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INTRODUCTION

2

BIOLOGY

3

GRAPH THEORY

In this chapter we review basic graph theory and explain how these terms are applicable in the context of biological neural networks. We begin with the definition of directed graphs:

3.1 DEFINITIONS & BASICS

References for this chapter: <http://nlab.mathforge.org/nlab/show/graph>, <http://nlab.mathforge.org/nlab/show/quiver>, (Bang-Jensen and Gutin 2008)

Definition 3.1.1 (Directed graphs). A **directed pseudograph** G consists of two finite (, non-empty?) sets V , the *set of vertices* of G , and E , the *set of edges* of G , and two maps

$$s, t : E \rightarrow V,$$

the *source* and *target functions* of G . A **directed multigraph** is a directed pseudograph without *loops*, that is the map $d = (s, t) : E \rightarrow V^2$ already maps to $V^2 \setminus \Delta_V$, where $V^2 = V \times V$ denotes the cartesian product and $\Delta_V = \{(x, x) | x \in V\} \subseteq V^2$ the diagonal. Similarly, a **directed loop graph** is a directed pseudograph where d is injective. Finally, a **simple directed graph** can be defined as a directed pseudograph where d is both injective and already maps to $V^2 \setminus \Delta_V$.

Thus, in simple directed graphs, neither parallel edges nor loops - edges between the same vertex - are allowed, whereas directed multi-graphs and directed loop graphs admit one of them respectively.

Say something about what "directed graph" means here.

Given a directed graph G , we denote with $V(G)$ the set of vertices of G and call it the **vertex set** of G . Analogously, the **edge set** $E(G)$ of G denotes the set of edges of G . This means, for a directed graph specified as $G = (V_G, E_G, s_G, t_G)$, we have

$$V(G) = V_G \quad \text{and} \quad E(G) = E_G.$$

A **morphism** $\phi : G \rightarrow H$, between two directed graphs $G = (V_G, E_G, s_G, t_G)$ and $H = (V_H, E_H, s_H, t_H)$, consists of a pair of maps $\phi_V : V_G \rightarrow V_H$ and $\phi_E : E_G \rightarrow E_H$, such that

$$s_H \circ \phi_E = \phi_V \circ s_G \quad \text{and} \quad t_H \circ \phi_E = \phi_V \circ t_G,$$

that is such that the following diagram commutes:

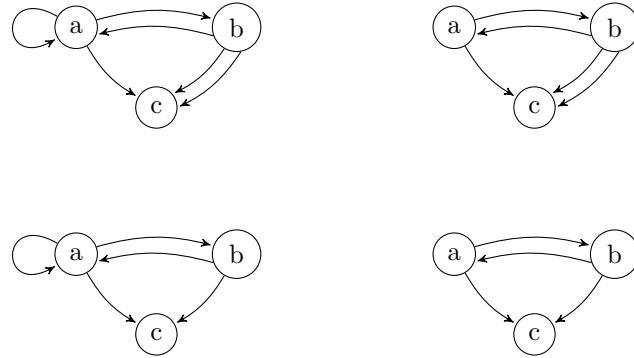


Figure 3.1: From top left to bottom right, typical examples of the defined graph types: A) directed pseudograph, B) directed multigraph, C) directed loop graph D) simple directed graph.

$$\begin{array}{ccc} E_G & \xrightarrow{\phi_E} & E_H \\ s_G \downarrow t_G & & \downarrow s_H t_H \\ V_G & \xrightarrow{\phi_V} & V_H \end{array}$$

A morphism $\varphi : G \rightarrow H$, between two directed pseudographs G and H is an **isomorphism**, if the maps $\varphi_V : V_G \rightarrow V_H$ and $\varphi_E : E_G \rightarrow E_H$ are bijective. Two directed pseudographs are called *isomorphic* if there exists an isomorphism inbetween them.

Remark The last definition implies that, if there exists an isomorphism $\varphi : G \rightarrow H$, an isomorphism $\psi : H \rightarrow G$ can be found. This isomorphism is, of course, easily constructed via $\psi_V : V_H \rightarrow V_G, v \mapsto \varphi_V^{-1}(v)$, $\psi_E : E_H \rightarrow E_G, e \mapsto \varphi_E^{-1}(e)$.

Definition 3.1.2 (Weighted directed graphs). A **weighted directed graph** is a directed graph G along with a mapping $\omega : E(G) \rightarrow \mathbb{R}$, called the *weight function*. Similarly, a **vertex-weighted directed graph** is a directed graph with a mapping $\nu : V(G) \rightarrow \mathbb{R}$.

Remark (heavy draft), title: A directed graph category for biological neural networks, in a bordered box?

Certainly, a weighted directed pseudograph is the most fitting mathematical modelling to the biological situation, since self connections and multiple synapse are not only plausible (source?) but the rule. However there is one abstraction we can make by adding together the synaptic weights - NEST is doing it..

Also think about **inhibitory**, **excitatory**. Suggestion: edge weights $\omega : E(G) \rightarrow \mathbb{R}^+$ and vertex weights $\nu : V(G) \rightarrow \{-1, 1\}$. Synaptic weight $\text{syn}(e)$ for edge e is then

$$\text{syn}(e) = \nu(s(e)) \omega(e).$$

Benefit: Synapse from one neuron are either excitatory or inhibitory but not mixed as in bio.

Equivalent definiton for directed loop graphs A directed loop graph G can be equivalently defined as a pair of finite(**, non-empty?**) sets V , the *set of vertices* of G , and $E \subseteq V^2$ the *set of edges* of G . For an edge $(x, y) \in E$, we call x the *source* and y the target of the edge (x, y) .

Source and target functions are then uniquely determined as the projections on the first and second component, $s = \text{pr}_1, t = \text{pr}_2 : E(G) \rightarrow V$. Conversely, the edge set $E(G) \subseteq V^2$ can be determined from the source and target functions as $E := \{(s(e), t(e)) | e \in E\}$. The trivial identities $(x, y) = (\text{pr}_1(x, y), \text{pr}_2(x, y))$ and $\text{pr}_1(s(e), t(e)) = s(e)$ with $\text{pr}_2(s(e), t(e)) = t(e)$ quickly verify the equivalence of the definitions.

Given a directed loop graph G , we often assume the graph to be given in this form and write edges as $e = (x, y)$. Note that this concept is more complicated to introduce for directed pseudographs, since parallel edges e and e' should to be differentiated in the egde set of G , establishing the need for $E(G)$ to be a multi- or indexed set, notions we are trying to avoid in this document.

From now on any *directed graph* is assumed to be a directed loop graph. Although most, if not all, concepts work for directed pseudographs just as well, we want to start to heavily use the canonical edge representation, which when talking about pseudographs makes problems as mentioned before.

More Notation - Check, do I really need this? For a pair of vertex sets $X, Y \subseteq V(G)$ of a directed graph G we write

$$(X, Y)_G = \{(x, y) \in E(G) | x \in X, y \in Y\}$$

for the set of edges with source in X and target in Y . For vertex sets with a single element $X = x$, we also write $(x, Y)_G$ and mean the edges with source x and target in Y .

In- and out-degree For a directed graph G the **in-degree** $d_G^-(x)$ of a vertex x is defined as the number of edges of G with target x , that is

$$d_G^-(x) = |(V(G), x)_G|.$$

Similarly, the **out-degree** $d_G^+(x)$ of x is defined as

$$d_G^+(x) = |(x, V(G))_G|,$$

the number of edges in G with source x .

Side In some literature about directed graphs (Bang-Jensen), loops are *not* counting towards the in- or out-degree of vertex. In the light of neural network however, we specifically want to count loops as well.

A basic property of the in- and out-degree in directed graphs is that number of in-degrees of every vertex, as well the sum of every out-degree, equal the total number of edges:

Proposition 3.1.1. *In every directed graph G , we have*

$$\sum_{x \in V(G)} d^-(x) = \sum_{x \in V(G)} d^+(x) = |E(G)|.$$

Proof. Since $(V(G), x)_G \cap (V(G), y)_G = \emptyset$ for $x \neq y$, we can write

$$\sum_{x \in V(G)} d^-(x) = \left| \bigcup_{x \in V(G)} (V(G), x)_G \right| = |(V(G), V(G))_G| = |E(G)|.$$

Analogously for the out-degree. \square

Walks and distances

Let G be a directed graph (what does it mean here?). A **walk** W in G is an alternating sequence $(x_1, e_1, x_2, e_2, x_3, \dots, x_{n-1}, e_{n-1}, x_n)$ of vertices x_i and edges e_i from G , such that

$$s(e_i) = x_i \quad \text{and} \quad t(e_i) = x_{i+1}, \quad \text{for } i = 1, \dots, n-1,$$

that is, such that the vertices are connected by the edges inbetween them. We denote the set of vertices (x_1, \dots, x_n) of W as $V(W)$ and the sequence of edges (e_1, \dots, e_{n-1}) as $E(W)$ (need it?).

The vertices x_1 and x_n are called the *end vertices* of W and we also say that W is an (x, y) -walk. The **length** of W is defined as the length of the sequence of edges; a walk consisting of only one vertex has length zero. colon, really?

Definition 3.1.3 (Distance). The **distance** of two vertices x, y in a directed graph G (means?), is defined as the minimum length of an (x, y) -walk, if any such walk exists, otherwise $\text{dist}(x, y) = \infty$. In short,

$$\text{dist}(x, y) = \inf\{|E(W)| \mid W \text{ is } (x, y)\text{-walk}\}.$$

| $E(W)$ | is not explained. Necessary?

Proposition 3.1.2. *The distance function $\text{dist} : V(G) \times V(G) \rightarrow \mathbb{N}$ of a directed graph G satisfies the triangle equality,*

$$\text{dist}(x, z) \leq \text{dist}(x, y) + \text{dist}(y, z), \quad \text{for } x, y, z \in V(G).$$

Proof. Let x, y, z be vertices in G . If either no (x, y) -walk or (y, z) -walk exists, the inequality holds by definition. Other wise, let W be an (x, y) -walk of minimal length and let U be a (y, z) -walk of minimal length. Certainly, by concatenating W and U we obtain an (x, z) -walk of length $|E(W)| + |E(U)| = \text{dist}(x, y) + \text{dist}(y, z)$, proofing that

$$\text{dist}(x, z) \leq \text{dist}(x, y) + \text{dist}(y, z).$$

\square

More to do:

- summarize category of directed (weighted) pseudographs
- weights!
- vertices will also be called nodes and neurons, edges will also be connections or synapses.
- subgraphs
- vertex set, edge set $E(G), V(G)$.
- $\omega(e)$ is weight, connection strength or synaptic weight (as a side remark)
- extend to category of weighted directed pseudographs (isomorphisms)
- path
- adjacency matrix
- converses of graph related to opposite category?
- in- and out-degree
- triangle inequality for distance, $\text{dist}(x, z) \leq \text{dist}(x, y) + \text{dist}(y, z)$

3.2 RANDOM GRAPH THEORY

For this chapter, as it is common and practical when talking about random graphs, we move away from the abstract notion of graphs and their equivalence classes and consider *labeled graphs*, where the edge set of a graph with n vertices takes the form $V = \{1, \dots, n\}$.

3.2.1 Erdős-Rényi graphs

References: Newman, Erdos1960, Erdos1959, Gilbert1959, Wikipedia, ([West 2000](#))

Definition 3.2.1 (Terms used). Graphs with n vertices: $G^n = \{G | G \text{ is graph (means??)}, |V(G)| = n\}$

Expected number of edges in a directed Erdős-Rényi graph (DERG)
 $X : G^n \rightarrow \mathbb{R}, G \rightarrow |E(G)|$, discrete random variable, with probability distribution $G(n, p) = B(n^2, p)$, binomial distribution. That is, distribution of X via probability mass function $P(X = k) = \binom{n^2}{k} p^k (1 - p)^{n^2 - k}$

$p)^{n^2-k}$. Thus $E(X)$ equals expect edges in DERG. We have of course, since $G(n, p)$ binomial,

$$E(X) = pn^2. \text{ (if self - edges!)}$$

Then, of course, the **mean in- and out-degree** is

$$\langle d^{\text{in}} \rangle = \langle d^{\text{out}} \rangle = \frac{\langle |E(G)| \rangle}{|V(G)|} = np.$$

Does this make sense? Define everything properly!!

3.2.2 Random Graph Model - Gilbert

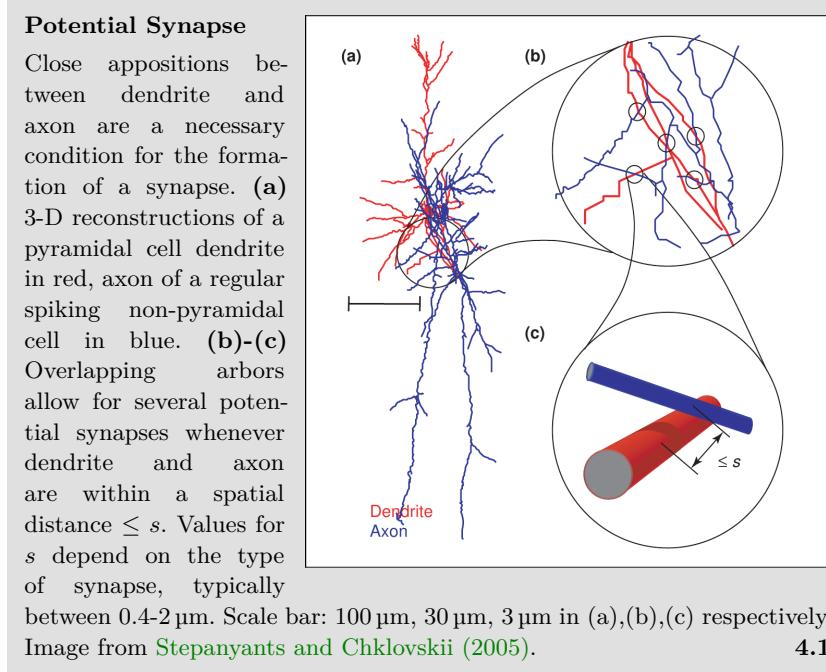
4

NETWORK MODEL

Referring to anisotropic characteristics in local cortical circuits of the rat's brain, a network model implementing anisotropic tissue geometry is developed. The introduction of a rewiring algorithm and qualitative anisotropy measure lay the foundation for the analysis of structural aspects of this model in Chapter 5.

4.1 ANISOTROPY IN NEURAL CONNECTIVITY

Neurogeometry addresses the problem of inferring synaptic connectivity from the geometric shapes of axon and dendrites. A fundamental concept in this field is that of a *potential synapse* (Stepanyants et al. 2002). Defined as the potential axonal-dendritic connection of two neurons, present whenever the axon of one neuron is within a spatial distance s of the dendrite of the other, it is a necessary, although not sufficient, condition for the formation of a synaptic connection (Figure 4.1). The existence of such close appositions solely depends on dendritic and axonal anatomy; identification of defining morphological characteristics in both axon and dendrite would therefore allow for a model of local network connectivity, assuming for example that a certain ratio r of potential synapses turn into active contacts independently. It is the hope that such a model, motivated from the geometry of a neuron's functional compartments, not only displays inherent patterns of connectivity similar to what has been observed in biological networks, but also proofs itself as a testing ground for how this connectivity may affect network dynamics.



high variability in
axonal
morphology

Finding stereotypical anatomical characteristics however is difficult, as axonal morphology is, in general, highly diverse (Debanne 2004). Across different species, distinct regions in the central nervous system and different neuron types, axons display a wide variety of shapes characterized by morphometric parameters such as total length, branching complexity and axonal extent (Ropireddy et al. 2011). Typical exam-

ples of distinct morphology include the T-shaped axons of cerebellar granule cells branching only at a singular point (Ramon and Cajal 1911), and axons of hippocampal CA3 pyramidal cells, which, in stark contrast, may feature up to 40 branches resulting in a total length of axon collaterals of up to 12 mm (Ishizuka et al. 1990).

It is therefore imperative to confine this analysis to a specific brain region and neuron type. In this study, we set the focus on circuits of pyramidal cells in the mammalian cortex. More specifically, local circuits of thick tufted layer V pyramidal neurons in the rat's somatosensory cortex have been the target of advanced experimentation (Song et al. 2005; Perin et al. 2011; Romand et al. 2011; Ramaswamy et al. 2012), and will serve as a benchmark for results in neural morphology and network connectivity in this report.

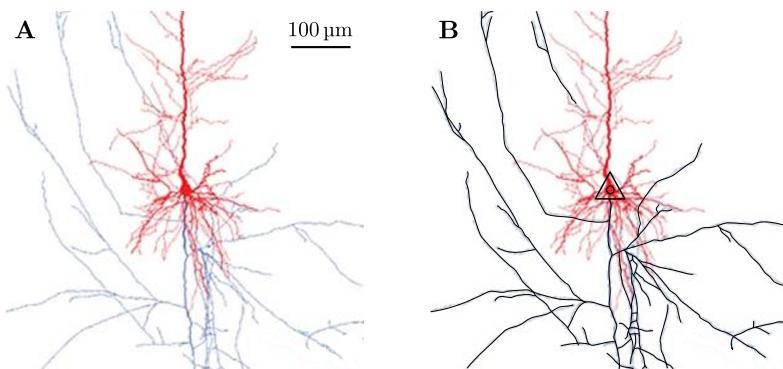


Figure 4.2: Tracing axonal branching of a pyramidal cell In a 3-D model reconstructed from biocytin-labeled thick-tufted layer V pyramidal cells in the somatosensory cortex of postnatal (day 14) Wistar rats, Romand et al. (2011) depict dendritic compartments in red, axonal compartments in blue. **A)** A 600 μm window centered on the soma of the pyramidal cell shows the main stem of the cell's axon projecting downwards in a straight line, collaterals branching at various angles. **B)** Using image manipulation software, axon morphology was manually traced and is emphasized in black.

Axonal morphology of pyramidal cells in the cerebral cortex is well described. From the soma the single main stem of the axon originates and projects downwards, describing a trajectory closely resembling a straight line (Braitenberg and Schüz 1998). At arbitrary points along this path, collaterals branch off at various angles and constitute themselves linear paths until they further ramify or terminate. Displaying a high degree of ramification, axonal trees of cortical pyramidal cells build, in general, complex structures (Petersen et al. 2003; Ramaswamy et al. 2012). Cortical slice experiments analyzing neural anatomy are typically constrained by a slice thickness of 300 μm . On this scale, 3-D reconstruction from labeled thick tufted layer V pyramidal cells reveals

cortical axons
form straight lines,
arborize profusely

characteristic morphology of the axonal tree (Figure 4.2). The downwards projecting, straight axon branches at several points, forming collateral branches that travel in linear path as well.

In a statistical view, this characteristic axonal morphology results in high axon branch densities along the main stem, whereas distant regions display a relatively low density (Figure 4.3). Specifically, axon collaterals do not cluster around the soma but align with the main stem's projection. As presence of an axonal branch constitutes a necessary condition for a potential synapse, a higher concentration of potential and, subsequently, realized synapses is expected in regions of high branch density. For a coherent picture of local connectivity profiles, however, dendritic morphology needs to be considered as well.

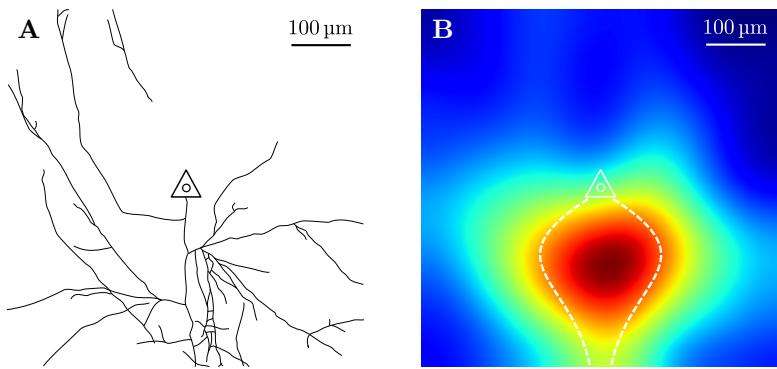


Figure 4.3: Illustrating axonal branch density In a sample of 5 reconstructions from thick-tufted layer V pyramidal cells (Romand et al. 2011), tracing axonal morphology illustrates characteristic branch density along the axon's main stem. **A)** Example of extracted axonal tree. Outline manually traced using image manipulation software. Soma indicated by triangle. Original data from Romand et al. (2011). **B)** Overlaying 5 axonal trees extracted as in A), applying a Gaussian filter and displaying high axon densities in warm colors, illustrates the characteristic higher branch densities along the axon's main stem.

basal dendrites dominate local connectivity

Dendritic anatomy of cortical pyramidal cells is inherently bipartite. From the soma several *basal dendrites* emerge and extend into arbitrary directions, branching profusely until they terminate. The single *apical dendrite* emerges from the apex of the pyramidal cell and ascends in a linear trajectory, forming occasional collateral branches until finally terminating into the apical tuft, where the dendrite branches several times to form a tree like structure (Feldman 1984). On the scale of typical cortical slice thickness, however, the apical dendrite is cut off and the basal dendrite dominates the dendritic morphology and potential of dendritic-axonal connections (Figure 4.4). The radial extension of dendritic branches results in a high concentration of dendritic branches

around the soma, much in the contrast to the findings of axonal branch densities before.

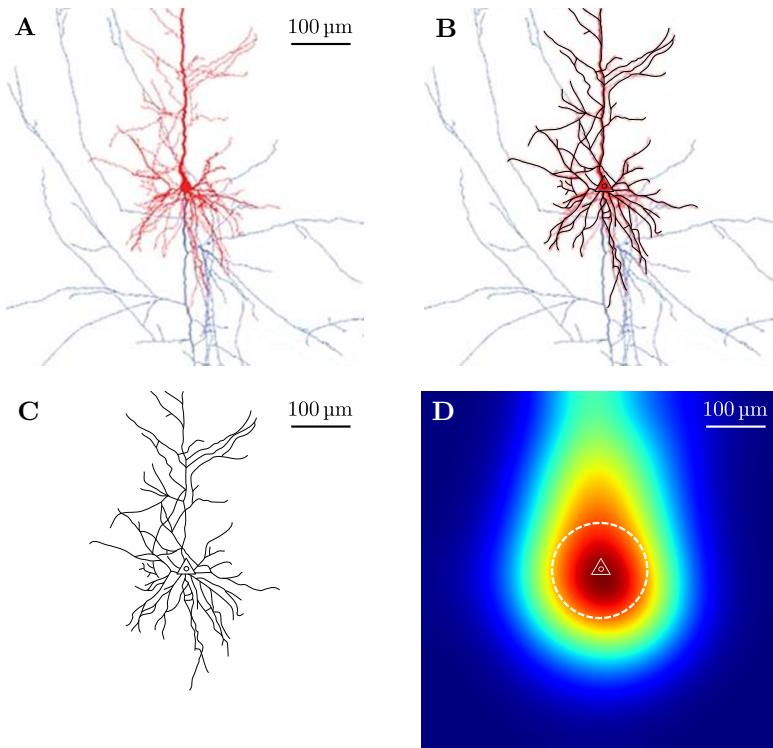


Figure 4.4: Dendritic morphology and branch density Using neuronal morphology of thick-tufted layer V pyramidal cells recorded by Romand et al. (2011), dendritic anatomy is traced and combined to illustrate high branch density around the soma. **A)** In a 600 μm window centered on the soma, basal dendrites (red) are visible extending around the soma. The ascending thick apical dendrite (red) is cut off and apical tuft is not shown. **B)-C)** Manual tracing of dendritic outlines in five samples (one shown), allows for clearer identification of stereotypical morphology and later analysis. **D)** Combining 5 dendritic outlines as shown in C) and subsequent Gaussian filtering reveals the relatively high dendritic branch density around the soma.

Combining the above results of dendritic and axonal branch densities in the light of neurogeometry, a clear concept of anisotropy of neural connectivity emerges. As dendritic branches of potential post-synaptic targets extend radially from the soma and do not display a preferred direction, target neurons for outgoing synaptic contacts originating from a single pyramidal cell, cluster around the downwards projecting axon (Figure 4.5). In their in-depth study, Stepanyants and Chklovskii (2005) confirm the overrepresentation of potential synapses along the axon for pyramidal cells. Consistent with the notion that stereotypical morphology of pyramidal cells is intrinsic to the local network's connectivity

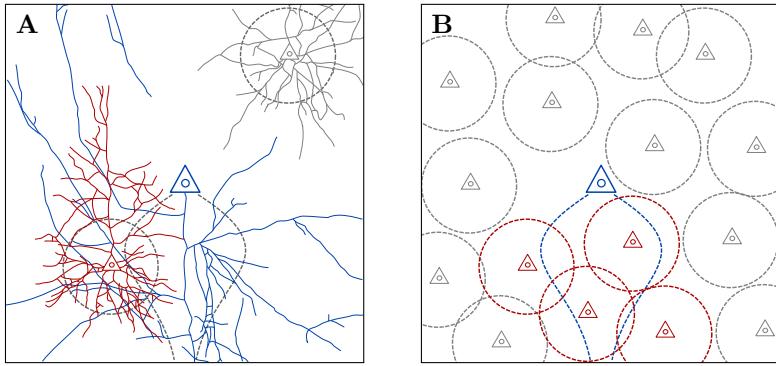


Figure 4.5: Connected neurons of a single pyramidal cell align with axonal projection Reducing the full axonal (blue, cf. Figure 4.2) and dendritic trees (red, gray, cf. Figure 4.4) as shown for two neurons in A) to their stereotypical axonal (blue) and dendritic profiles (red, gray) in B), demonstrates how connected neurons (red) tend to cluster around the pre-synaptic axon's profile, as spatial closeness constitutes a necessary condition for the formation of contacts. Unconnected neurons (gray) are found distant from the axon's projection, but not necessarily distant from the soma.

profile, they also find that anisotropy of this degree is *not* present in spiny stellate neurons located in lower-layer-4.

4.2 ANISOTROPIC GEOMETRIC GRAPH MODEL

With this in mind, we propose the following model: On a square surface of side length e , a number of N point neurons are randomly, uniformly distributed. Connected neighbors are then calculated for each neuron separately and independently, by determining the randomly, uniformly distributed direction of the neuron's axon. In this direction the axon traverses over the surface describing a straight path, terminating only when an edge of the surface is reached. Directed contacts are made with every neuron that is within a width $w(x)$ of the axon's trajectory, where in general w depends on the axon length x at this point.

Algorithm in Python, in connectivity stored in graph tool (Peixoto 2014)

To employ this model to generate networks, a set of parameters needs to be chosen. The network size N is solely determining computational efforts in numerical calculations and has thus been set as $N = 1000$. Side length of the surface is a priori and, relative of

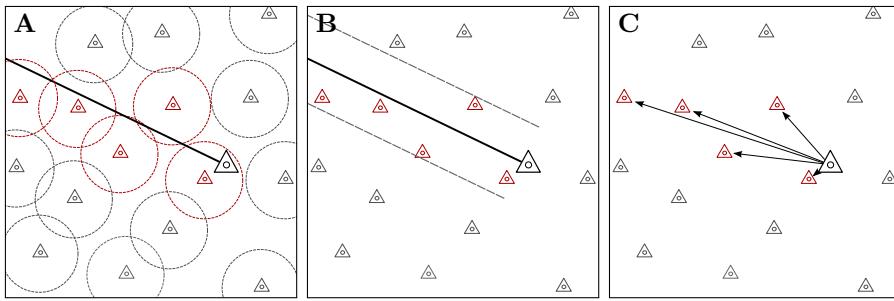


Figure 4.6: Interpretations of network model Here constant width w coinciding with dendrite radius

The final parameter is then the axon-profile width w . In their analysis of connectivity of thick-tufted layer V pyramidal cells in neonatal rats (day 14), Song et al. (2005) report an overall connection probability of $p = 0.116$, consistent with prior reports of a cortical connection probability of $p \approx 0.1$.

Having no further evidence at the time on how to select axon width, we set $w(x)$ to be constant. This leaves

to the overall connection probability p can be approximated by

$$p = \frac{Lw}{E^2},$$

where L is the average length of the axon.

With this parameter set we generate a sample of 25 graphs

4.3 DISTANCE DEPENDENT CONNECTIVITY

Random Graph Model section 3.2.2

In Gilbert's random graph model $G(n, p)$, probability of connection p is independently chosen and a fixed value for all vertex pairs. The anisotropic geometric graph model introduced in the last section is itself a random graph model - node positions as well as preferred directions of connection are randomly, uniformly distributed. In contrast to Gilbert's model however, neither is the probability of connection between a given vertex pair independent of the realization of other edges in the graph, nor is it a fixed value - probabilities strongly depend on internode distance in the anisotropic geometric graph model introduced.

Analyzing dependencies in the anisotropic model, specifically by identifying prevalent patterns of connectivity and relating these modes of non-randomness to biological findings, is the main focus of Chapter 5. However, such structural correlations may not necessarily be an inherent feature of the network's anisotropy - distance dependent connectivity alone, as imposed by the model's specific geometry, may be the cause for emerging dependencies. It is therefore a crucial initial task to map the anisotropic model's distance dependent connection probability. Inferring connection probability as a function of internode distance and comparing it with computational results, in this section we explore distance connectivity of the anisotropic network model, securing a vital component in the analysis of structural features.

Consider a graph G . In Gilbert's random graph model the probability p for a edge between nodes $v, w \in V(G)$ to be realized is a fixed value; in a geometric graph it is more generally a function of the distance between the nodes, $d(v, w)$. In short, we write $p(x)$ to denote the probability that a vertex pair of distance x is connected,

$$p(x) := P[(v, w) | d(v, w) = x].$$

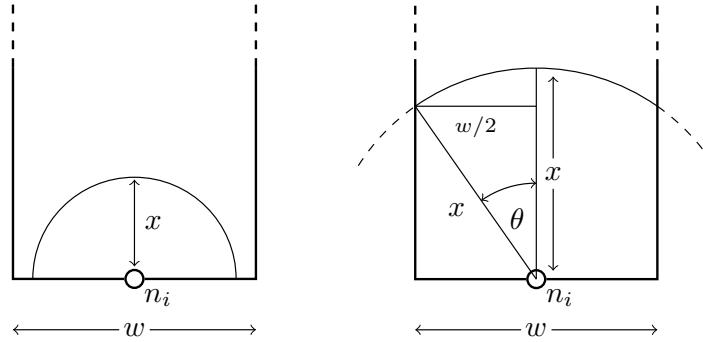
Owning to the abstract geometric model we defined, this connection probability is easily computed.

Proposition 4.3.1. *In the anisotropic geometric graph model distance depend connection probabilities are computed as*

$$p(x) = \begin{cases} 0.5 & \text{for } x \leq w/2 \\ \frac{1}{\pi} \arcsin\left(\frac{x}{2w}\right) & \text{for } x > w/2. \end{cases}$$

Proof. To see this, consider a given source vertex v at $(0, 0)$ and a possible target w , such that $d(v, w) = x$. We may then express the target coordinates as $xe^{i\varphi}$, $0 \leq \varphi < 2\pi$.

Figure ?? illustrates for which angles φ the node w becomes a valid target for an edge from v . This intervall



For a general v make coordinate transformation

□

We can verify this result by computationally extracting the distance dependencies in the sample graphs generated.

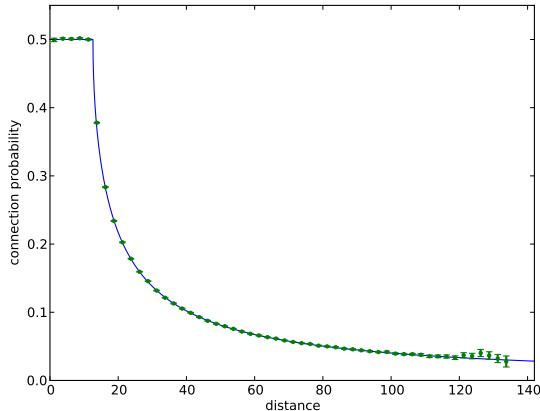


Figure 4.7: Distance dependent connection probabilities

4.4 REWIRING METHODS

In the network configuration introduced in section 4.2 strong directional anisotropy is present: Edges originating from one node “point in the same direction”, that is they connect to other nodes which cluster around a. In this section we introduce an algorithm

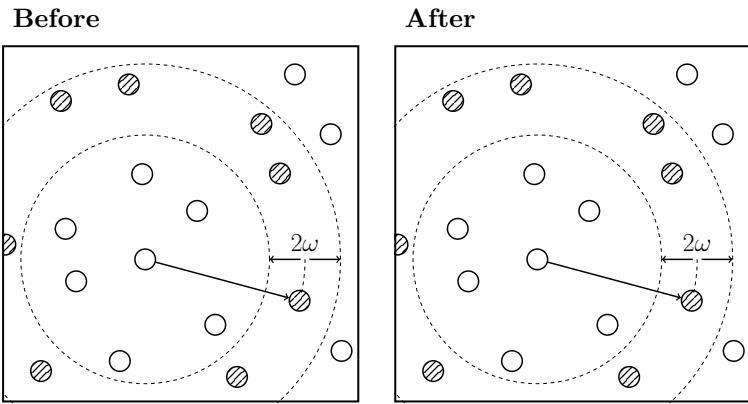


Figure 4.8: Rewiring

4.5 ANISOTROPY MEASURE

4.6 SUMMARY AND DISCUSSION

5

STRUCTURAL ASPECTS

Subjecting the directionally heterogeneous network model to a critical examination of its structural features, we identify prevalent patterns of connectivity and relate theoretical and computational results to findings from experiments in the rat's visual cortex.

5.1 INTRODUCTION

Investigation of the brain's connectivity is an ongoing endeavour. Concurrent collaborative efforts like the Human Connectome Project [HCP], the Open Connectome Project [OCP] and the Allen Brain Atlas [ABA], intent on mapping the 'wiring' of the brain, as well as the continued development of experimental techniques and computational resources, demonstrate the great interest in advancing this field.

Research in brain connectivity spreads over the whole scale of the brain; from the mapping of fiber pathways between brain regions at the macroscopic level, to the synaptic connections of individual neurons on the microscale, researchers are trying to identify the links that enable the brain its characteristic cognitive abilities. In the search for structural connections, these links are of anatomical nature. However, statistical dependencies and causal relationships between the distinct computational units in the brain are being researched with equal emphasis (Sporns 2007).

Connectivity in the context of the directionally heterogenous geometric networks introduced in ??, refers in this chapter to structural links. So far, we have only briefly mentioned that the network's nodes should be interpreted as individual neurons; to allow for a discussion of functional relationships between nodes, we have yet to provided a physical description of a neuron's function. As such, we will here explore the network's structural connectivity, modeling synaptic contacts between axon and dendrites of individual neurons.

HUMAN
Connectome
PROJECT
humanconnectome.org

Open Connectome
Project
[openconnectome-
project.org](http://openconnectome-project.org)

ALLEN BRAIN ATLAS
brain-map.org

Synaptic Connectivity

In the local cortical circuits the anisotropic geometric model was derived from, synaptic connectivity is a major mode of configuration. In those networks, connectivity has been determined to be neither completely random nor exclusively specific [Source]. Recurring patterns of connectivity have been identified by several reports (Sporns and Kötter 2004; Song et al. 2005; Perin et al. 2011).

The impact of this structural specificity discovered in local networks is shown to be significant; while the linking of network structure and network dynamics remains an active field of research, several studies were able to employ computational and theoretical models to establish such a connection. A study by Zhao et al. from 2011, for example, demonstrates how second order connectivity statistics affect a network's propensity to synchronize (Zhao et al. 2011). In the same year, Alex Roxin reported on the influence of in- and out-degree distributions on dynamics of neural network (Roxin 2011). Later, Pernice et al. were able to link structural connectivity to spike train correlations in neural networks (Pernice et al. 2011).

Mapping synaptic connectivity in experiments

Experimentally, paired intracellular recordings are used to determine synaptic connectivity in cortical slices. Using two electrodes, one inserted in the cell and one outside the cell, a single intracellular recording allows for measurement of a cell's membrane potential (Brette and Destexhe 2012)(Weckstrom 2010). Simultaneous recordings from multiple neurons are then able to infer synaptic connectivity by evoking an action potential through current injection in one neuron and observing the change of membrane potential in the other cells (Song et al. 2005).

While techniques for paired intracellular recordings are rapidly developing, their ability to capture connectivity patterns of large networks is yet very limited. To this date, the connectome of *C. Elegans* remains the outstanding exception of a connectivity configuration that has been fully mapped [Source]. Even in the state-of-the-art experiment conducted by Perin et al., using a setup capable of recording up to twelve neurons simultaneously, the authors note that an investigation of degree distribution was not carried out, due to lack of sufficient data (Perin et al. 2011).

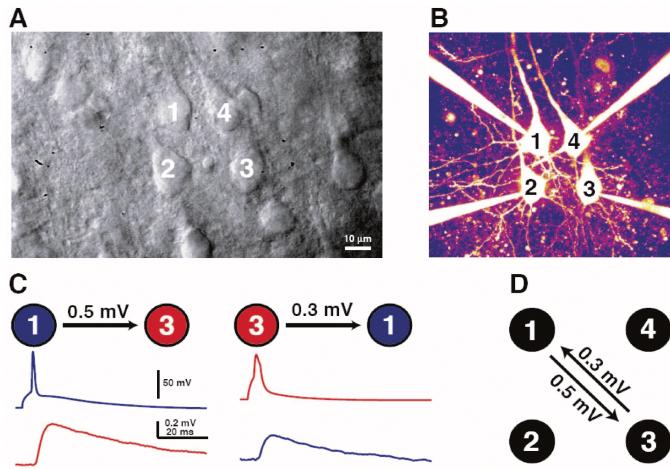


Figure 5.1: Song et al. use quadruple whole-cell recordings, observing simultaneously the membrane potential of four neurons. **A)** Contrast image showing four thick-tufted L5 neurons **B)** Fluorescent image of the same cells after patching on **C)** Evoking an action potential in the presynaptic neuron causes characteristic membrane potential change in the postsynaptic neuron **D)** Inferring synaptic connectivity from the EPSP waveform observed in C). Image from (Song et al. 2005).

Exploiting the benefits of a geometrical model

Working with a geometrical network model and its computational implementation, such restrictions disappear; the full information about the network, in form of its connectivity matrix, is given at point in time and can be easily queried for. Experiments that may take days to perform *in vivo*, can be completed in a matter of seconds *in silico*. As such, geometrical models lend themselves to extensive examination of their structural aspects.

In trying to exploit these advantages, two approaches present themselves. One may construct a network model that extrapolates the known biological configuration; a full structural examination of these networks could possibly expose relevant patterns not yet observed. For this approach a sophisticated understanding of the biological configuration is critical. Neuron morphology, however, is difficult to describe and extract.

*Extrapolation vs.
reduction*

For this analysis we suggest a reductionist approach. Having motivated an abstract model reflecting a cortical network's directional heterogeneity, we distinguish emerging patterns of connectivity, specific to directionally heterogeneous networks, from results, that only indirectly stem from the network's anisotropy, in the hopes to be able to characterize

the significance of directional heterogeneity in structural connectivity of cortical circuits.

Structural aspects of the heterogeneous model

In this chapter we subject the directionally heterogeneous network model introduced in ?? to a critical analysis of its structural aspects. General network topology, as well as specific modes and patterns of connectivity, are to be identified and laid out for comparison with findings in biological neural networks.

*employing
anisotropy
measure*

In an effort to map out structural features that can be directly associated with the network's directional heterogeneity, it is crucial to differentiate such findings from results that are only indirectly caused by the network's anisotropy. To this end, already in ?? we developed a measure to quantify the degree of anisotropy prevalent in a given network; throughout this chapter we will now frequently employ this measure to determine which structural aspects are originating from the network's heterogeneity, and which aspects are to be attributed solely to the network's distance dependency.

Accordingly, results from this investigation are categorized in two sections: The first section, 'Section 2', describes structural aspects that can not be directly attributed to the model's anisotropy. The second section, 'Section 3', then presents results that are truly features of network's directional heterogeneity.

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