

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:

1.1 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 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:

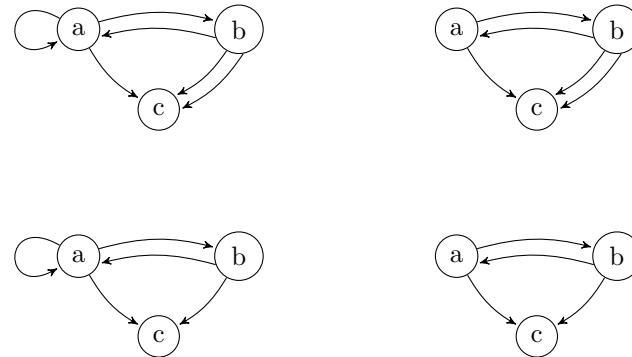


Figure 1.1: From top left to bottom right, typical examples of the defined graph types: A) directed pseudograph, B) directed multigraph, C) directed loop graph D) simple directed graph.

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

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 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 1.3. *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 1.4 (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 1.5. *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, $\text{dist}(x, z) \leq \text{dist}(x, y) + \text{dist}(y, z)$

1.2 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 $V = \{1, \dots, n\}$.

1.2.1 Erdős-Rényi graphs

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

Definition 1.6 (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!!

1.2.2 Random Graph Model - Gilbert

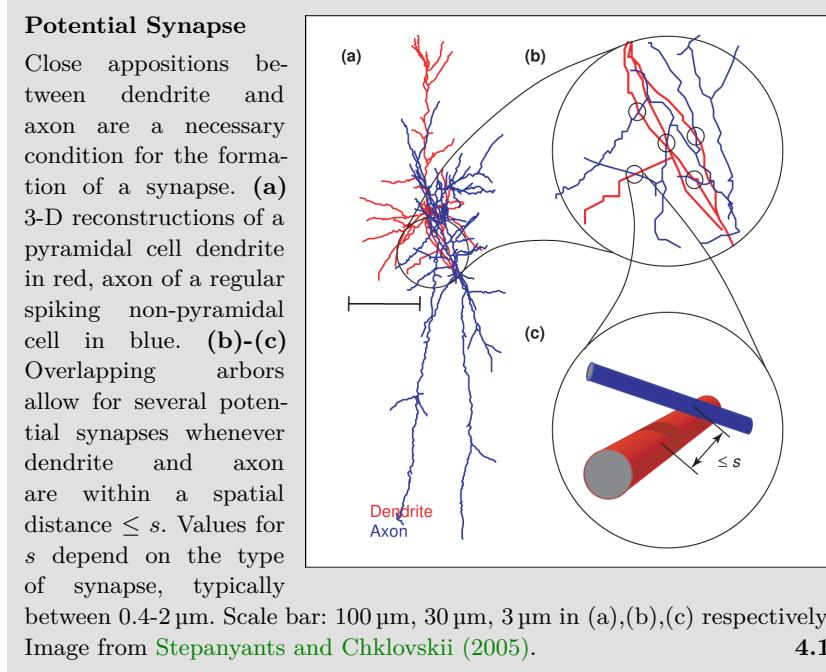
2

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 ??.

2.1 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 2.1). 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.

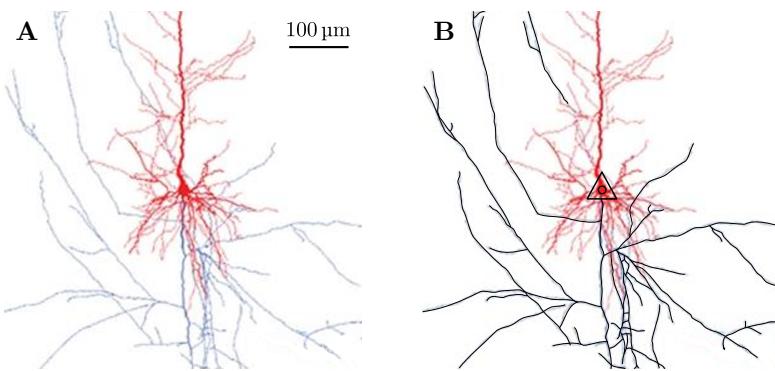


Figure 2.2: Tracing axonal branching of a pyramidal cell In a 3-D model reconstructed from biocytin-labeled thick-tufted layer V pyramidal cells in the somatosensory cortex of postnatal (day 14) Wistar rats, Romand et al. (2011) depict dendritic compartments in red, axonal compartments in blue. **A)** 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 2.2). 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 2.3). 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.

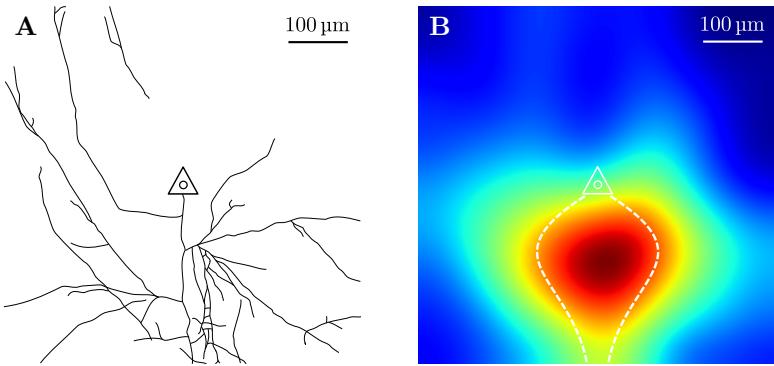


Figure 2.3: Illustrating axonal branch density In a sample of 5 reconstructions from thick-tufted layer V pyramidal cells (Romand et al. 2011), tracing axonal morphology illustrates characteristic branch density along the axon's main stem. **A)** Example of extracted axonal tree. Outline manually traced 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 2.4). 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.

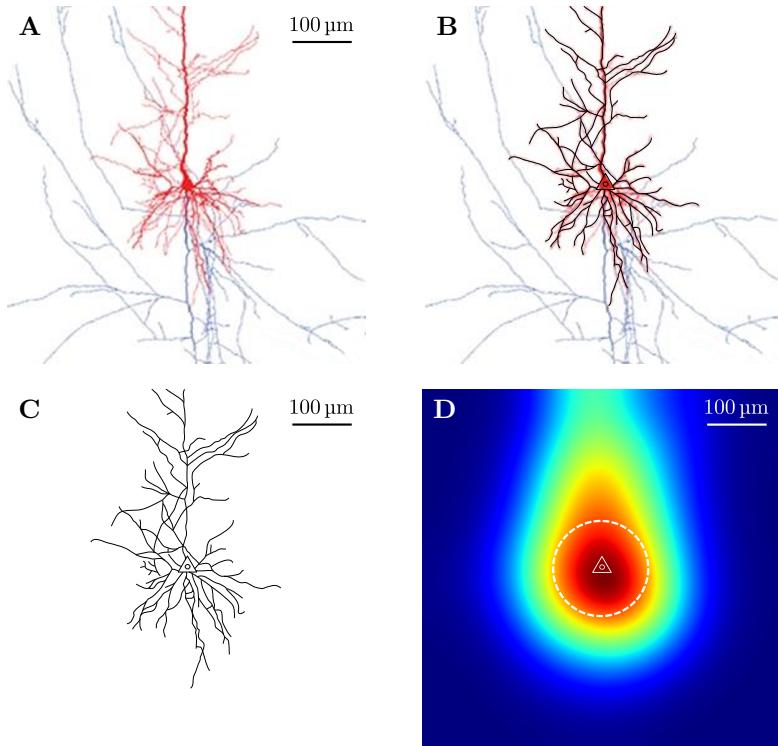


Figure 2.4: Dendritic morphology and branch density Using neuronal morphology of thick-tufted layer V pyramidal cells recorded by Romand et al. (2011), dendritic anatomy is traced and combined to illustrate high branch density around the soma. **A)** In a 600 μm window centered on the soma, basal dendrites (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 2.5). 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

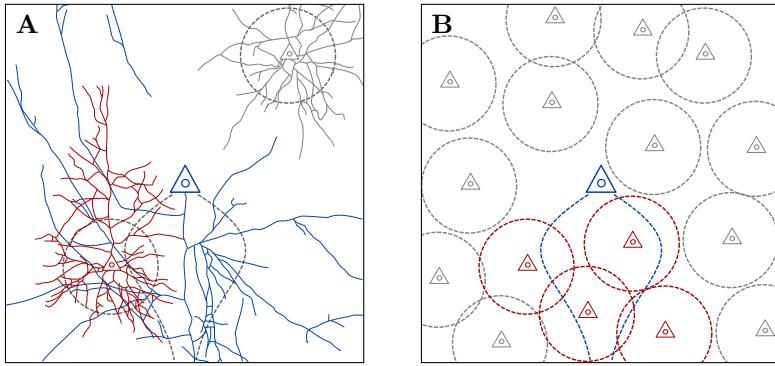


Figure 2.5: Connected neurons of a single pyramidal cell align with axonal projection Reducing the full axonal (blue, cf. Figure 2.2) and dendritic trees (red, gray, cf. Figure 2.4) as shown for two neurons in A) to their stereotypical axonal (blue) and dendritic profiles (red, gray) in B), demonstrates 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.

2.2 ANISOTROPIC GEOMETRIC GRAPH MODEL

In this section we formulate a model of network connectivity incorporating anisotropy as outlined in the last section. A

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 (Figure 2.6).

The implementation of arbitrary axonal orientation is crucial to the model. Although cortical axons are described as consistently projecting downwards (Braitenberg and Schüz 1998, cf. Section 2.1), combining exclusively vertically aligned axons with the simplified axonal and dendritic morphological profiles would result in a “vertically staggered connectivity” - neurons could then only project to targets located below

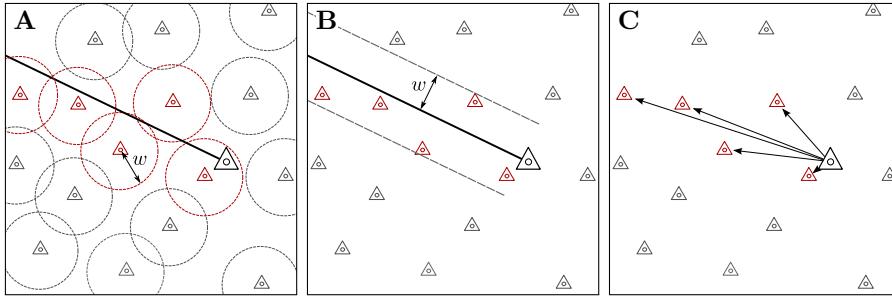


Figure 2.6: Anisotropic geometric network model and interpretations of width parameter w Illustrating the process of finding connections for one neuron (large triangle, black), the axon describes a linear trajectory in an arbitrary direction and until terminating on the surface's edge. Target neurons (red) are encountered along the path within a distance w , which is in **A**) interpreted as a dendritic radius or, equivalently, in **B**) as a “bandwidth” of the axon. Connections to the encountered targets are then established as projections in **C**), consistent with the directed nature of synapses in biological networks (cf. Chapter ??).

them. It is in fact not a vertical alignment of axon orientation, but the anisotropy in neural connectivity - the observation of neuronal targets aligning with the axonal projection - that this model tries to capture.

We will commonly refer to the model defined above as the *anisotropic geometric network model*. The resulting object of a realization of the model is a directed graph. More formally we define realizations as:

Definition 2.1 (Anisotropic geometric graph). Let $n \in \mathbb{N}$ and $e, w \in (0, \infty)$. An *anisotropic geometric graph* $G(n, e, w)$ then consists of a tuple (G, p, a) , of a simple directed graph G with $|V(G)| = n$ and maps

$$p : V(G) \rightarrow [0, e]^2, \quad a : V(G) \rightarrow [0, 2\pi),$$

such that for every vertex pair $v, w \in V(G)$ and edge $e \in E(G)$ with $s(e) = v$ and $t(e) = w$ exists if and only if $\leq w$.

The subsequent is a study of anisotropic geometric graphs. To enable this analysis, some prior work which composes the rest of this chapter. Integral to is a numerical implementation. The anisotropic network model is

2.3 NUMERICAL IMPLEMENTATION

for numerical considerations was achieved in Python. Using convenient

N Normal distribution. E . For a in N

Computational implementation was achieved by

Implementing the model as an algorithm in Python, we obtain .

in connectivity stored in graph tool ([Peixoto 2014](#))

Harnessing the computational implementation, we generated a sample of 25 networks with following parameters.

determine
parameter set to
generate sample
graphs

To harness the numerical implemenation to generate networks, a set of parameters needs to be chosen. The network size N is solely governing computational efforts in subsequent calculations and has thus been set as $N = 1000$. As shown in ??, only the quotient of the side length parameter e and axon width w . As such, side length e is arbitrarily set as $e = 100$ and leaves axon width for determination.

First, we determine w to be constant. Although simplistic profiles ([Figure 2.3](#)) and makes for characteristic distance distribution as we will see later ([Figure 2.8](#)), more in line with idea of abstractness and simplicity. For small w then, the overall connection probability p can be approximated as

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

where L is the average length of the axon until it terminates on a surface edge.

Proposition 2.2. *Average L*

Proof. Hello

□

Having established the connection between ,

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

With this parameter set we generate a sample of 25 graphs

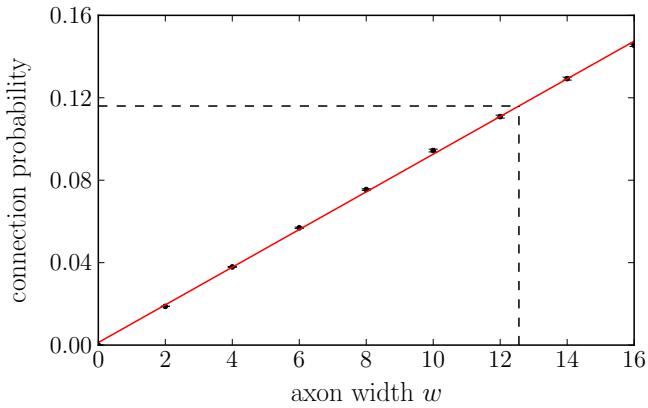


Figure 2.7: Tracing axonal branching of a pyramidal cell In a 3-D model reconstructed from biocytin-labeled thick-tufted layer V pyramidal cells in the somatosensory cortex of postnatal (day 14) Wistar rats, Romand et al. (2011) depict dendritic compartments in red, axonal compartments in blue. **A)** 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.

2.4 DISTANCE DEPENDENT CONNECTIVITY

Random Graph Model section 1.2.2

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 ???. 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,

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

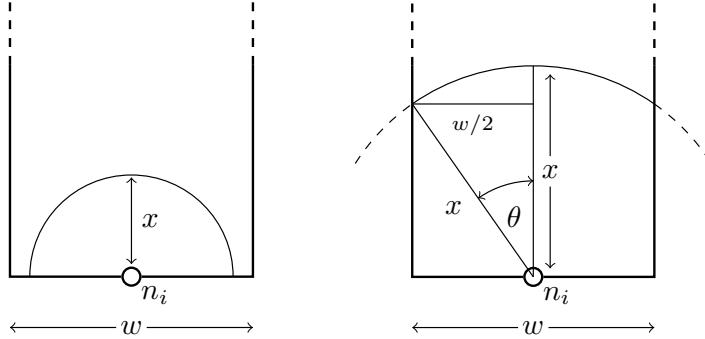
Owning to the abstract geometric model we defined, this connection probability is easily computed.

Proposition 2.3. *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.

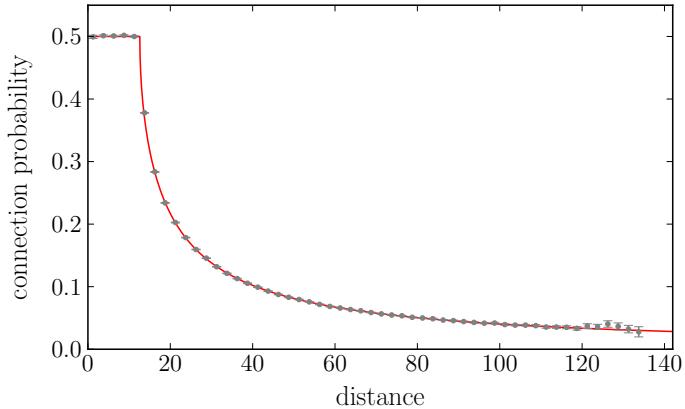


Figure 2.8: Predicted distance-dependent connection probability profile is matched by numerical computation In a 3-D model reconstructed from biocytin-labeled thick-tufted layer V pyramidal cells in the somatosensory cortex of postnatal (day 14) Wistar rats, Romand et al. (2011) depict dendritic compartments 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.

2.5 REWIRING

*eliminate
anisotropy
through rewiring*

It is in our highest interest to compare results to. To this end we introduce an algorithm that preserves distance-dependent connectivity as found in Proposition 2.3, but eliminates anisotropy in network connectivity by consecutively rewiring existing connections to new suitable targets.

```

1 _paths = sys.argv[1:1+params.n_data_sets]
2 _sets = []
3
4 data_path in data_paths:
5 pfile = open(data_path, "rb")
6 data_sets.append(pickle.load(pfile))
7 pfile.close()
8
9
10 sys.argv[1+params.n_data_sets]
11 pt IndexError:
12 label = img_label.labelstr
13 :
14 label = sys.argv[1+params.n_data_sets]
```

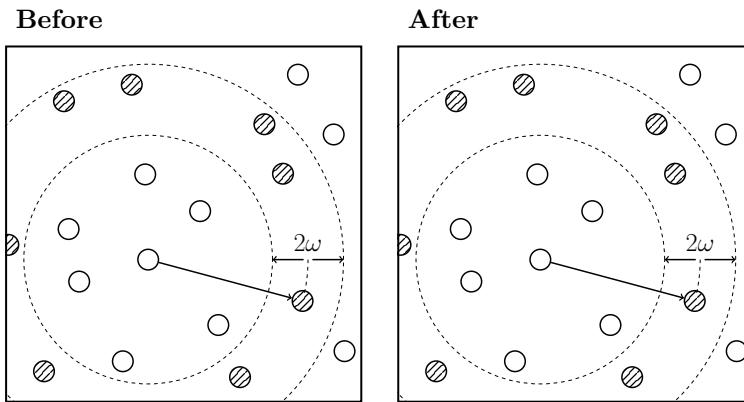


Figure 2.9: Rewiring

2.6 ANISOTROPY MEASURE

2.7 SUMMARY AND DISCUSSION

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