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Chromatic and Anisotropic Cross-Recurrence Quantification Analysis of Interpersonal Behavior

Ralf F.A. Cox, Steffie van der Steen, Marlenny Guevara, Lisette de Jonge-Hoekstra, and Marijn van Dijk

Abstract Cross-recurrence quantification analysis (CRQA) is a powerful nonlinear time-series method to study coordination and cooperation between people. This chapter concentrates on two methodological issues related to CRQA on categorical data streams, which are commonly encountered in the behavioral sciences. Firstly, we introduce a more general definition of recurrence as ‘behavioral matching’, which can be applied to several kinds of matches simultaneously, visualized by a color coding. We will refer to this as *cross-matching*, and to the resulting quantification procedure as *Chromatic* CRQA. Secondly, cross-recurrence plots of categorical data often prominently consists of rectangular structures. This calls for a differential analysis of vertical and horizontal lines, rather than of diagonal lines. We introduce a simple procedure for this, referred to as *Anisotropic* CRQA. Both procedures are demonstrated with empirical studies on children’s problem-solving behavior and by means of a model simulation. The authors hope that the ideas presented here increase the power and applicability of CRQA in the behavioral sciences, and that this chapter serves as a stepping stone for their mathematical and methodological development.

1 Introduction

Behavioral scientists intend to study human behavior as it unfolds in time, aiming to capture the behavioral regularities at the different time scales that apply to a given task and context, and within the existing methodological constraints. These regularities are the key to understanding the processes underlying social behavior, learning and development. Typically the measurement scale of the behavioral dimension (eye movements, speech) is nominal in such studies, and signifies the specific set of categories (gaze here or there, say this or that kind of word) into which the researcher wishes to compress the behavior under study. Data collection hence results in an ordered sequence of observed behavioral categories. When the research context involves two people who are engaged in some form of interaction, the collected data set consists of two such categorical behavioral streams. The task at hand then is to analyze these streams in order to unravel the dynamic organization of the interactions.

To date, one of the best nonlinear techniques to analyze such data, which exploits the temporal structure of the behavioral streams, is recurrence quantification analysis (RQA) and its bivariate cousin cross-recurrence quantification analysis (CRQA). Both RQA and CRQA were originally designed for time series variables of a continuous measurement scale [1] [2] [3] [4]. In the past decade, several methodological advances made these techniques more appropriate for the analysis of categorical data, for instance as collected in the behavioral sciences. As a result CRQA has found its way into the study of interpersonal behavior, and has now been applied successfully to explore, for instance, syntactic coordination between children and parents [5] [6], eye movement synchronization between speakers and listeners [7] [8], mother-infant gaze during a still-face procedure [9], infant-parent visual coordination in joint attention [10], nonverbal attunement in social interaction [11] [12] [13], and transitions in parent-child conflict conversation due to intervention [14]. In all these cases CRQA has provided valuable and unique knowledge about interpersonal coordination and its relation to other psychological constructs or its development.

Specific methodological issues which typically arise in CRQA on categorical time series (and which set it apart somewhat from CRQA on continuous time series) have been encountered in most if not all of the studies listed above. Although several of these issues have been noted, described and (sometimes even) solved in an ad hoc fashion (see also [15] [16] [17] [18]), they have yet to be addressed more generally and more formally. Here we will focus on the following main issues, which are relevant to the behavioral sciences:

The first issue pertains to the definition of recurrence. Recurrence is essentially operationalized in a rather straightforward way akin to mimicking, that is, as ‘being of the same behavioral category’. However for interpersonal coordination to be successful, oftentimes, entirely different behaviors of the two interacting persons are called for (from the same functional behavioral class), for instance, being silent as the other person speaks. Recurrence procedures should be able to keep track of this, which necessitates a proper generalization of the concept of recurrence. As a corollary this creates the opportunity of distinguishing and analyzing different kinds of recurrences within one context.

The second issue has to do with the prominent rectangular structures which are common in cross-recurrence plots (CRPs) of categorical time series (see Figure 1). These structures reflect some persistence in the interaction, partly due to the coarse-grained nature of the measurement. It makes sense to focus the analysis on the non-diagonal line measures (*LAM*, *TT*, *MaxL*), because for categorical time series these are often more reliable and informative. In addition, a differential analysis of the CRQA-measures along the horizontal and vertical directions in the (anisotropic) CRP might help to tear apart the respective contributions of each of the two subsystems to the dynamics.

Concretely, the goal of this methodological chapter is twofold: First, to introduce an alternate definition of cross-recurrence as cross-matching, for coupled dynamical systems measured on a

nominal scale. Second, to initiate the development of recurrence procedures that enable the analysis of asymmetry in such systems, based on anisotropy in the CRP. To dub their existence we will call these methodological variations *cross-matching* and *Chromatic CRQA* and as *Anisotropic CRQA*, respectively. The merit of the proposed techniques will be demonstrated by two empirical studies and a model simulation. Note that although these issues will be presented somewhat more formally than has been done previously, no claims are made about mathematical rigour and methodological completeness.

2 Cross-Matching and Chromatic Quantification Analysis

2.1 *Cross-matching procedure*

There are numerous contexts and tasks in everyday behavior for which the atom of dyadic interaction is not defined on the basis of an equal or similar behavioral state for the two interacting people. More often than not effective and efficient interpersonal coordination requires individuals to behave quite differently from each other and sometimes even perform opposite actions in a coupled way (e.g. [11] [19] [20] [21]). In addition, frequently behavioral scientists wish to keep track of, distinguish between, and relate several behavioral atoms, and wish to distil their temporal structure. The canonical concept of recurrence, that is, detecting similar behavioral categories at the same or any other moment in time, is not sufficiently powerful or accurate to capture the coordination dynamics of the interaction in those cases (cf. [16]). A variation of this basic procedure based on ‘behavioral matching’ should then be applied, so as to provide more flexibility in the analysis as well as a richer set of outcome measures.

The cross-matching (where ‘cross’ refers to the analysis of two time series) procedure on categorical data uses a fairly simple parameter setting for the analysis. It is largely similar to the canonical cross-recurrence procedure for categorical data which essentially reflects the typical arrangement of categorical data, but implements the research or context dependent choice of what recurrence should entail based on some desired matching of categories in the two time series. Taking an embedding dimension of 1 and a delay of 1 for the phase space reconstruction usually works well (e.g. [15] [22]). Setting the radius or threshold to 0 classifies ‘perfect’ recurrence within the reconstructed phase space, articulating a matching choice where behavioral categories in the two time series need to be equal to qualify as recurrent. Other matching choices can also be understood in terms of the radius parameter, when one realizes that the reconstructed phase space for categorical data has a discrete topology and the radius parameter can only take integer values.

However, a more efficient and direct way to implement cross-matching and the subsequent chromatic quantification analysis is by means of the following procedure.¹

The basic parameterization outlined above actually entails that the CRP can be drawn without any formal phase space reconstruction. In fact, the CRP is constructed by plotting all congruent appearances of some pre-specified matching values within a pair of time series in a plane, by placing one of the time series along the horizontal axis and the other along the vertical axis. In this way the CRP represents all those instances when the behavioral state of one subsystem at some moment in time is matched appropriately by the behavioral state of the other subsystem at the same or any other moment in time during the observation. This essentially generalizes the canonical ‘recurrence’ notion by a more appropriate ‘behavioral matching’ notion, specified by the researcher beforehand on theoretical or practical grounds in a specific context. And since this can readily be executed for more than one combination of categories simultaneously, cross-matching enables the distinction between several kinds of behavioral matches. The different matches can be tracked by means of a color coding. A straightforward way to implement this is by constructing multiple cross-recurrence matrices $CR_{i,j}(color)$, one for each *color*. That is, one cross-recurrence matrix is constructed for each desired kind of match between the behavioral states of the dyadic partners on the two axes of the CRP. By applying this procedure, all recurrences of the different kinds of matching are represented by differently colored dots in the plane, resulting in a patchwork or multi-colored checkerboard CRP (see Figure 1).

A straightforward application of the cross-matching procedure can be found for instance in the context of turn-taking in a conversation. For instance, in a study by Reuzel et al. [12] [13], speech rhythms of two conversing people were analyzed, by tracking in their nonverbal time series those instances where only one of the interlocutors was talking (‘matches’) and marking as ‘non-matches’ those instance where both were talking or where both were silent. So recurrence was defined as ‘talking’ (code 1) in one time series and ‘silent’ (code 0) in the other. The other combinations (0-0 and 1-1) were non-recurrent. This characterization of interlocutors nonverbal behavioral matching provided a meaningful partitioning of this particular interaction. In this way, it was demonstrated that people achieved interactional synchrony in their speech rhythm, which was related to the perceived quality of the conversation.

¹ Note that recoding the data oftentimes will also do the trick. However, complex cases with multiple matches and non-matches require a more general and powerful approach. Interestingly, this also gives rise to a set of additional measures, as will become clear further on.

Figure 1. A patchwork or multi-colored checkerboard CRP produced by the cross-matching procedure, forming the basis for Chromatic CRQA. In this case two different matches of behavioral categories were distinguished, depicted by a red and blue color code, together with the non-matching white areas. (For more details see Section 2.3.)

2.2 Chromatic CRQA

Fundamental to regular CRQA is that the spatial layout of dots in the CRP gives rise to several interesting recurrence measures [23]. Together the recurrence measures reveal the hidden structure concealed in the shared dynamics of the interacting subsystems across all possible time scales. The simplest measure of Chromatic CRQA, based on multiple kinds of behavioral matching (i.e. colors in the CRP), is the *recurrence rate (RR)* of a *color*:

$$RR(colour) = \frac{1}{N^2} \sum_{i,j=1}^N \mathbf{CR}_{i,j}(colour), \quad (1)$$

where $\mathbf{CR}_{i,j}(color)$ are the cross-recurrence matrices underlying the CRP with respect to each individual *color*. $RR(color)$ quantifies the density of one kind of match of behavioral states in the CRP. In other words, $RR(color)$ reflects the extent to which the behaviors of one subsystem match those of the other subsystem in a specific way, across all possible time scales. As such, $RR(color)$ is a basic measure of the coordination between the two subsystems. Note that this definition equals that of the regular $RR(\epsilon)$, for some radius ϵ , when the canonical concept of recurrence is applied.

A related measure is the *relative recurrence rate* (rRR) of a *color*:

$$rRR(colour) = \frac{\sum_{i,j=1}^N \mathbf{CR}_{i,j}(colour)}{\sum_{colour} \sum_{i,j=1}^N \mathbf{CR}_{i,j}(colour)}, \quad (2)$$

quantifying which proportion of the entire amount of behavioral matches (i.e. all colored dots) is of a particular kind (i.e. of a specific *color*). In other words, $rRR(color)$ expresses the relative contribution of the different kinds of behavioral matches across all possible time scales to the overall coordination.

The other measures of Chromatic CRQA related to the diagonal and non-diagonal line structures in the CRP are straightforward generalizations of their regular definitions, which can be found, for instance, in [23]. Each of the measures can be calculated for the desired kinds of behavioral matches separately, that is, based on their respective cross-recurrence matrices $\mathbf{CR}_{i,j}(color)$. A number of the measures, viz. $rDET(color)$ and $rLAM(color)$ can also be calculated relative to all the colors included in the CRP, similar to $rRR(color)$ above.

2.3 Application of Chromatic CRQA: Children's dyadic problem solving

As an example application of Chromatic CRQA in the behavioral sciences, consider the following recent study on dyadic interaction between school-aged children in the context of science and technology education [24]. In six subsequent sessions over a period of 11 months, data was gathered about interpersonal behaviors of seven dyads of children with a mean age of 5.1 years, while they performed hands-on problem-solving tasks. For 20-25 minutes in each session, each child's individual interactive behaviors were coded at 1 Hz using five mutual exclusive behavioral categories: No work, Passive work, Copy work, Parallel work, and Collaborative work (for details see paper).

In this study the attractor dynamics of a small set of (predefined) quasi-stable states was analyzed, by applying Chromatic CRQA. To this end the five individual categories above, which potentially give rise to 25 a-priori combinations, were conceptually coarse grained by means of cross-matching into three dyadic attractor states 'distributed dyadic interaction' (DDI) and 'unequal dyadic interaction' (UDI) and 'no dyadic interaction' (NDI), which were tracked separately. It should be noted that not all combinations were possible. Children could not copy each other at the same time, and collaboration always involved both individuals.

Figure 2 shows the discrete state space of the dyadic interaction. DDI indicates that both children were actively engaged with the task and contributed to the solution. This dyadic interaction is the result of matching either collaborative-collaborative or parallel-parallel behaviors. UDI indicates that only one child was contributing to the solution while the other child was not active by the matching of three individual behaviors: parallel-no work, parallel-passive and parallel-copy. NDI refers to all other matches of behaviors that do not result in DDI or UDI. The result of the cross-matching procedure for one particular dyad is shown in Figure 1.

Figure 2. State space or ‘behavioral matrix’ of dyadic problem-solving, presenting the potential combinations of dyadic interaction states. The colored areas define the behavioral matches used for Chromatic CRQA. The axis values represent the individual behaviors: No work (1), Passive work (2), Copy work (3), Parallel work (4), and Collaborative work (5). DDI (*red*) corresponds to distributed dyadic interaction, UDI (*blue*) to unequal dyadic interaction, NDI to no dyadic interaction. The dashed areas indicate impossible combinations (i.e. non-matches), which entered the analysis in the same category as NDI.

The research questions of the study addressed how the dyadic interactions developed over six sessions in terms of the relative strength of the dyadic attractor states DDI, UDI and NDI, and how this attractor dynamics was related to task performance. In the confinement of this example we will only present the basic results with respect to coordination based on the relative recurrence rates of DDI, UDI, and NDI. The full article, however, also includes analyzes of other CRQA-measures concerning the non-diagonal line structures in the CRP [24].

As said, the recurrence rate provides a basic measure for the coordination between subsystem. To scale the degree of coordination and analyze the relative strength of the three quasi-stable states a baseline is needed. This baseline is readily provided by the discrete topology of the state space, with the color codes based on behavioral matching overlaying the 25 cells, as shown in Figure 2.

This generates a-priori probabilities for the relative recurrence rates $rRR(color)$ as follows: When *color* is *red* (DDI) the baseline is 8% (i.e. 2 of 25 cells), for *blue* (UDI) it is 24% (i.e. 6 of 25 cells), for *white* (NDI and other non-matches) it is 68% (i.e. 17 of 25 cells). If the empirical $rRR(color)$, especially $rRR(red)$ and $rRR(blue)$, significantly differ from these baselines this indicates coordination in the dyadic interaction. That is to say, children’s behavioral systems involved in the problem-solving task are governed by a shared dynamics, with a non-random, non-uniform coupling between subsystems.

Figure 3 shows the $rRR(color)$ of the two quasi-stable states DDI and UDI across all sessions, for four of the dyads in the study separately and averaged (dotted black line). It is clearly visible that $rRR(red)$, referring to DDI, is above baseline (full black line) for the entire series of six sessions. In contrast, $rRR(blue)$, referring to UDI, hovers around baseline (full black line). This makes DDI the predominant attractor state throughout the six observations. This basically implies that the distributed interactions remained more recurrent than the unequal interactions. This example briefly shows how Chromatic CRQA can reveal the coupling of both unequal and distributed ‘matches’ across all possible time scales and enables their comparison.

Figure 3. Relative recurrence rates, $rRR(red)$ and $rRR(blue)$, for the two quasi-stable states DDI and UDI, respectively, for four dyads, over the six sessions.

3 Anisotropic CRQA

3.1 Analysis of Anisotropic CRPs

As can be seen in Figure 1, most colored dots in the CRP are not isolated but arrange to form rectangular and line structures. The “checkerboard texture” in Figure 1 generally indicates recurrence domains which reveal metastability in the dynamics [25], an observation also made within the framework of symbolic dynamics [26] [27] [28] [29]. In fact, the predominant formation of non-diagonal structures, as opposed to diagonal structures, is a typical feature of categorical time series, and is obviously related to the discrete topology of the phase space. (Note that this also appears when applying canonical recurrence, without matching and the color

coding.) The rectangular and line structures provide information about the attractor dynamics of the interacting subsystems. They particularly inform about the strength and direction of the coupling between the two subsystems under investigation, as will be demonstrated later.

Thus far recurrence procedures have focused on diagonal lines with the measures *DET*, *MeanDiagLine*, *MaxDiagLine* and *ENT*, and vertical lines with measures *LAM*, *TT* and *MaxVertLine* ([23]; see below). However, as noted earlier, with categorical time series dots mostly do not appear on diagonal lines but rather are part of non-diagonal structures. In addition, it is clearly visible in Figure 1 that these non-diagonal line structures extend in two directions in the CRP, both horizontally as well as vertically. This directionality can potentially provide differential and complementary information about the coupling between the two subsystems represented by the time series along the two axes. Generally, line structures indicate instances where behavioral categories which are briefly expressed by one subsystem are accompanied by episodes of lingering in the matching behavioral category by the other subsystem. For instance, a vertical line structure in the CRP represents that a brief occurrence of some behavior in the time series along the horizontal axis is either followed (when above the Line-of-Synchrony) or preceded (when below the Line-of-Synchrony), with some delay, by a much longer occurrence of the matching behavior in the times series along the vertical axis.

Anisotropic CRQA, both in its cross-matching and cross-recurrence version, is founded on the general observation of anisotropy in the CRP, that is, on direction dependence along the two axes of the plot. Calculating the recurrence measures for the horizontal and vertical line structures separately, and allowing for their comparison, can easily be performed by first computing the transpose matrices, $\mathbf{CR}_{ij}^T(\text{color})$, of the cross-recurrence matrices $\mathbf{CR}_{ij}(\text{color})$. Subsequently, the algorithm ‘*tt*’ from Marwan’s crp toolbox for Matlab (available at <http://www.recurrence-plot.tk>) can be applied to all $\mathbf{CR}_{ij}(\text{color})$ as well as all $\mathbf{CR}_{ij}^T(\text{color})$. The ‘*tt*’ function computes the distribution of the length of the vertical line structures in the recurrence plot. Based on these distributions of both the vertical and the horizontal line lengths, the corresponding direction-specific non-diagonal CRQA-measures can be calculated. This will be explained below for canonical cross-recurrence (or: cross-matching of a single kind) for the sake of simplicity.

The first measure derived from the non-diagonal line structures is *laminarity*, defined as the proportion of colored dots that are part of a vertical (LAM_V) or horizontal (LAM_H) line structure. Laminarity reflects the degree to which subsystems are ‘trapped’ into expressing matching behaviors for some period of time. LAM_V depicts how much the subsystem on the vertical axis constitutes larger structures, whereas LAM_H does so for the subsystem on the horizontal axis. Second, *trapping time* is the average length of either the vertical (TT_V) or horizontal (TT_H) line structures. TT is measured in units of time and estimates how long subsystems are, on average, lingering in a specific state. If TT_V is high, the system on the vertical axis tends to be trapped in relatively long periods of the same behaviors that are matched by the subsystem on the horizontal axis at some point, and for high TT_H the system on the horizontal axis tends to be trapped in relatively long periods of the same behaviors that are also expressed by the other subsystem at

some point. Finally, *maximum line* also gives information about maximum duration of the non-diagonal line structures, with $MaxL_V$ being the length of the longest vertical line and $MaxL_H$ the length of the longest horizontal line. In other words, $MaxL$ measures the duration of the longest behavioral matching for each subsystems. High $MaxL_V$ means that the vertical subsystem is lingering for a long period in a single (matching) behavior, whereas $MaxL_H$ means that the horizontal subsystem lingers for a long period in a single (matching) behavior.

3.2 Application of Anisotropic CRQA: Asymmetric gestures-speech attunement

In this example, the data do not concern dyadic interaction as in the previous examples, but two behavioral dimensions. More specifically we were concerned with the verbal and nonverbal problem-solving skills of children. This example study of Anisotropic CRQA addresses the coupled dynamics of children’s gestures (i.e. manual kinesics and task manipulations) and speech as they construct cognitive understanding [30]. Contrary to the mainstream approach applied in most studies in this field, gestures were considered as in-the-moment actions, originating from an underlying complex dynamical system which is rooted in cognitive and perception-action subsystems. CRQA helps us to get a more detailed understanding of the role of gestures in learning and of their dynamic coordination with speech and cognitive processes.

The data of 12 children with a mean age of 5.4 years were analyzed. Children’s expressed gestures and speech during a hands-on science task were scored in a common metric, which was based on their skill level as defined by dynamic skill theory [31]. Within this theory, a total of ten hierarchically ordered levels of cognitive skills (either actions or verbalizations) can be distinguished, divided over three tiers: sensorimotor, representational, and abstract. Anisotropic CRQA was performed on the (categorical) skill-level time series of children’s gestures and speech. First the cross-matching as introduced above was applied: Skill levels of speech and gestures belonging to the same tier were considered behavioral matches of a specific kind. They received a designated color in the CRP, where blue was reserved for the sensorimotor tier, red for the representational tier, and green for the abstract tier. In Figure 4 an example CRP is shown of the coupled gesture-speech subsystems. Note that in the following presentation of part of the results the color coding does not play a role. In other words, in the context of this example the data were not subjected to Chromatic CRQA for the sake of brevity (however see [30] for a more extensive account).

Figure 4. Example CRP of the coupled gesture-speech subsystems for a single child, demonstrating the color coding for the three skill tiers used in the cross-matching procedure, with blue for sensorimotor, red for representational, and green for abstract (did not occur here). The child's speech is represented along the horizontal axis, gestures along the vertical axis.

Results of the Anisotropic CRQA on the vertical and horizontal line structures in the CRP, for all 12 children in the study are shown in Table 1. Monte Carlo permutation tests² revealed that all vertical line measures were significantly higher than the horizontal line measures (all p -values < .01), with respectable effect sizes: $d(LAM_V > LAM_H) = 2.01$; $d(TT_V > TT_H) = 1.72$; $d(MaxL_V > MaxL_H) = 1.31$. This was not only true at the group level, but also for all children separately for LAM and TT and for 9 out of 12 children also for $MaxL$. This finding reveals an asymmetric dynamic attunement of gestures and speech, with gestures relatively more regularly and more rigidly displaying the same-tier skill level compared to speech. For the proposed meaning in terms of the difference in coupling between gestures and speech, we refer to the simulation study in Section 4.

² These tests can readily be applied to small sample sizes or unequal groups of data, in this case to determine the statistical significance (p -value) of the differences between the line structures. The test repeatedly (e.g., 1000 times) compares the observed difference to the difference found within a range of simulated data drawn from the original sample. The p -value is computed by dividing the number of times the observed or a bigger difference occurs in these random samples by the number of drawn samples.

Table 1. Overview of *RR* and Anisotropic CRQA-measures (V = vertical lines; H = horizontal lines) of all 12 children in the study, not specified for color.

Child	<i>RR</i>	<i>LAM_V</i>	<i>LAM_H</i>	<i>TT_V</i>	<i>TT_H</i>	<i>MaxL_V</i>	<i>MaxL_H</i>
1	.013	0.99	0.91	5.2	3.4	21	7
2	.019	1.00	0.89	6.4	3.8	19	10
3	.004	0.97	0.69	4.3	2.6	12	3
4	.011	1.00	0.89	7.4	5.1	26	11
5	.002	0.89	0.90	3.2	3.1	5	6
6	.010	0.96	0.70	6.6	2.6	16	5
7	.009	0.98	0.92	5.8	4.0	18	12
8	.006	0.97	0.62	4.8	2.8	12	5
9	.025	0.99	0.92	6.3	5.1	15	15
10	.016	1.00	0.79	6.0	5.5	25	27
11	.002	0.96	0.63	5.4	2.7	18	3
12	.018	1.00	0.79	8.3	3.6	24	6
Mean	.011	0.98	0.81	5.8	3.7	17.6	9.2

4 Model Example of Anisotropic CRQA

In order to facilitate the interpretation of the Anisotropic CRQA-measures and to serve as a non-empirical illustration of Anisotropic CRQA on categorical time series, the following model of two time-discrete oscillators will briefly be explored:

$$\begin{aligned} y_1(n+1) &= \sin(\pi \cdot y_1(n)) + c_1 \sin(\pi \cdot y_2(n)), \\ y_2(n+1) &= \sin(\pi \cdot y_2(n)) + c_2 \sin(\pi \cdot y_1(n)). \end{aligned} \quad (3)$$

The model consists of a system of two coupled difference equations with coupling parameters c_1 and c_2 , which represent the coupling strength between the oscillators y_1 and y_2 .

The behavior of the model will be assessed in a coarse grained fashion to realistically simulate data as it is commonly collected in the behavioral sciences. Specifically, two dichotomous time series, x_1 and x_2 , will be constructed by applying the following rule:³

$$x_i(n) = \text{round} \left[\frac{y_i(n) - \min(y_i(n))}{\max(y_i(n)) - \min(y_i(n))} \right], \quad i \in \{1,2\}. \quad (4)$$

Although there is some resemblance with a Kuramoto model ([32] [33])⁴, this is by no means the incentive of the present simulations. However, a potential connection to human behavior would be, for instance, and without any claim of validity, two people's gazes during a conversation. The

³ This basically constructs a symbolic dynamics by introducing a static encoding of the time series (see e.g. [26] [27]).

⁴ In fact written in this way the system models a system of three asymmetrically coupled Kuramoto oscillators under a specific set of parameter settings, among which, in particular equal intrinsic frequency.

model articulates the (dichotomized) dynamics of the weakly coupled oculomotor and cognitive systems of the two individuals, in terms of a pair of nonlinear coupled oscillators. Variable y_1 represents one person's eye movements over time on some continuous spatial dimension and variable y_2 that of the other person. When transcribed at the behavioral level in terms of the distinct categories (1) looking at the other person's face and (2) looking away from it, which is not uncommon in the behavioral sciences (e.g. [9] [12] [13]; see also [7] [8]), the resulting time series x_1 and x_2 are dichotomous.

Simulations will focus on the relation between relative coupling strength in the model and the Anisotropic CRQA-measures, that is, the measures of vertical and horizontal line structures in the CRP. The CRP will be based on straightforward cross-recurrence of the discrete-time dichotomized time series x_1 and x_2 .

Model simulations for both the continuous and coarse-grained variables and the related CRPs of the dichotomous system are given in Figure 5, for two parameters settings, over 100 time steps, after transient. The parameter settings are drawn from a 'realistic' area of the parameters space (c_1, c_2) . The impression of being realistic is based on a visual comparison of time series and CRPs of the model outcomes and the empirical data encountered in previous studies (esp. [12] [13]). We admit that this reflects no robust mathematical or other kind of formal criterion at this point. However, we would like to stress once more that the model is not intended as a realist model of some type of behavior. It merely serves as a demonstration of Anisotropic CRQA and to provide some directions for interpretation of anisotropy in CRPs.

Figure 6 shows how the relative difference in coupling strength, $(c_1 - c_2) / (c_1 + c_2)$, is related to the relative difference in vertical and horizontal line measures LAM , TT and $MaxL$, in two separate and realistic parts of the parameters space. These graphs reveal a strong association between coupling and anisotropy, for the Anisotropic CRQA-measures LAM and TT but not for $MaxL$, in both parameter ranges.

Results like these remains difficult to interpret however, since the relation between coupling and synchronization in complex dynamical systems is not straightforward and might rely heavily on the specifics of the chosen model and parameter range (cf. [23]).

Figure 5. Time series and CRPs for (a) $c_1 = 3.0$ and $c_2 = 2.5$, with resulting $RR = 0.51$, vertical line measures $LAM_V = 0.73$, $TT_V = 3.88$, $MaxL_V = 9$, horizontal line measures $LAM_H = 0.62$, $TT_H = 2.38$, $MaxL_H = 4$, and (b) $c_1 = 1.8$ and $c_2 = 2.0$, with resulting $RR = 0.50$, vertical line measures $LAM_V = 0.73$, $TT_V = 3.46$, $MaxL_V = 6$, horizontal line measures $LAM_H = 0.65$, $TT_H = 2.82$, $MaxL_H = 6$.

5 Discussion

In the present chapter we tried to extend the existing recurrence procedures for the study of coupled dynamical systems which are measured on a nominal scale, by introducing two novel methodological variations: Chromatic CRQA, using cross-matching, and Anisotropic CRQA, based on anisotropy in the CRP. These advancements facilitate the study of a wider class of phenomena in the behavioral sciences and the detection of asymmetry in the dynamic organization of interpersonal behavior, respectively.

Several issues related to these procedures need to be developed further, in order for them to reach their full potential in the behavioral sciences. We will touch upon a few of these open-ends only briefly below. First, and foremost, the formal description as presented in this chapter should be extended and improved, with a focus on mathematical rigour and methodological completeness. This will allow the proposed methodological variations to be embedded in the larger framework of recurrence based methods (see [23]).

(a)

(b)

Figure 6. Relative difference in coupling strength $(c_1 - c_2) / (c_1 + c_2)$, for (a) $c_1 = 2$ and $c_2 \in \{1.5 : 0.05 : 2.5\}$ and (b) $c_1 = 4$ and $c_2 \in \{3.5 : 0.05 : 4.5\}$, on the horizontal axis, and its relation to the relative difference in vertical and horizontal line measures LAM , TT and $MaxL$, on the vertical axis.

Second, applying Chromatic CRQA and Anisotropic CRQA, especially when done conjointly, results in substantial increase in the amount of measures to be considered, compared to regular CRQA. Specifically, there is a new set of measures for each added behavioral match (i.e. color) and the number of measures almost doubles with the anisotropic analysis. However, the possibility of directly comparing the (relative) measures pertaining to the different kinds of matches in Chromatic CRQA reduces this problem to a large extent. Also, as already demonstrated, for Anisotropic CRQA, a focus on the (relative) differences of the anisotropic measures is probably the best way to express and detect asymmetries in the dynamics. The modeling approach initiated in Section 4 might be pursued further to find out which combinations of measures are most informative in specific contexts.

Third, subsequent efforts in the development of these procedures should look into the overlap between the anisotropic measures of rectangular structures. Since recurrent points within a rectangular structure are always part of both a horizontal line and vertical line at the same time,

they ‘count’ for the measures in both directions. This is not the case for isolated recurrent points, or for those that form a line. Distinguishing between rectangular and (actual) line structures might provide a more reliable estimate of the anisotropy in the CRP and of the coupling between subsystems. Another promising way to deal with this is to quantify the rectangular structures directly, for instance in terms of their ‘area’ (i.e. horizontal length $\times$ vertical length), ‘asymmetry’ (i.e. horizontal length divided by vertical length), number, entropy etcetera (cf. [34]).

Fourth, and finally, the application of the behavioral matching procedure and chromatic analysis to a single system measured on a nominal scale might be interesting to pursue as well. Chromatic RQA on one categorical time series would give additional and unique information about the structural connections between different behavioral modes of a system. It might even be possible to (in a way) reverse the technique, and use recurrence measures to detect which behavioral matches are most dynamically stable in the behavior. Finally, it is not unlikely that even Anisotropic RQA and Anisotropic CRQA of continuous times series might find an application within a specific research context.

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