A copulas approach to neuronal networks models

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Abstract

Simultaneous recordings from groups of neurons request to improve models. To switch from single unit description to multivariate models describing the coding activity of two or more neurons, we propose to use the copula notion. This mathematical object catches the coupling properties and allows a mathematical description of the dependencies between two or more random variables. Its use is here illustrated by means of toy examples and further applications are discussed.

1 Introduction

Data from simultaneous recording of groups of neurons allow to detect the existence of precise temporal relations in sequences of spike intervals, referred to as 'spatiotemporal patterns' and brain theories emphazise the role of temporal coding. Several experimental and theoretical observations support the hypothesis of the existence of dynamical cell assemblies as organizational principle of higher brain activity ([1, 3, 26, 12, 28, 27]). The cell assembly is formed by a population of neurons that spontaneously organizes on the basis of a sequence of input patterns of spikes and reproduces the same spatio-temporal activity whenever the same input pattern is presented ([2, 14]). Moreover, syntony of firing, i.e. correlated activity of firing at variable coarse grain time scales (cf. [9]), suggests that the same neuron might participate to distinct cell assemblies following the kind of brain process associated to the coding schema enabled by the "ignition" of the cell assembly

itself. For a brief but deep analysis of features and problems involved in neural coding and spike trains relationships see for example [24].

Mathematical models of single neuronal units are used to help the understanding of neuronal coding mechanisms and it exists a large literature on this topic. Hogkin and Huxley type models and leaky integrate–and–fire stochastic models are typical examples of single neuron spiking activity models, for a review see for example [25, 23]. On the contrary there have been few attemps to develop mathematical models to describe small or large neuronal networks and the existing results are mainly of simulation type. Cross-correlation histograms are a precious support to the study of relationships between neurons and hence to the analysis of multivariate models, but they photograph a mean behavior and can lose part of the information. It seems of interest to develop alternative methods to keep into account the complete bivariate or multivariate behavior avoiding to lose information in the averaging procedure. The use of the entire information contained in the spike train becomes useful both from the statistical and model point of view. Hence we focus here on a methodology capable of capturing the structure of dependencies between random variables.

Multivariate models are an investigation topic also in areas different from neurosciences such as financial markets models, cf. for example [15]. In that context copulas are a mathematical tool largely used to study dependency properties. In this paper we propose to mutuate this approach to study multiple spike trains dependencies. Compared to the joint distribution approach or correlation-based approach, a copula model is a more convenient tool in studying the dependence structure. In statistics, a copula is a function that connects the marginal distributions to restore the joint distribution and different copula functions represent different dependence structures between variables (cf. [20]). In a copula model, the primary task is to choose an appropriate copula function and a corresponding estimation procedure. Marginal distributions play a role as nuisance functions. This reorientation seems perfect to investigate spatio temporal patterns in spike trains. Indeed non significative patterns can be thought as random patterns arising from the fortuite merging of the marginals while significative ones should be related with the dependency structure determined by common inputs to the neurons.

Despite their diffusion in market models copulas have not yet been used in neuroscience context and the only exception is an insufficiently underlined paper by Jenison and Reale [16]. However many applications of the copula notion in neuroscience could be made. Indeed they are a good mathematical tool to develop models but they can also be used for statistical studies of data or to simulate specific dependencies structures to understand causes that can generate significative patterns.

The paper is organized as follows. In Section 2 we review some basic concepts about copulas while in Section 3 we introduce the basic ideas for the use of copulas in neurosciences and we use two toy models for the coupling of two neurons to illustrate the usefulness of the method. We postpone to future papers other applications of the copula notion to real data analysis or to the simulation of specific dependency structure for counting processes. By means of the proposed toy models we also show how some dependency structure can become unobservable using cross correlograms while they are visible with the copula approach.

2 Copula definition and first properties

To define a copula we first consider k uniform random variables $U_1,...,U_k$ on $[0,1]\times...\times[0,1]$ that are assumed not necessarily independent but related through their joint distribution function as

$$C\left(u_1,...,u_k\right)=P\left(U_1\leq u_1,...U_k\leq u_k\right). \tag{2.1}$$

The function C is called "copula". Consider now $k\geq 2$ arbitrary marginal distribution functions $F_1\left(x_1\right),...F_k\left(x_k\right)$, then it is easy to check that the function

$$C\left[F_1\left(x_1\right),...F_k\left(x_k\right)\right]=F\left(x_1,...,x_k\right), \tag{2.2}$$

defines a multivariate distribution function with marginals $F_1\left(x_1\right),...,F_k\left(x_k\right)$. Sklar estabilished that also the converse is true, indeed he proved that any multivariate distribution function F can be written in the form of Equation (2.2). Hence any joint distribution function admits a copula representation. Sklar's theorem also claims that if the marginal distributions are continuous then there is a unique copula representation.

Note that eq. (2.2) defines different multivariate distributions if marginals are changed. Otherwise, the coupling structure does not change with marginal distributions, while it varies if the copula function is changed. The copula is invariant under increasing and continuous transformations, i.e. it is scale free, hence avoiding the assumption that dimensions of the marginals are independent.

The joint study of several spike trains requests the use of multivariate distributions. An extensive literature in statistics deals with nonnormal multivariate distributions; see, for example [19, 18]. Many multivariate distributions have been developed as extensions of univariate distributions, examples being the bivariate Pareto, bivariate gamma, and so on. These types of distributions have a set of disadvantages: i) each bivariate family is built with respect to specific marginal distributions whose change implies the rebuilding of a new bivariate family, ii) extensions to more than just the bivariate case are often unhandy, and iii) the parameters characterizing the dependency between the components appear both in the marginal distributions and in the joint distribution. A technique to construct multivariate distributions that overcomes these difficulties is based on copula functions.

The word copula comes from Latin where it refers to a connection and is used in linguistics to refer to a proposition that links a subject to a predicate. In statistics literature, the idea of copulas arose as early as the 19th century in the context of the search of non-normality in multivariate cases. The word "copula" was first used in a mathematical sense by Sklar (1959) who defined it, provided some fundamental properties and proved the fundamental theorem which bears his name. Mathematically a copula is a function which joins or "couples" a multivariate distribution function (i.e. the distribution of two or more random variables) to its one-dimensional marginal distribution functions. A useful property of copulas is that they are scale free. Indeed, as Fisher (1997) notes in the Encyclopedia of Statistical Sciences, "Copulas [are] of interest to statisticians for two main reasons: first, as a way of studying scale-free measures of dependence; and secondly, as a starting point for constructing families of bivariate distributions, ...". In probability

theory, copulas functions are used to couple marginal distributions to form flexible multivariate distribution functions.

The simplest example of copula, in the bivariate case, is the independent copula which is defined as $C(u,v) = uv, (u,v) \in [0,1] \times [0,1]$. More complex copula functions usually contain one or more parameters, which are also called association parameters. If only one parameter appears in a copula function, this parameter usually reflects the strength of the dependence. Consider for example the following copula function,

$$C_\theta(u,v) = uv \exp(-\theta \ln u \ln v), \qquad \theta \in (0,1], (u,v) \in [0,1] \times [0,1]. \tag{2.3}$$

For $\theta = 0$ it reduces to the independent copula. A continuous copula $C(u,v)$ can also be characterized through its probability density function, given by

$$c\,(u,v) = \frac{\partial C\,(u,v)}{\partial u \partial v}. \tag{2.4}$$

For example, the independent copula has probability density function $c\,(u,v) = 1, (u,v) \in [0,1] \times [0,1]$, i.e. the dependence is flat on $[0,1] \times [0,1]$. In Fig. 1 we compare the bivariate densities when marginals are independent with the case of dependence corresponding to the copula (2.3). Different couples of marginals are considered in this figure.

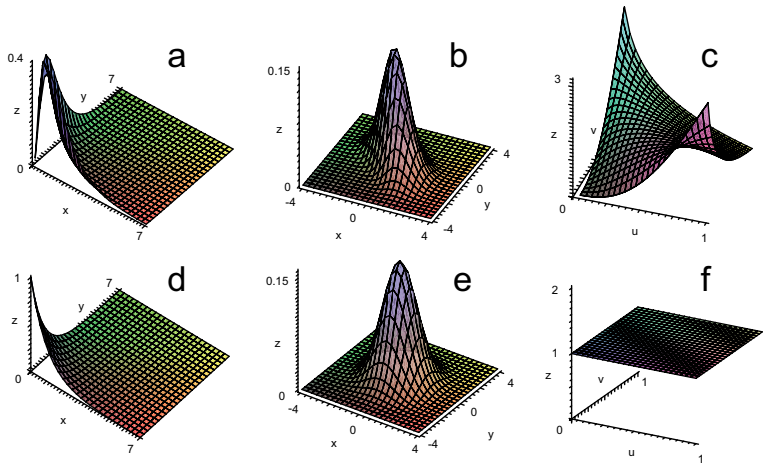

Figure 1: Joint density functions for a couple of random variables (X,Y) (panels a,b,d,e) and density functions of the corresponding copulas (panels c,f). In panels a and b, the marginal distributions are two Exponential random variables of parameter 1 and two standard Gaussian random variables respectively. The marginals are coupled by the copula function in eq. (2.3), whose density is represented in panel c, for $\theta = 1$. In panels d and e, the same marginal distributions as in panels a and b respectively are coupled with the independent copula, whose density is represented in panel f.

Working with copula models has important advantages compared to joint distributions. Indeed it is more flexible in applications, since, when the scatter of the data does not fit any known family of joint distributions, it may be difficult to specify the joint

distribution. Using copulas, we can first estimate the marginal distributions and then estimate the copula. This two step approach allows the use of single neuron models for the marginal spike activity description. Furthermore in a copula model approach the dependence function is explicitly expressed and this allows to relate directly the effect of an input on the network to the copula structure. Despite Sklar's theorem that guarantees the existence of the copula function it is not always easy to identify the copula. Various methods exist both from model and statistical point of view (cf. [20, 17]), but we will not focus on the mathematical details which are out of the scope of this paper.

3 Copulas in neurosciences

The long lasting interaction between mathematics and neurosciences has allowed the formulation of a variety of models for single neuron coding activity. Depending upon the grade of detail included in the mathematical description, the proposed models can range from phenomenological ones, like leaky integrate–and–fire type models, to detailed biophysical ones, like Hodgkin and Huxley models. The theoretical study of these models and their variant has occupied mathematicians for a couple of decades since seventies and has request strong mathematical efforts. Nowadays specific numerical techniques and analytical results for single neuron activity models are available. Single neuron models were developed when the experimental techniques allowed the recording only from a single neuron. The variety of results on input–output relationships descending from the use of these models has then maintained their interest for scientists.

Since more than two decades have been developed multielectrodes that, with an increasing level of technology, allow to record simultaneously from two or more neurons. The necessity then arises to formulate models for networks and to analyze data coming from the activity of two or more neurons. This implies two main directions for the research:

1. the development of suitable statistical methods;
2. the development of multivariate mathematical models.

As far as the first topic is concerned the typical approach consists in using crosscorrelograms. This method has allowed important progresses in the study of temporal patterns but does not suggest specific rules to build models, being difficult its reading in terms of cause effect features that go beyond the basic ones such as excitation, inhibition and independency. The second topic is largely considered in the literature where small and large network have been considered with different methods. Unfortunately the largest part of these models renounce the analytical approach and make use of simulation algorithms or to computer science approaches.

Use of copulas could open new research direction both on statistical and model view point.

1. Statistical methods

Given experimental data simultaneously recorded from two or more neurons it may be interesting to determine the copula that fits the data. This corresponds to look for the

copula coupling two or more point processes and is a subject of statistical investigation implying many mathematical open questions (cf. for example [17, 22, 6, 8, 21]).

A first step of the study should consider a simpler frame. In many single neuron models one focus on the time, when an action potential is elicited and the collection of spikes intertimes is studied as a sample from independent identically distributed random variables. In this frame, one could investigate the dependency between $T_1, ..., T_k$ where k is the number of neurons recorded. This implies the study of the collected data recovering their marginal distribution, i.e. the distribution of each $T_i, i = 1, ..., k$, and the copula structure catching their multivariate dependency. Statistical methods to select the right copula and to estimate its parameters are discussed in [7, 11, 10] while in [30] one can find instruction for R code software to use copulas for fitting data.

Limiting the attention to the coupling of times until the first spike of different neurons, we can use scatterplots of the copula to argue particular dependencies and to hypothesize the copula expression. Then, the estimation of different association indexes, such as the correlation coefficient ρ, or the Kendall's τ or the Spearman's ρ can give hints on the estimation of the parameters of the copula (for a precise definition of the cited measures of dependence see for example [20]).

An extensive study on data should be performed to recognize the copulas that can fit different experimental instances, in the hope to recognize some law in the coupling procedure that could allow to make hypothesis on the mechanisms generating the different shapes. This approach requests the availability of a large quantity of recordings of stationary spike trains and may open some practical problems besides to the mathematical ones. We postpone the study on recorded data to a future paper.while here we limit ourself to the use best fit statistical tests to analyse simulated data.

1. Modeling approach

Statistics can help to understand observed features on neural networks, suggesting how to fit experimental data to determine a statistical model. When the statistical model can be related with special cause effect features it also helps to understand the rules governing the phenomenon. Alternatively one can have a partial phenomenological knowledge of the physical laws governing the network connections. In these cases one can formulate a mathematical model catching the rules governing the phenomenon. When one studies the coupling between spike times of different neurons in simultaneous activity one can argue the type of connections between neurons and use this information to formulate models. A similar approach was fruitful of consequences in single neuron leaky integrate and fire models. After the pioneering work [13], that was partly motivated by statistical evidences, an enormous literature has appeared on possible features that had to be inserted in a "good" model (spontaneous membrane potential decay, presence of reversal potentials, refractory period) and on the consequences of each new variation (see [5] for a review on the subject). Working in analogy with those models we should focus on the sources of coupling between neurons to determine a copula catching the dependency structure. Hence coupling models and marginal behaviors are inserted in the model. Eventually, marginals can be described by means of standard models for single neuron activity. This

approach should help to distinguish random patterns, related to marginal distributions, from significant ones, related to the coupling effect.

Copulas can catch the dependencies between two or more random variables and models for groups of neurons could be built in perfectly analogy with models of two or three neurons. Having in our mind the simple illustration of the methodology and of its power we limit ourself to the discussion of two toys examples. These examples do not pretend any realism but they are simple enough to illustrate the importance of copulas to researchers without a strong mathematical background. Extensions to larger dimensions can introduce further mathematical difficulties, that should be solved, but conceptually should not change the approach.

3.1 Two neurons coupled by a third one

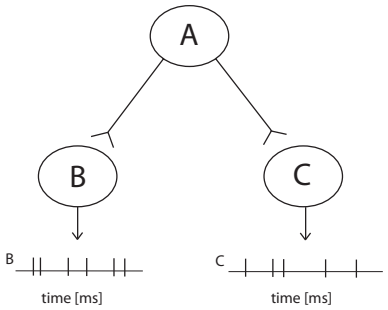

Figure 2: Two neurons, B and C, both receiving the same inputs from neuron A.

Let us consider a small network composed by three neurons, A, B and C, as illustrated in Fig. 2. Let T_A, T_B and T_C be the times of firing of units A, B and C respectively, in the absence of connections between the three units. Let A be excitatory for both neurons B and C, so that an action potential generated by neuron A makes both B and C fire simultaneously. Hence, in the presence of connections between the elements of the network, the firing times of B and C are

$$\begin{aligned} \tau_B &= \min(T_A, T_B), \\ \tau_C &= \min(T_A, T_C). \end{aligned} \tag{3.1}$$

For simplicity let us assume that T_A, T_B and T_C are exponentially distributed with parameters $\lambda_A, \lambda_B, \lambda_C$ respectively. In this case simple computations (cf. Appendix 1) show that the spiking times of neuron B and C, (τ_B, τ_C), are coupled through the copula function

$$C(u,v) = \min\Big((1-u)^{1-\alpha}(1-v), (1-v)^{1-\beta}(1-u)\Big) + u + v - 1, \tag{3.2}$$

where $\alpha = \frac{\lambda_A}{\lambda_B+\lambda_A}$ and $\beta = \frac{\lambda_A}{\lambda_C+\lambda_A}$. The survival copula for (τ_B, τ_C) is the well known Marshall-Olkin copula, cf. [20]. Fig. 3 illustrates the probability density function of the copula (3) and Fig. 4 shows the corresponding scatterplots of the joint variables (τ_B, τ_C).

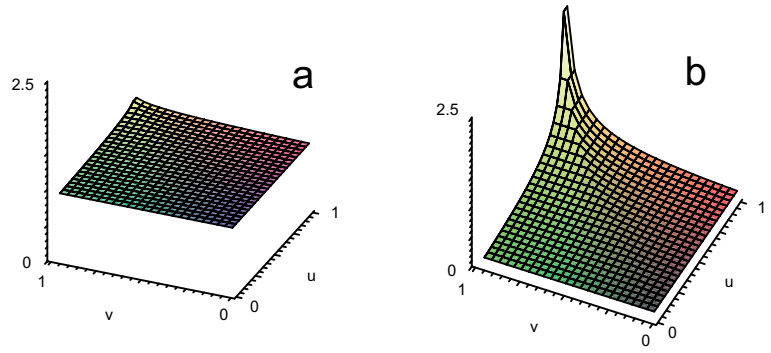

Figure 3: Density function of the copula (3.2) for $\lambda_B = \lambda_C = 20$ ev/s and $\lambda_A = 1$ ev/s (panel a), $\lambda_A = 100$ ev/s (panel b).

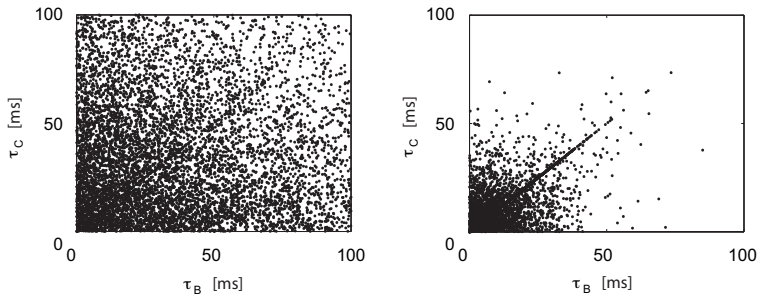

Figure 4: Scatter plot of the couple (τ_B, τ_C), with joint distribution given by the copula (3.2), for $\lambda_B = \lambda_C = 20$ ev/s and $\lambda_A = 1$ ev/s (left panel), $\lambda_A = 100$ ev/s (right panel).

The coupling effect of neuron A is illustrated by the presence of a large number of points on the diagonal line of Fig. 4–right panel. Indeed these points correspond to the synchronous firing of neurons B and C, induced by A.

The model above introduced is very simple and gives only the joint distribution of the interpike intervals (τ_B, τ_C). In order to get the two spike trains, given the interspike intervals (ISIs), we should build the corresponding sequence of successive spikes events. The most natural method to do it is to paste one after the other the ISIs generated with distributions τ_B and τ_C. However, this method definitely destroys the coupling between the two spike trains. Indeed, the coupling between the ISIs of cells B and C joins together two inter-times, but if the coupled ISIs are separated by other spikes (and constructing the spike train it could happen due to the relative delays gradually accumulated), the dependency is lost. In other words we could say that the coupling of (τ_B, τ_C) is a first-order dependency and it hides when the coupled spikes are separated becoming higher-order intervals (see for example Fig. 5, left panel).

The simplest choice which preserves the coupling between B and C is to build the spike trains pasting the joint realizations of (τ_B, τ_C) one after the other, as shown in Fig. 5, right panel.

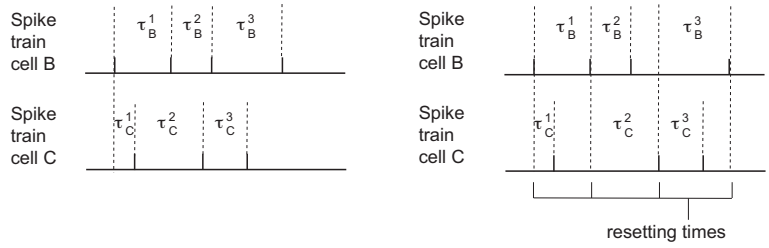

Figure 5: Resetting procedure to build the spike train from the random variable (τ_B, τ_C). The system is reset after the generation of the couple of spikes, from B and from C.

Let us remark that this model is quite unrealistic but it is simple enough to show some features of the association property in the two time series. The law used to model this network and to generate the time series guarantees the presence of a dependence between the ISIs of neurons B and C. The copula in eq. (3.2) captures the dependency between the spikes of neurons B and C and this dependency is maintained in the subsequent spikes of the two neurons.

The coupling is catched also by the cross-correlation histograms shown in Fig. 6. From there we deduce that cells B and C, with high probability, fire simultaneously, but no suggestions about the modeled network that could produce such an output is given. Furthermore the observed dependency cannot be used to build the bivariate distribution of (τ_B, τ_C) without the aid of the copula notion.

Even if very simple, the model above introduced is more adequate to deal with the problem than it seems at first sight. Indeed the hypothesis of independent Exponential distribution of the marginal firing times T_A, T_B and T_C in the absence of connections, could be replaced with any other probability distribution, getting similar results as before for the distribution in the presence of connections between the cells A, B and C as given

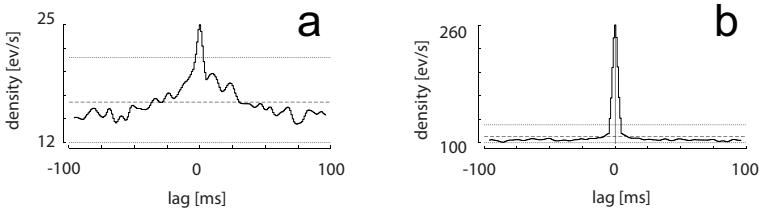

Figure 6: Cross-correlation histograms of the spike trains of cells B (trigger) and C (follower), for $\lambda_B = \lambda_C = 20$ ev/s and $\lambda_A = 1$ ev/s (panel a), $\lambda_A = 100$ ev/s (panel b). Note that the vertical axes in the two panels have different ranges.

in Fig. 2. Given that T_A, T_B and T_C, in the absence of any connection, are independent and identically distributed (and this is quite weak and natural assumption), the copula that joins (τ_B, τ_C) is again given by equation (3.2), with parameters $\alpha = \beta = 0.5$. This claim can be proved both theoretically (but for simplicity we omit here the calculations) and statistically, performing the goodness of fit test illustrated for example in [10, 4].

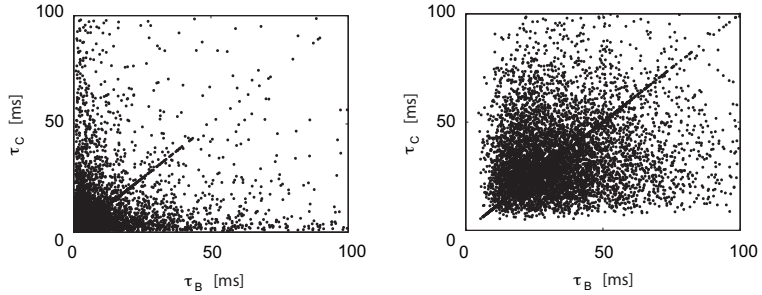

Figure 7: Scatter plot of the couple (τ_B, τ_C), with Inverse Gaussian marginal distributions, with parameters (common to the three identical marginal distribution in the absence of connections) $\mu = 0.2$ mVms^{-1}, $S = 10$ mV, $x_0 = 0$ mV and $\sigma^2 = 20$ mV^{2}ms^{-1} (left panel), $\sigma^2 = 1$ mV^{2}ms^{-1} (right panel).

For example let us consider T_A, T_B and T_C independent identical Inverse Gaussian (IG) random variables. Let us recall that the IG is the ISI distribution of a neuron modeled as a perfect integrator, with drift μ, diffusion coefficient σ^2, threshold S and resetting potential x_0 as will be considered later in eq. (3.3). In Fig. 7 are illustrated the scatterplot of the joint variables (τ_B, τ_C) given by the expressions (3.1) for two different choices of the parameters. Even if the patterns of plotted points can be recognized as very different with respect to the ones given in Fig. 4 where the marginal times T_A, T_B and T_C were Exponentially distributed, the copula that joins them is again given by equation (3.2) (in both cases the statistical test for the goodness of fit gives p–value ¿ 0.5).

We would like to stress that this result means that even if the marginal distributions, and hence the joint distributions, are changed the copula is the same, meaning that it describes the deep structure of the dependency rid of the marginal behaviors. Hence finding the copula that fits real data gives informations on the dependency between he

registered units and may suggest a model of the network that could produce the sampled spike trains.

3.2 Two neurons subject to the same random input

Let us consider two neurons, D and E, modeled as perfect integrators, i.e. the membrane potentials V_t^D and V_t^E respectively are given by the stochastic differential equations

$$dV_t^D = \mu_D dt + \sigma_D dW_t^D, \tag{3.3}$$
$$dV_t^E = \mu_E dt + \sigma_E dW_t^E, \tag{3.4}$$

with $V_0^D = V_0^E = 0$ mV, σ_D and σ_E positive (σ_E^2 is measured as $\mathrm{mV}^2\mathrm{ms}^{-1}$) and W_t^D and W_t^E are two independent Brownian motions. The parameters μ_D and μ_E are called drift terms and can be interpreted as the intensity of the external inputs arriving to the neuron, while σ_D and σ_E are called diffusion coefficients and accounts for the variability of the incoming inputs. In this model, when the membrane potential attains a threshold value S, the neuron releases a spike and the membrane potential is reset to its resting value, V_0^D and V_0^E respectively. Hence the ISIs correspond to the subsequent first passage times T_D and T_E (FPT) of the membrane potential processes through the threshold S. For a review see for example [25]. It is well known that the mean and variance of the ISI distribution are:

$$\mathbb{E}(T_D) = \frac{S}{\mu_D}, \qquad \mathrm{Var}(T_D) = \frac{S\sigma_D^2}{\mu_D^3}, \tag{3.5}$$

and completely similar equations hold for neuron E.

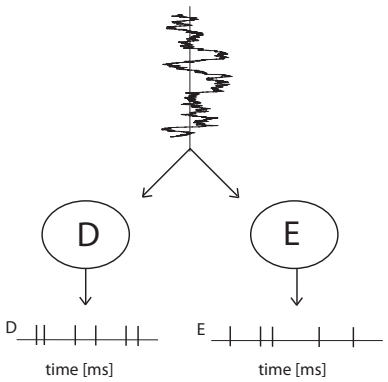

Figure 8: Neurons D and E receive the same input signal.

We consider here a generalization of this model where the two neurons D and E are subject to the same random input term, as in Fig. 8. Since the post-synaptic potentials arriving to a neuron have large variability and fluctuations in time, the hypothesis that the input parameter is a random variable is quite natural. However it seems reasonable to assume that neurons included in the same network could share the same inputs. Hence μ_D and μ_E are no more considered constant parameters, but a random variable that

we suppose exponentially distributed with parameter λ. Notice that larger values of λ imply smaller mean values for the drift parameter and hence larger mean interspike times $\mathbb{E}(T_D) = \mathbb{E}(T_E)$. The presence of the common input determines a coupling between spike times of the two neurons, as illustrated in Fig. 9. Both scatter plots show a high density

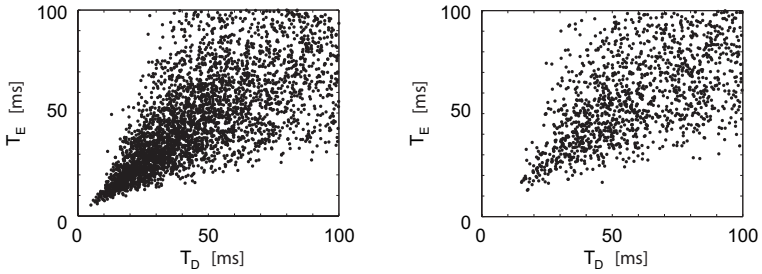

Figure 9: Scatter plot of the couple (T_D, T_E), for $S = 10$ mV $, \sigma_D^2 = \sigma_E^2 = 1$ mV^{2}ms^{-1} and $\lambda = 5$ (left panel), $\lambda = 10$ (right panel).

of events around the diagonal line, $T_D = T_E$, but as λ increases, and hence the mean interspike intervals becomes larger, the pattern of points increases its variability. This feature is related to the increased value of $\mathrm{Var}(T_D)$ and $\mathrm{Var}(T_E)$, cf eq. (3.5). Analytical computations can be performed only in a very specific instance but a statistical study of the joint ISI distribution shows that the resulting copula is well fitted by the Gumbel copula (cf. [20]).

Using this model we generate two spike trains with the same resetting procedure proposed in the previous Section, cf. Fig. 5. We plot the corresponding cross-correlation histograms in Fig. 10. The cross-correlation histograms recognize the coupling between

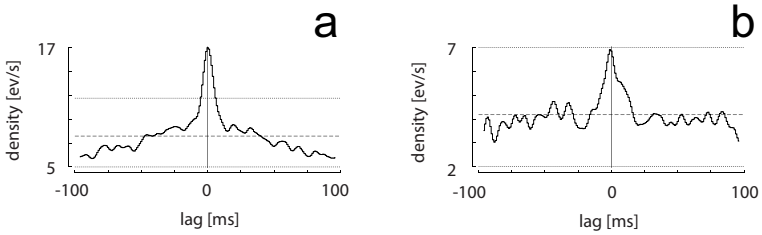

Figure 10: Cross-correlation histograms of the spike trains of cells D (trigger) and E (follower), for $S = 10$mV $, \sigma_D^2 = \sigma_E^2 = 1$ mV^{2}ms^{-1} and $\lambda = 5$ (panel a), $\lambda = 10$ (panel b).

the two spike trains when λ is small enough (Fig. 10–a), while the peak around lag zero is not statistically significant when λ increases, cf. Fig. 10–b. This fact illustrates a deeper ability of copulas in recognizing eventually weak dependencies and suggests to introduce the use of copulas in data analysis in order to recover dependencies that could be hidden using crosscorrelograms.

Moreover we would stress that once the copula is estimated from data, it may give a hint of the modeled interactions between cells that could produce the registered data. Hence, it appears that copulas are a useful tool both to describe the dependency identified

from data and to suggest a most probable model of interaction between the units involved in the analysis.

4 Conclusions

An alternative approach to the study of coupling of two or more neurons is proposed by suggesting the use of the notion of copula. Advantages of this approach are illustrated by means of unrefined examples that do not pretend any realism but allow to show some difficulties related with the use of crosscorrelograms. This is a preliminary work on the subject and future works should consider more sophisticated models. In particular coupling of counting processes through copulas seems a direction that should be investigated although the available mathematical results on this topic seem not yet well suited to be applied to neurosciences. Furthermore a statistical study of simultaneously recorded data, devoted to the recognition of the copula fitting the data, could give some light on the coupling mechanisms governing the network suggesting the most probable model that gives the registered data. Finally, we would like to suggest the use of copulas for the simulation of large networks, according to an agent based approach (cf. [29]). This should allow the study of long term association properties and eventually of macroscopic features of a large network. Copulas seem particularly well suited for this goal since methods exist for recursive generation that allow to move from coupling of two objects to coupling of a larger number of objects.

Appendix

Let T_A, T_B and T_C be independent Exponential random variables of parameters λ_A, λ_B and λ_C respectively. Let $\tau_B = \min(T_A, T_B)$ and $\tau_C = \min(T_A, T_C)$. The goal is to find the copula function C such that

$$C(F_B(x), F_C(y)) = H(x, y) \tag{4.1}$$

where F_B and F_C are the marginal distribution functions of τ_B and τ_C, and H is the joint distribution function of the couple (τ_B, τ_C).

Let us denote the joint survival function as $\bar{H}(x, y) = \mathbb{P}(\tau_B > x, \tau_C > y)$. Hence we have

$$\begin{aligned} \bar{H}(x,y) &= \mathbb{P}(\min(T_A,T_B) > x, \min(T_A,T_C) > y) \\ &= \mathbb{P}(T_A > x, T_B > x, T_A > y, T_C > y) \\ &= \mathbb{P}(T_B > x, T_C > y, T_A > \max(x,y)) \\ &= \mathbb{P}(T_B > x)\mathbb{P}(T_C > y)\mathbb{P}(T_A > \max(x,y)) \\ &= \exp[-(\lambda_B x + \lambda_C y + \lambda_A \max(x,y))]. \end{aligned} \tag{4.2}$$

The marginal survival function $\bar{F}_B$ is given by

$$\begin{aligned}\bar{F}_B(x) &= \mathbb{P}(\min(T_A, T_B) > x) \\ &= \mathbb{P}(T_A > x, T_B > x) \\ &= \exp[-(\lambda_A + \lambda_B)x],\end{aligned}$$

and analogously $\bar{F}_C(y) = \mathbb{P}(\min(T_A, T_C) > y) = \exp[-(\lambda_A + \lambda_B)y]$. Hence, being $\max(x, y) = x + y - \min(x, y)$, eq. (4.2) can be rewritten as

$$\begin{aligned}\bar{H}(x, y) &= \bar{F}_B(x)\bar{F}_C(y)\exp(\lambda_A \min(x, y)) \\ &= \bar{F}_B(x)\bar{F}_C(y)\min(\mathrm{e}^{\lambda_A x}, \mathrm{e}^{\lambda_A y}) \\ &= \bar{F}_B(x)\bar{F}_C(y)\min(\bar{F}_B(x)^{-\lambda_A/\lambda_B+\lambda_A}, \bar{F}_C(x)^{-\lambda_A/\lambda_C+\lambda_A}).\end{aligned}$$

It follows that the survival copula function, defined as $\bar{C}(\bar{F}_B(x), \bar{F}_C(y)) = \bar{H}(x, y)$, is given by

$$\bar{C}(u, v) = uv\min(u^{-\alpha}, v^{-\beta}),$$

where $\alpha = \frac{\lambda_A}{\lambda_A+\lambda_B}$ and $\beta = \frac{\lambda_A}{\lambda_A+\lambda_C}$. Given that the relation between the survival copula and the copula functions is given by

$$C(1 - u, 1 - v) = \bar{C}(u, v) - u - v + 1,$$

we finally get that

$$C(u, v) = \min\Big((1 - u)^{1-\alpha}(1 - v), (1 - v)^{1-\beta}(1 - u)\Big) + u + v - 1.$$

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