Notes on inferring connectivity (Bente's problem) [draft]

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17 October 2019; updated 7 November 2019

Notes on Bente's problem about inferring connectivity. This is just a memo, not meant to be detailed or precise.

1 Synopsis of the problem

We're considering neurons in some specific region of the mouse brain, and neurons some other specific region, which connect to those in the first region. Let's call the first *target region*, and the second *input region*. Our question is, roughly: how many neurons in the input region project, on average, to a single neuron in the target region?

Our question actually concerns several input regions at once. For the moment we focus on making inferences for one input region only, but the calculation will generalized to several input regions later. Considering several at once will actually improve the results, even if just a little.

The observations and data we use: in several mice a small number of neurons in region A – *starter neurons* – are infected with a virus. This virus spreads, with time, to neurons – *input neurons* – that projects to the starter neurons. The virus can't spread further than that. Some of the infected neurons will be in region B. The virus also leads to colouring of starter and input neurons. Each mouse is killed after several days (different for each mouse) and the starter and input neurons are counted. So our data are the number of starter and input neurons for several mice.

There's a complication: if the mouse is killed too early, the virus hasn't had the time to spread to all input neurons. If the mouse is killed too late, the starter cells decay and are no longer visible. So we also need to guess, for each observed mouse, whether there were additional starter neurons, no longer visible, and what proportion of input neurons have been reached by the virus. As data we have the number of days between virus injection and killing, for each mouse. This complication for the moment is set aside to simplify the initial calculation, but will be taken into account later.

Now let's sketch a schematic picture of our problem in order to make our question more precise and to discuss possible strategies.

2 Formulation and strategies

The strategies we can consider vary in their complexity, both both conceptual and mathematical. This complexity reflects the *hierarchic* depth at which we analyse our problem. What do we mean by 'hierarchy'? For example, we could study the similarities and dissimilarities (say, means and deviations) of the connections from the input region to *one* neuron. Then we can study how these similarities and dissimilarities are themselves similar and dissimilar across all target neurons in *one* mouse. And finally we can study how these higher-order similarities and dissimilarities are themselves similar and dissimilar across all mice. This approach would have a three-level hierarchy. As an opposite example, we could study the similarities and dissimilarities of all connections to all target neurons in all mice, in a way pooling across target neurons and mice at once. This approach would have only a one-level hierarchy.

The hierarchic depth at which we analyse our problem constrains the kind of questions we can ask and the kind of mathematical approximations we can use. In the second example above we would be forsaking the possibility of asking across-mouse variability. In the first example above our mathematical formulae would be very complex.

Here's a first schematic picture of our inference.

We consider a very large number of mice: those we have observed and all those that we might observe in the future or we could have observed in the past. For our inferences to be valid, these mice must be judged 'similar' in some respects. Let's label each mouse with an index $m = 1, 2, \dots$. For each mouse, we consider all neurons constituting its input region, labelling them $i = 1, 2, \dots, K_m$, and all neurons constituting its target region, labelling them $j = 1, 2, \dots, L_m$. The values of the three labels m, i, j may be arbitrary or carry some information. For example, m could reflect a temporal order, and i, j could each reflect a topographical order. The number K_m of neurons in the input region and the number L_m in the target region are different for each mouse m.

Now that we've labelled the mice and their neurons in the two regions, we can consider specific statements about their connections, for example

> *In mouse $m = 3$, the neuron $i = 5$ in the input region projects to the neuron $j = 4$ in the target region*

which can be either true or false. The situation described by these statements is visualized in fig. 1: we have a grid for each mouse; each row i in the grid represents a neuron in the input region, each column j a neuron in the target region. If in mouse m neuron i projects to neuron j, then we colour the corresponding entry i, j in grid m in black, or we can associate the number 1 with it; if it doesn't project, then we use white or the number 0.

Mathematically we represent these statements and the grids of fig. 1 with these quantities:

$$c_{mij} = \begin{cases} 1 & \text{if neuron } i \text{ projects to neuron } j \text{ in mouse } m, \\ 0 & \text{if neuron } i \text{ doesn't project to neuron } j \text{ in mouse } m. \end{cases} \tag{1}$$

For most of these statements we'll never be able to ascertain whether they're true or false, obviously. But they make our question and our data more precise.

First, let's see how our question can be expressed in term of these statements.

We imagine to check every neuron i in the target region of every mouse m. For each such neuron we count how many neurons from the input region project to it. Let's call this number N_{mi}. From the point of view of fig. 1 we're considering every column from every grid, in turn, and counting how many black entries it has. If we were able to perform

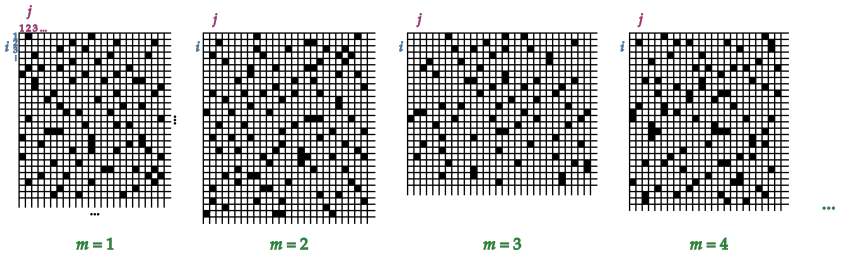

Figure 1 Imaginary layout of the connectivity from input to target region for all mice examined

these observations, at the end we could build a histogram of the numbers (N_{mi}), showing the proportion of neurons in the target region that have 0 inputs from the input region, or 1 input, 2 inputs, n inputs, and so on. These values would be the bins of the histogram. The number of bins is large – as much as the largest number of neurons that could make the input region of a mouse. Denote by F_n the proportion (between 0 and 1) of neurons that receive n inputs. This proportion is calculated from all numbers (N_{mi}) by

$$F_n = \frac{\sum_{mi} \delta(N_{mi} = n)}{\sum_m L_m} \equiv \frac{\text{number of } N_{mi}\text{s equal to } n}{\text{total number of neurons in target regions}}. \qquad (2)$$

The whole histogram is the set of proportions $\boldsymbol{F} \coloneqq (F_0, F_1, \dots)$.

This histogram can give one definite meaning to the question 'how many inputs from the input region does a neuron in the target region have on average?': we are asking 'what the mean of the histogram?', that is,

$$\text{average number of inputs} = \sum_n n\, F_n \equiv \frac{\sum_{mi} N_{mi}}{\sum_m L_m}. \qquad (3)$$

But the histogram would tell us even more, for example the percentage of target neurons that receive between 100 and 200 inputs from the input region, obtained by summing $F_{100} + \dots + F_{200}$.

It's good to keep in mind that our question could also be approached in slightly different ways, leading to different secondary questions. For example, we could construct a histogram for the number of inputs for each mouse individually, thus obtaining several $\boldsymbol{F}^{(m)} = (F^m_0, F^m_1, \dots)$, one for each m. Then we could ask: 'what is the average connectivity histogram for a mouse?', that is,

$$\frac{1}{\text{number of mice}} \sum_m \boldsymbol{F}^{(m)} \qquad (4)$$

and also ask how much such histogram can vary from mouse to mouse.

These alternative questions are important in view of possible approximations in our assumptions and maths.

For example, if we assume that all target neurons from all mice can be somehow pooled together – which makes the maths easier – then we are forsaking the possibility of analysing the individual connectivity histograms.

Although we'll never be able to construct such a histogram, we can nevertheless guess, from our observations in a small set of mice, what kind of shape and numerical values it could have. So our goal is to determine the probability

$$\mathrm{p}(\text{histogram} \mid \text{data}, I) \tag{5}$$

for each possible histogram, given the data collected in our observations and any other information I we have, including our present knowledge of brain biology.

These probability above can be found using the rule for conditional probabilities:

$$\mathrm{p}(\text{histogram} \mid \text{data}, I) \propto \mathrm{p}(\text{data} \mid \text{histogram}, I) \times \mathrm{p}(\text{histogram} \mid I). \tag{6}$$

To calculate these we need to determine our initial probability distribution $\mathrm{p}(\text{histogram} \mid I)$ for all possible histograms. In fact we need to determine the initial probability of a couple more things, for example the total number of neurons in the input region K_m, for each mouse m. All other probabilities are calculated from this initial probability distribution.

In the next section we discuss and analyse several alternative assumptions that we can use to build the distribution $\mathrm{p}(\text{histogram} \mid I) \equiv \mathrm{p}(\boldsymbol{F} \mid I)$. Some of these assumptions are approximate or unrealistic, yet unfortunately necessary for making the problem mathematically tractable. After discussing the alternatives we'll choose specific ones to arrive at formulae that we can use with the data. The discussion of the alternatives is useful because we can step back and try to change the less realistic assumptions if we see that our formulae don't work well.

3 Initial probability distribution

The assumptions we use to build our initial probability distribution $\mathrm{p}(\boldsymbol{F} \mid I)$ are about the symmetries of our problem.

The first symmetry is very intuitive and compelling. Take the distribution of numbers of inputs for a given mouse m: (N_{m1}, N_{m2}) ***

In order to formulate the initial probability distribution $\mathrm{p}[(c_{mij}) \mid I]$ we explore the symmetries of our problem.

Let's analyse two approximate symmetries first. Consider a specific mouse m.

the answers to our question Q2 and the statement of our experimental observations are built up from the specific statements (10). For example, the statement *In mouse # 3, neuron # 1 in the target region receives input from 2 neurons in the input region* is equivalent to the composite statement *In mouse # 3, neuron # 1 in the target region receives input from neurons # 1 and # 2, or # 1 and # 3, or # 1 and # 4, or … in the input region*, which we can express as

$$(C_{311} \text{ and } C_{312}) \text{ or } (C_{311} \text{ and } C_{313}) \text{ or } \cdots \\ \text{or } (C_{312} \text{ and } C_{313}) \text{ or } (C_{312} \text{ and } C_{314}) \text{ or } \cdots \tag{7}$$

Let's denote such kind of statement with

$$C_{mij} \coloneqq \textit{In mouse } m\textit{, neuron } i \textit{ in input region projects to neuron } j \textit{ in target region} \tag{8}$$

and let's introduce the quantity

$$c_{mij} = \begin{cases} 1 & \text{if } C_{mij} \text{ is true,} \\ 0 & \text{if } C_{mij} \text{ is false.} \end{cases} \tag{9}$$

We can rephrase it in two different ways; it's the second that probably interests us:

Q1. If we examine a new neuron in region A in a new mouse, how many neurons in region B will project to it? The possible answers to this question are: 0, 1, 2, and so on.

Q2. If we examine all neurons in region A in a very large sample of mice, and for each neuron we count how many neurons from region B project to it, then what are the frequencies with which we'll observe 0 connections, 1 connection, 2 connections, and so on? One possible answer could be this distribution:

$$0\text{: } 0.1\%, \quad 1\text{: } 0.3\%, \quad \dots, \quad 1\,000\text{: } 24\%, \quad \dots$$

another answer could be this distribution:

$$0\text{: } 0.02\%, \quad 1\text{: } 0.07\%, \quad \dots, \quad 1\,000\text{: } 31\%, \quad \dots$$

and so on, for all possible distributions of frequencies.

For the first question we must give a distribution of probability over all possible answers 0, 1, and so on. For the second the probability is distributed over all possible frequency distributions.

The answers to these two questions and their probabilities are connected; in particular, from the second we can obtain the first. The second is more informative, because it gives us also a range of variability.

Our analysis will also produce probabilities for other another quantity: how many neurons are there in region B, in the next mouse we observe?

We must consider the set of mice that have been observed and those that will be observed in the future. Let's label each mouse with an index m. For our inferences to be valid, these mice must be judged 'similar'.

Now that we've labelled the mice and their neurons in the two regions, we can make several concrete statements, such as

> *In mouse # 64, the neuron # 931 in the input region projects to the neuron # 1 488 in the target region.*

which can be either true or false. Let's denote such kind of statement with

$$C_{mij} \coloneqq \textit{In mouse } m\textit{, neuron } i \textit{ in input region projects to neuron } j \textit{ in target region} \tag{10}$$

and let's introduce the quantity

$$c_{mij} = \begin{cases} 1 & \text{if } C_{mij} \text{ is true,} \\ 0 & \text{if } C_{mij} \text{ is false.} \end{cases} \tag{11}$$

Obviously for most of these statements we'll never be able to ascertain whether they're true or false. But the answers to our question Q2 and the statement of our experimental observations are built up from the specific statements (10). For example, the statement *In mouse # 3, neuron # 1 in the target region receives input from 2 neurons in the input region* is equivalent to the composite statement *In mouse # 3, neuron # 1 in the target region receives input from neurons # 1 and # 2, or # 1 and # 3, or # 1 and # 4, or … in the input region*, which we can express as

$$(C_{311} \text{ and } C_{312}) \text{ or } (C_{311} \text{ and } C_{313}) \text{ or } \cdots \\ \text{or } (C_{312} \text{ and } C_{313}) \text{ or } (C_{312} \text{ and } C_{314}) \text{ or } \cdots \tag{12}$$

The probabilities of such combinations are completely determined once we give an initial joint probability distribution for all statements (10) and their negations, which is equivalent to the joint distribution of

$$\mathrm{p}[(c_{mij}) \mid I] \equiv \mathrm{p}(c_{111}, c_{112}, c_{113}, \dots \mid I) \tag{13}$$

conditional on the information I that we have before doing the experiments and the observations.

Now, we'll want the probability of a specific answer A to our question, conditional on the data D we observed: $\mathrm{p}(A \mid D, I)$. By the rule of conditional probability we obtain it as

$$\mathrm{p}(A \mid D \text{ and } I) = \frac{\mathrm{p}(A \text{ and } D \mid I)}{\mathrm{p}(D \mid I)}. \tag{14}$$

The probabilities in the numerator and denominator can be obtained from our main joint probability (13) using the basic rules of the probability calculus.

So our strategy is as follows:

1. Quantitatively determine the initial joint probability $\mathrm{p}[(c_{mij}) \mid I]$.
2. Resolve the answers to question Q2 in terms of the basic statements C_{mij}.
3. Resolve the experimental observations in terms of the basic statements C_{mij}.
4. Calculate the probabilities in (14).

We now face these steps in turn. We shall discuss several possible alternative assumptions and conceptual or mathematical approximations that we can make in order to proceed.

4 Initial probability distribution

In order to formulate the initial probability distribution $\mathrm{p}[(c_{mij}) \mid I]$ we explore the symmetries of our problem.

Let's analyse two approximate symmetries first. Consider a specific mouse m.

For each neuron i in the input region, we can approximately judge as equally likely that it will connect to any of the neurons j in the target region. This means that our initial probability distribution should remain

the same if we swap some values of the index j, with m and i fixed. For example, the probability that neuron #3 in the input region projects to neuron #2 in the target region and does not project to neuron #5 should be the same if we exchange 2 and 5 in that statement. And similarly for combinations of such statements:

$$\mathrm{p}(c_{m\,3\,2}=1, c_{m\,3\,5}=0 \mid I) = \mathrm{p}(c_{m\,3\,2}=0, c_{m\,3\,5}=1 \mid I). \tag{15}$$

This symmetry is an approximation: if the indices i and j bear some information about the neurons' locations, our probability should reflect the possibility that nearby neurons may connect more easily, for example.

We have an analogous approximate symmetry under exchanges of the input-neuron index i for fixed target neuron j.

These two approximate symmetries together are important because they greatly restrict the possible values of our initial probability distribution $\mathrm{p}[(c_{mij}) \mid I]$. The result they lead to[1] is mathematically difficult for me, however. To further simplify the problem I make an even rougher approximation: that the symmetries above hold not just for i and j separately, but for any pairs of them. This assumption is even more unrealistic than the previous two, because it gives the same probability to the situation where each input neuron is connected with only one, distinct, target neuron, as to the situation where only one input neuron is connected to all target neurons, and all other input neurons are unconnected.

With this approximation the joint probability distribution for a given mouse m assumes the following form, by de Finetti's representation theorem:[2]. Take a set of k_m input neurons and l_m target neurons, and consider all possible connections c_{mij} between them, with $i = 1, \dots, k_m$ and $j = 1, \dots, l_m$. Then

$$\begin{aligned}\mathrm{p}[(c_{mij}) \mid m, I] &= \int_0^1 \mathrm{d}\nu_m \; \mathrm{p}(\nu_m \mid I) \prod_{ij} \left[{\nu_m}^{c_{mij}} \, (1-\nu_m)^{1-c_{mij}}\right] \\ &\equiv \int_0^1 \mathrm{d}\nu_m \; \mathrm{p}(\nu_m \mid I) \; {\nu_m}^{k_m l_m f_m} \, (1-\nu_m)^{k_m l_m (1-f_m)}.\end{aligned} \tag{16}$$

Here $k_m l_m f_m = \sum_{ij} c_{mij}$ is the total number of connections between the k_m input neurons and the l_m target neurons, and $0 \leqslant \nu_m \leqslant 1$ is the

[1] Hoover 1979; Aldous 1981; Diaconis et al. 1981. [2] De Finetti 1930; Hewitt et al. 1955; Heath et al. 1976; Diaconis 1977; Diaconis et al. 1980; Dawid 2013.

population-averaged number of connections from the *whole* input region to the *whole* target region. The probability distribution $\mathrm{p}(\nu_m \mid I)$ expresses our beliefs about the total number of connections from input to target region in mouse m. The formula above is valid only if k_m and l_m are small (say, one tenth at most) compared to their region sizes.

The probability distribution for the connections present in different mice can be obtained by combining the expressions above for each m. To do this we need the initial joint probability distribution

$$\mathrm{p}[(\nu_m) \mid I] \equiv \mathrm{p}(\nu_1, \nu_2, \dots \mid I) \tag{17}$$

for the total number of connections in several mice.

Our question has another symmetry, more realistic than the previous two. We don't believe any of the mice to be examined to be special with respect to the others, nor we do believe that the particular order in which they are observed has any relevance. This means that our initial probability distribution above should be invariant with respect to permutations of the index m. Then we obtain the following expression, again by de Finetti's theorem:

$$\mathrm{p}[(\nu_m) \mid I] = \int \mathrm{d}\theta \; \mathrm{p}(\theta \mid I) \prod_m q(\nu_m \mid \theta), \tag{18}$$

where q is a distribution that depends on the parameter θ, and $\mathrm{p}(\theta \mid I)$ is our initial probability distribution for this parameter.

The parameter θ in principle represents every possible distribution – or histogram – of the total number of connections across the mice. For example, a particular θ can say that 7% of mice had 10^6 connections, 11% had 5×10^7 connections, and so on. The above formula sums over all such possible distributions. There is an infinite of such distributions, so the integral is over an infinite-dimensional space. When we calculate this integral with this full generality, we're using a so-called *non-parametric* method. But for mathematical simplicity we can also decide to restrict our attention to histograms of specific shape, such as a normal for example. In this case the integral is restricted to a finite-dimensional space and we're using a *parametric* method.

Combining the initial probability distributions (16) and (18) we finally obtain our initial probability distribution for a joint set of statements

(C_{mij}):

$$\mathrm{p}[(c_{mij}) \mid I] = \iint \mathrm{d}\theta \; \mathrm{d}\boldsymbol{\nu} \; \mathrm{p}(\theta \mid I) \; \prod_{mij} \Big[q(\nu_m \mid \theta) \; {\nu_m}^{c_{mij}} \; (1-\nu_m)^{1-c_{mij}} \Big], \tag{19}$$

where $\boldsymbol{\nu} \coloneqq (\nu_m)$.

5 Statements of the questions and of the data

Bibliography

('de *X*' is listed under D, 'van *X*' under V, and so on, regardless of national conventions.)

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