




# Methodology for identification, visualization, and clustering of similar behaviors in dyadic sequences analyzed through the longitudinal actor-partner interdependence model with Markov chains

Mégane Bollenrucher<sup>a</sup>  , Joëlle Darwiche<sup>a</sup>  & Jean-Philippe Antonietti<sup>a</sup> 

<sup>a</sup>University of Lausanne, Switzerland

**Abstract** ■ The longitudinal actor-partner interdependence model (L-APIM) is frequently used to study dyadic relationships over time. When one deals with categorical longitudinal data, Markov chains emerge as a valuable analytical tool. This approach allows for the identification of interaction patterns in the L-APIM framework through the examination of the transition matrix. In the context of dyadic sample, investigating the similarity of behaviors between individuals becomes important. To address this question, visualization and grouping analysis are employed, providing valuable tools for discerning relationships with behavioral data. We introduce a novel methodological approach to ascertain such behavioral similarity using the probabilities into the transition matrix. In this article, we describe the utilization of multidimensional scaling and hierarchical clustering for identifying analogous behaviors within a dyadic sample. We illustrate the complete methodology using a simulated dataset. Codes in **R** language are included for implementation.

**Keywords** ■ Dyadic sequence; APIM model; Markov chains. **Tools** ■ R.

 [megane.bollenrucher@unil.ch](mailto:megane.bollenrucher@unil.ch)

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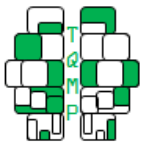
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## Introduction

The actor-partner interdependence model (APIM) is increasingly used to analyze data from two individuals, such as partners, friends, and parent and child (Kenny, 1996). The classic APIM can be used to analyze static behavior, including the influence of depression on marital satisfaction. When data is collected over several short periods, such as several successive days, the data reveals changes in the behavior of each individual over time while considering the mutual influence of each member of the dyad. An adaptation of the APIM, called the longitudinal actor-partner interdependence model (L-APIM), is used to analyze this data (Estrada et al., 2020). When the data are categorical, these dyadic sequences can be modeled using homogeneous Markov chains. When this method is adopted, the sequences are summarized in count matrices, which allow the probabilities transition matrix to be estimated as in the classic Markov chains setup (Bollenrucher et al., 2023).

L-APIM analysis allows for the identification of various interaction patterns: actor-partner (APM), actor-only (AM), partner-only (PM), and independence (IM). The APM is the general case, in which each individual's responses depend on that individual's and their partner's previous responses. The AM is characterized by responses hinging solely on the actor's previous answers, and the PM is marked by responses linked exclusively to their partner's previous answers. In the IM, the responses do not exhibit temporal dependence. When dyadic sequences are modeled using Markov chains, a test based on the maximum likelihood ratio is used to identify which interaction pattern each individual adopts (Bollenrucher et al., 2023). These different types of interaction patterns imply different processes in the dyadic relationship.

Consider the following example: Heterosexual romantic partners are questioned every day for a month about their sexual desire with the following question *Did you have sexual desire yesterday?* and they can answer *yes* or *no*. Fo-



cusing on the analysis of the woman's sequence, the likelihood ratio test is used to identify her interaction pattern. If the test indicates an APM, it means that actor and partner effects are considered. In other words, her previous answers and her spouse's previous answers influence the sequence of the woman. If the identified type is an AM, the spouse's answers have no effect. Respectively, if it is a PM, the woman answers have no effect. If the pattern of interaction is independent, neither actor nor partner influences the sequence. The type is identified at the individual level. The same analysis can be done on the man's sequence. This analysis is conducted on a unique dyad. However, in research, it is more common to collect data on a sample of individuals, or in this case, on a sample of dyads.

In unique case analysis, the focus is on examining intradyad consistency to determine whether both members of the dyad engage in similar types of interactions. The shift from unique to multiple case analysis is rooted in the desire to extend research questions and findings beyond intra dyad analysis (Kenny et al., 2020). Embracing a multiple case analysis approach facilitates the formulation of interdyadic research questions, such as understanding the differences between dyads or determining the characteristics common to individuals who share the same interaction pattern.

### ***Similarity and Dissimilarity in Dyadic Sequences***

The question of similar behaviors in the dyadic sample makes it possible to provide a more in-depth analysis than that of individual's interaction pattern. The focus can be on the similarity of behaviour between both members of the dyad, but also between each individual in the sample, allowing for an intra and inter dyad analysis' perspective. Consequently, it is necessary to establish a way of analyzing the similarity (or dissimilarity) between the behaviors of individuals summarized in probabilities transition matrices. Two complementary approaches are used to visualise and group similarities (Buja et al., 2008-06).

Multidimensional scaling (MDS) is used to visualize and reduce the dimensionality of data while preserving the pairwise similarity or dissimilarity relationships between data points (Borg & Groenen, 1997). The aim is to provide a low-dimensional representation of data points that maintains their relative distances or similarities as accurately as possible (Buja et al., 2008-06). In other words, MDS is used to create a visual representation that illustrates the measured distances between the transition matrices of each pair of individuals within the sample. The graphical representation provides an initial understanding of the level of similarity between individuals. Clustering analysis is used to group similar data points together based on certain characteristics or features (James et al., 2021). It is a data anal-

ysis technique that is intended to group similar data points together into clusters, in which points in the same cluster are more similar to each other than to those in other clusters (Hastie et al., 2009). The main goal of clustering is to highlight inherent patterns or structures within a dataset without requiring predefined labels (Hastie et al., 2009). The application of the MDS and the clustering into categorical dyadic sequences is intended to visualize and group the individuals based on their probabilities transition matrices because they contain all the information about the behavior during the sequence.

### ***Aims and Outline***

The main goal of this article is to develop a methodology to deal with a dyadic sample when the data are categorical sequences. This work is centered on the concept of similarity with the aim to identify, visualize and cluster individuals that share similar behavior. This approach complements the identification of each individual's interaction patterns. The procedure focuses on the importance of transition probabilities in the transition matrix. It is important to understand the impact of these probabilities on the graphical representation and the grouping of individuals. To develop this methodology, we will use multiple steps. To facilitate this work, we will exclusively use simulated data. In the initial section of the article, we will provide an explanation of the methodology, focusing on theoretical aspects of MDS and clustering. We will also analyze the impact of transition probabilities and its possible consequences on the various analyses proposed. In the second part, we propose a complete illustration of the methodology applicable for analyzing a sample of dyads. Finally, we will summarize the methodology and conclude with suggestions for future improvements.

### **Multidimensional Scaling and Clustering Analysis on Probabilities Transition Matrix**

#### ***Theoretical aspects***

#### *Some Recall on Markov Chains Modeling for L-APIM*

Markov chains can be adapted to model dyadic sequences (Bollenr ucher et al., 2023). The transition matrices are individual and are represented as in Equation 1 for each individual for a case with two possible states for the response, as in the example proposed above. Although each individual possesses a distinct transition matrix, it is constructed using conditional probabilities associated with the states in which both members of the dyad were present at the previous time point. We use the following notations:  $T$  for the length of the chains,  $t$  for any time measurement,  $S$  for the number of possible states, and  $s$  for any state. In this arti-



cle,  $S = 2$  because the possible answers to the question are *yes* or *no*.

$$TP = \begin{matrix} & & 1 & 2 \\ \begin{matrix} (1, 1) \\ (1, 2) \\ (2, 1) \\ (2, 2) \end{matrix} & \begin{pmatrix} p_{1|11} & p_{2|11} \\ p_{1|12} & p_{2|12} \\ p_{1|21} & p_{2|21} \\ p_{1|22} & p_{2|22} \end{pmatrix} \end{matrix} \quad (1)$$

For to each interaction pattern, namely APM, AM, PM, and IM, the structure of the transition matrix is different. The interaction pattern can be defined using a likelihood ratio test (LRT) (Bollenrucher et al., 2023).

Markov chains can be used to model the individuals' behavior in a transition matrix. By conducting an LRT test, the pattern of interaction derived from the APIM conceptual model can be identified. However, it is important to note that this information might necessitate additional analysis because individuals who fall under the same interaction type may exhibit variations in their behavior. For example, an individual may adopt a behavior oriented toward their partner while responding *yes* or *no* to the given question. The interaction pattern remains the same, but the transition probabilities are different. Equation 2 represents the transition matrix for a PM. The PM implies that only the state in which the partner was at time  $t - 1$  is considered. Consequently, lines 1 and 3 of Equation 2 are identical, as are lines 2 and 4. Therefore, the number of degrees of freedom in this equation is two. This equation can be written without conditional probabilities as in Equation 3, in which  $p_j$  can take any value between 0 and 1 and  $q_j$  is defined as  $1 - p_j$ . By forcing the transition probabilities to be the same depending on whether the individual was in state 1 or 2 at  $t - 1$ , the degree of freedom falls to one, as shown in Equation 4. Equations 5 and 6 illustrate cases in which  $p_1 \in (0.9, 0.1)$  and  $p_2 \in (0.7, 0.3)$ . Equations 7 and 8 illus-

trate the two distinct transition matrices that individuals can employ in cases of reciprocity, depending on whether  $p$  takes on values of 0.9 or 0.1. Although all four equations in the case with two degrees of freedom and the two equations in the case with one degree of freedom represent partner-oriented behavior, it is necessary to note that the transition probabilities in these matrices are entirely distinct. Consequently, the sequences corresponding to these matrices reflect different behavior. The individual could adopt an interaction pattern other than the partner-oriented pattern. The same kind of considerations about the matrices can be made for the APM and AM patterns, as shown in the Appendix. We will only develop the partner case in the article because it has fewer matrices than the APM while retaining the dyadic aspect.

$$TP^{PM} = \begin{matrix} & & 1 & 2 \\ \begin{matrix} (1, 1) \\ (1, 2) \\ (2, 1) \\ (2, 2) \end{matrix} & \begin{pmatrix} p_{1|\cdot 1} & p_{2|\cdot 1} \\ p_{1|\cdot 2} & p_{2|\cdot 2} \\ p_{1|\cdot 1} & p_{2|\cdot 1} \\ p_{1|\cdot 2} & p_{2|\cdot 2} \end{pmatrix} \end{matrix} \quad (2)$$

Equations 3 and 4 reveal that the partner-oriented transition matrix can be represented in two different forms depending on the number of degrees of freedom. Furthermore, the illustrative matrices show that the transition probabilities can take various values, resulting in numerous potential sequences. Hence, the key question centers around understanding how individuals in a sample of dyads group together when they share the same interaction pattern. Multidimensional scaling and clustering will be used to complete the analysis of the pattern of interaction. To assess the impact of the degree of freedom and the probabilities transition, we will conduct two analyses according to the degree of freedom and using various values

$$TP_{df=2}^{PM} = \begin{matrix} & & 1 & 2 \\ \begin{matrix} (1, 1) \\ (1, 2) \\ (2, 1) \\ (2, 2) \end{matrix} & \begin{pmatrix} p_1 & q_1 \\ q_2 & p_2 \\ p_1 & q_1 \\ q_2 & p_2 \end{pmatrix} \end{matrix} \quad (3)$$

$$TP_{df=1}^{PM} = \begin{matrix} & & 1 & 2 \\ \begin{matrix} (1, 1) \\ (1, 2) \\ (2, 1) \\ (2, 2) \end{matrix} & \begin{pmatrix} p & q \\ q & p \\ p & q \\ q & p \end{pmatrix} \end{matrix} \quad (4)$$

$$TP_{\substack{p_1=0.9, \\ p_2=0.7}}^{PM} = \begin{matrix} & & 1 & 2 \\ \begin{matrix} (1, 1) \\ (1, 2) \\ (2, 1) \\ (2, 2) \end{matrix} & \begin{pmatrix} 0.9 & 0.1 \\ 0.3 & 0.7 \\ 0.9 & 0.1 \\ 0.3 & 0.7 \end{pmatrix} \end{matrix} \quad (5)$$

$$TP_{\substack{p_1=0.1, \\ p_2=0.3}}^{PM} = \begin{matrix} & & 1 & 2 \\ \begin{matrix} (1, 1) \\ (1, 2) \\ (2, 1) \\ (2, 2) \end{matrix} & \begin{pmatrix} 0.1 & 0.9 \\ 0.7 & 0.3 \\ 0.1 & 0.9 \\ 0.7 & 0.3 \end{pmatrix} \end{matrix} \quad (6)$$

$$TP_{p=0.9}^{PM} = \begin{matrix} & & 1 & 2 \\ \begin{matrix} (1, 1) \\ (1, 2) \\ (2, 1) \\ (2, 2) \end{matrix} & \begin{pmatrix} 0.9 & 0.1 \\ 0.1 & 0.9 \\ 0.9 & 0.1 \\ 0.1 & 0.9 \end{pmatrix} \end{matrix} \quad (7)$$

$$TP_{p=0.1}^{PM} = \begin{matrix} & & 1 & 2 \\ \begin{matrix} (1, 1) \\ (1, 2) \\ (2, 1) \\ (2, 2) \end{matrix} & \begin{pmatrix} 0.1 & 0.9 \\ 0.9 & 0.1 \\ 0.1 & 0.9 \\ 0.9 & 0.1 \end{pmatrix} \end{matrix} \quad (8)$$



of  $p$ . The first analysis is done for the simplest case, namely the case with only one degree of freedom. The second analysis is done for the case with two degrees of freedom. The matrices presented before will be used to simulate the data. As they are represented only one pattern of interaction, we expect that individuals will be grouped according to the transition probabilities. Before delving into these analyses, we first address some general considerations regarding the two methods we employ.

### *Multidimensional scaling*

MDS is a statistical technique used in data analysis and visualization to represent the similarity or dissimilarity between a set of objects or data points in a lower-dimensional space (Borg & Groenen, 1997). It is essentially employed for visualizing complex relationships and patterns. At the first step, it is necessary to compute similarities or dissimilarities between the points. These could be distances, dissimilarity scores or similarity measures. This information is organized into a distance matrix, which quantifies the dissimilarity between each pair of objects in the dataset (Buja et al., 2008-06). The matrix is symmetric with zeros on the diagonal. MDS aims to reduce the dimensionality of the data while preserving the pairwise relationship as much as possible. The reduced-dimensional representation is used for visualization in  $2D$  or  $3D$ . Objects that are similar in the original dataset will be closer and those that are less similar will be farther. Hence, MDS is useful to understand the underlying structure of data (Borg & Groenen, 1997). Different algorithms, namely metric or non metric algorithm, exist to perform MDS depending on the nature of the data and the objectives.

In this work, we will calculate the Euclidean distance between the probabilities transition matrices between each individual in the sample before performing MDS to obtain a  $2D$  representation of the individuals' position. To calculate the distance between matrices, we use the `dist` function in **R**, and to calculate the multidimensional scaling, we use the `cmdscale` function.

### *Clustering Analysis*

Clustering is a fundamental concept in the field of data analysis and machine learning that helps reveal underlying structure in the data (James et al., 2021). It involves the process of categorizing data into classes based on their inherent attributes. It seeks to segment data points into clusters, where data points within the same cluster exhibit greater similarity to one another than to those residing in another clusters (Crane, 2014). This grouping process is driven by the notion that data points sharing similar characteristics should be closer in terms of metrics (Hastie et al., 2009). The distance metric measures the dissimilarity

between two data points (James et al., 2021). Multiple distance metrics exist. The most common are Euclidean distance, Manhattan distance, cosine similarity, and correlation distance (James et al., 2021; Hastie et al., 2009; Kaufman & Rousseeuw, 2009-09). Various clustering algorithms have been developed to address different types of data and objectives. Each method has its own strengths and limitations, making the choice of the appropriate algorithm dependent on the nature of the data and the specific goals of the analysis (Hastie et al., 2009). In this work, we use hierarchical clustering because it does not require prior knowledge about the number of clusters in the data, because it generates a hierarchy of clusters that can be cut at various levels.

Hierarchical clustering is the method used to group similar data points into nested clusters in a hierarchical manner using a tree-like structure (Kaufman & Rousseeuw, 2009-09). This tree-like structure is called a dendrogram (Hastie et al., 2009). This method can follow either an agglomerative (bottom-up) or divisible (top-down) approach (Cabezas et al., 2023). In the first case, each point in the database represents a cluster and the clusters are progressively grouped into larger clusters. In the second case, all the points in the database are in a single cluster, which is progressively split into smaller clusters. Visual analysis of the dendrogram provides insights into how the clustering algorithm operates on the data. Although it does not directly allow the optimal number of clusters to be chosen, it offers a general understanding of the clustering structure (Hastie et al., 2009). To determine the optimal number of clusters, additional factors need to be considered. The first is an index analysis (Charrad et al., 2014-09). In **R**, the `NbClust` library can be used to determine this number by considering several indices (Charrad et al., 2014-10). The second element is knowledge of the data, the assumptions made, and the trade-off between clusters that are too large or too small, which would compromise pattern discrimination. These elements can be enriched using the visual analysis provided by the MDS. Besides the way in which the cluster distance is calculated, the way in which the distance between data points is calculated is also important. The optimal solution to cut the tree on the dendrogram is linked with the linkage method. It defines how the distances between clusters are computed during the process. Multiple linkage methods exist such as single, complete, average, and Ward's linkage (Hastie et al., 2009). Because the linkage method determines how clusters are merged, the method's choice influences the clusters' size (Ward, 1963-03).

We perform clustering on the probabilities' distance matrix obtained before multidimensional scaling. We have chosen to use Ward's linkage method because it seems to be the most appropriate method according to the data. Indeed,

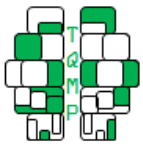
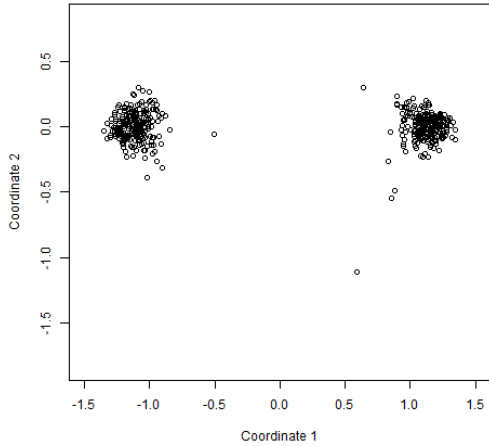
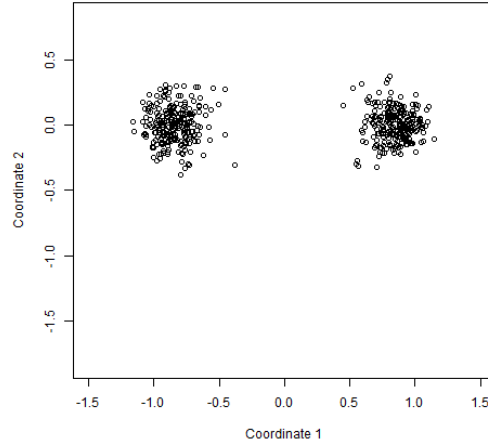


Figure 1 ■ Multidimensional scaling map for partner-only interaction pattern with different probabilities transition matrix.

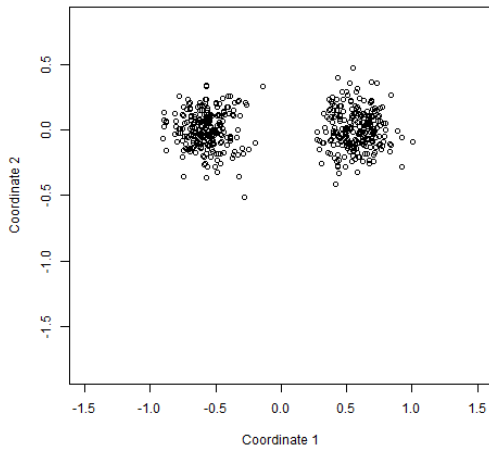
(a) Map for  $p \in (0.9, 0.1)$



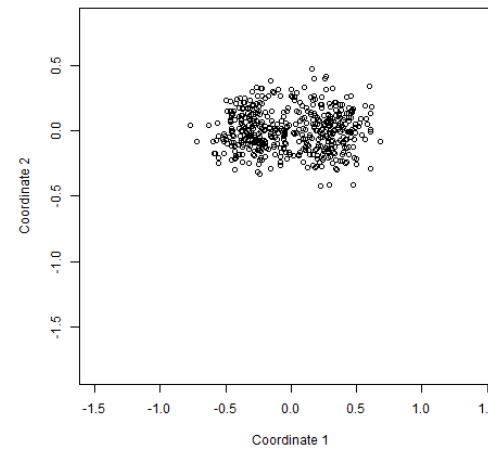
(b) Map for  $p \in (0.8, 0.2)$



(c) Map for  $p \in (0.7, 0.3)$



(d) Map for  $p \in (0.6, 0.4)$



it aims to create clusters that have minimal within-cluster variance, which leads to internally consistent clusters in term of probabilities. Moreover, Ward's linkage often leads to clusters that are easily interpretable. In R, we use the classic hclust function to perform agglomerative clustering with the specification for the method, with method="ward.D2".

### Influence Transition Probabilities

#### Case with one degree of freedom

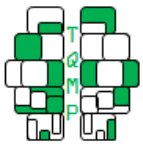
Equations 7 and 8 represent a situation in which the transition probabilities are notably distant from each other. Consequently, the sequences exhibit minimal variation. Returning to Equation 4, several cases and their reciprocals can be constructed by setting different values for p. To assess the impact of these transition probabilities' on the

differentiation of individuals' behavior, we will work with simulated data to cover several possible scenarios, namely  $p = 0.9, p = 0.8, p = 0.7, p = 0.6$ , as well as their reciprocals.

**Simulation Design.** The data are generated using the provided example, which involves the question *Did you experience sexual desire yesterday?* over a 90-day period. The possible answers are *yes* or *no*. This gives us the following data characteristics:  $T = 90$  and  $S = 2$ . Each database is simulated using 60 dyads.

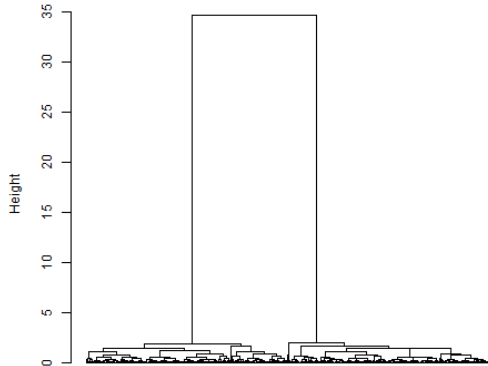
For each of the four scenarios outlined earlier, we generate databases encompassing all possible matrix interactions between the two individuals in a dyad. In the case of  $p = 0.9$  or  $p = 0.1$ , this entails creating databases in which both members possess a transition matrix akin to Equation 7, another set in which both members have a transition matrix similar to Equation 8, a third set in which women have



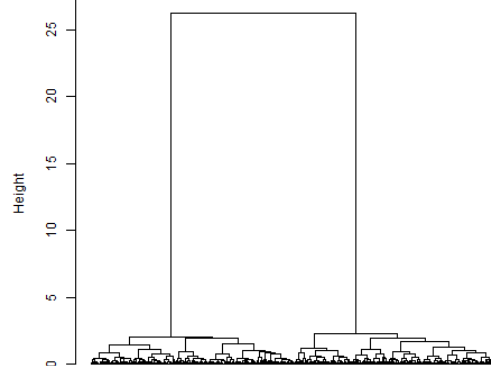


**Figure 2** ■ Dendrograms obtained during hierarchical clustering for partner-only interaction pattern with different probabilities transition matrix.

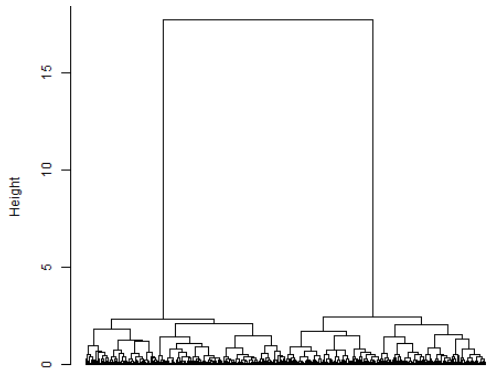
(a) Dendrogram for  $p \in (0.9, 0.1)$



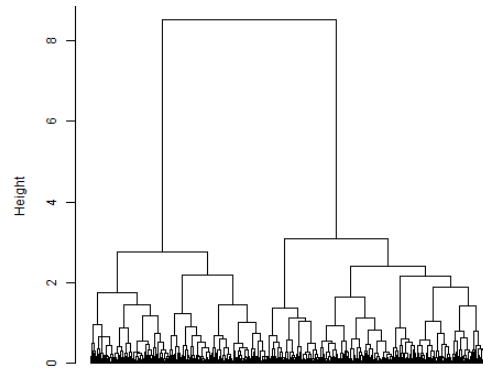
(b) Dendrogram for  $p \in (0.8, 0.2)$



(c) Dendrogram for  $p \in (0.7, 0.3)$



(d) Dendrogram for  $p \in (0.6, 0.4)$



a matrix resembling Equation 7 whereas men follow Equation 8, and lastly, a database reflecting the inverse of the previous configuration.

**Comparison for MDS.** Figure 1 shows a visual representation of the four simulated scenarios. With these four distinct scenarios, the initial observation from the figure indicates the existence of two groups instead of the anticipated four. The resulting hypothesis suggests that individuals are grouped based on the values of  $p$  rather than on combinations of transition matrices between the partners. This hypothesis means that the partner's only contribution is in the creation of the transition matrix. Once this transition matrix is done, the main element is the value of the transition probabilities. Moreover, it is evident that when transition probabilities exhibit significant disparities, as in the scenario presented in Figure 1a, two distinct groups of data points emerge. These clusters gradually draw closer together in the scenarios represented in Figures 1b and 1c, ultimately converging into essentially a single group in Figure 1d. This graphical representation yields several insights. First, it confirms the hypothesis that an addi-

tional analysis, complementary to the examination of interaction types, allows for the identification of varying behaviors in the same interaction pattern. Second, it shows that differentiation depends on the transition probabilities. When these probabilities are very close, reflecting a highly variable sequence, distinguishing between individuals becomes more challenging. In contrast, when the probabilities are notably different, individuals become more distinguishable from one another. Third, this visual representation leads to the assumption that clustering analysis will reveal two distinct clusters, effectively grouping individuals based on their transition probabilities. Moreover, it suggests that cluster membership derived from these probabilities will be more accurate when the probabilities exhibit significant disparities.

**Comparison for Clustering.** In the cluster analysis, the initial consideration is determining the appropriate number of clusters to apply. As mentioned previously, in the context of hierarchical clustering, this number can often be discerned by examining the dendrogram. Figure 2 shows the dendrograms for the four cases analyzed. It is evident



**Table 1** ■ Table of cluster membership with respect to the structure of the transition probabilities when both members of the dyad have a partner-only interaction pattern with a transition matrix with one degree of freedom

(a) Table of cluster membership with respect to the structure of the probabilities of transition for the case with  $p = 0.9$  and  $p = 0.1$

	$p_{fm} = 0.9$ $p_{sm} = 0.9$	$p_{fm} = 0.9$ $p_{sm} = 0.1$	$p_{fm} = 0.1$ $p_{sm} = 0.9$	$p_{fm} = 0.1$ $p_{sm} = 0.1$
Cluster 1	120	60	60	0
Cluster 2	0	60	60	120

(c) Table of cluster membership with respect to the structure of the probabilities of transition for the case with  $p = 0.7$  and  $p = 0.3$

	$p_{fm} = 0.7$ $p_{sm} = 0.7$	$p_{fm} = 0.7$ $p_{sm} = 0.3$	$p_{fm} = 0.3$ $p_{sm} = 0.7$	$p_{fm} = 0.3$ $p_{sm} = 0.3$
Cluster 1	120	60	60	0
Cluster 2	0	60	60	120

that in all scenarios, the most suitable number of clusters is two. This is the same result as the one obtained using the `NbClust` with the index of Calinski and Harabasz. We chose this index because it is one of the best performing (Charrad et al., 2014-09).

After we establish the appropriate number of clusters, the next step involves the analysis. In this context, each individual from the sample is assigned to a specific cluster. This allocation allows for an initial visual exploration, followed by an analysis of the relationship between the cluster affiliation of each individual and the structure of their respective transition matrix.

In Figure 3, the visual representation produced by MDS displays a map in which data points are color coded according to their assigned clusters. This visualization highlights that the clustering analysis has grouped the individuals according to their position on this map. Notably, in the first three scenarios, a distinct lack of color overlap implies a highly effective discrimination of individuals. In contrast, in the last scenario, some red and blue data points overlap, indicating that the discrimination is less effective.

Table 1 provides an overview of the number of individuals across clusters, taking into account the transition matrices of both members in the dyad. Examining the scenarios, it becomes apparent that Cluster 1 predominantly comprises individuals with transition matrices characterized by higher probabilities  $p$ , whereas Cluster 2 mainly consists of individuals with lower  $p$  values. To illustrate this with the previous example, we consider the cases of  $p = 0.9$  and  $p = 0.1$ . When both members of the dyad share a transition matrix resembling Equation 7, they are assigned to Cluster 1. Conversely, when both members of the dyad possess a transition matrix similar to Equation 8, they are assigned to

(b) Table of cluster membership with respect to the structure of the probabilities of transition for the case with  $p = 0.8$  and  $p = 0.2$

	$p_{fm} = 0.8$ $p_{sm} = 0.8$	$p_{fm} = 0.8$ $p_{sm} = 0.2$	$p_{fm} = 0.2$ $p_{sm} = 0.8$	$p_{fm} = 0.2$ $p_{sm} = 0.2$
Cluster 1	120	60	60	0
Cluster 2	0	60	60	120

(d) Table of cluster membership with respect to the structure of the probabilities of transition for the case with  $p = 0.6$  and  $p = 0.4$

	$p_{fm} = 0.6$ $p_{sm} = 0.6$	$p_{fm} = 0.6$ $p_{sm} = 0.4$	$p_{fm} = 0.4$ $p_{sm} = 0.6$	$p_{fm} = 0.4$ $p_{sm} = 0.4$
Cluster 1	114	69	66	17
Cluster 2	6	51	54	103

in Cluster 2. The same occurs true when the dyad members exhibit differing matrices. If women have a matrix akin to Equation 7 and men have one resembling Equation 8, the individuals are separated into the two clusters according to their matrix. Furthermore, the tables confirm the observations made with the visual analysis. In situations in which clusters are well separated, there is no misassignment. The overlapping points of Figure 3d are represented with the misassignment in Table 1d. Cluster 1 still predominantly encompasses transition matrices with high  $p$  values ( $p = 0.6$ ) but also includes some individuals with low  $p$  ( $p = 0.4$ ). A similar analysis applies to the second cluster. This indicates that the closer the transition probabilities are to  $\frac{1}{2}$ , the more challenging it becomes for the cluster analysis to distinguish between individuals.

In the case of one degree of freedom, the clustering analysis reveals that individuals tend to cluster based on their transition probabilities. This highlights that the combination of the dyads is not relevant. The next step is to show how clustering works when transition matrices have two degrees of freedom. The same analysis as previously proposed is conducted on a single scenario.

*Case with two degrees of freedom*

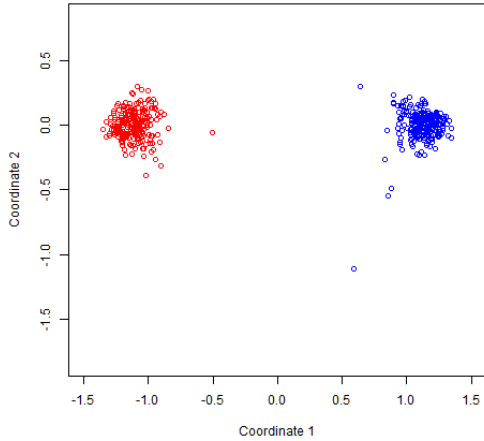
For the analysis with two degrees of freedom, we use the same case as before, namely transition matrices with partner interaction pattern. Equations 5 and 6 represent a case with two degrees of freedom. In Equation 5  $p_1 = 0.9$ , and  $p_2 = 0.7$  and in Equation 6 the counterpart is used with  $p_1 = 0.1$ , and  $p_2 = 0.3$ . We will use these matrices to simulate the data used for the analysis of clustering.

**Simulation Design.** The data are generated using the provided example, which involves the question *Did you experi-*

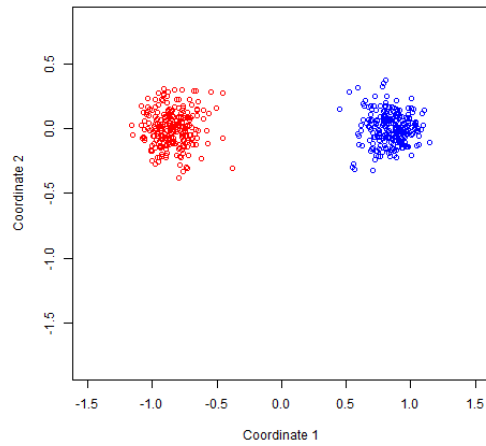


**Figure 3** ■ Clusters obtained from hierarchical clustering represented on the multidimensional scaling map for partner-only interaction pattern with different probabilities transition matrix. For each case, the red cluster groups together the individuals with the highest  $p$  value and the blue cluster those with the lowest  $p$  value.

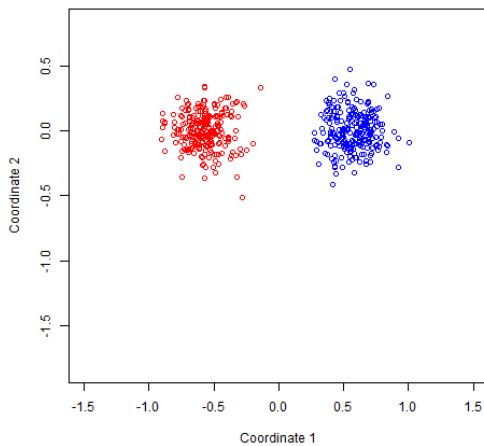
**(a)** Map for  $p \in (0.9, 0.1)$



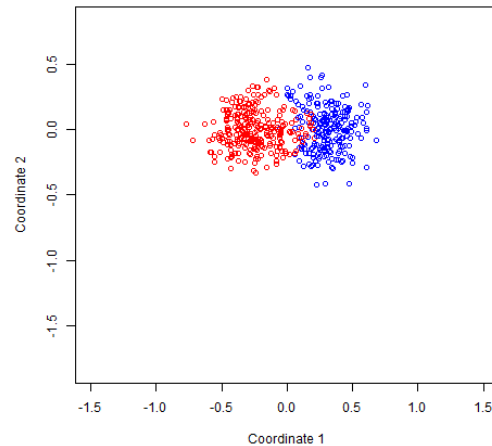
**(b)** Map for  $p \in (0.8, 0.2)$



**(c)** Map for  $p \in (0.7, 0.3)$



**(d)** Map for  $p \in (0.6, 0.4)$



ence sexual desire yesterday? over a 90-day period. The possible answers are *yes* or *no*. This gives us the following data characteristics:  $T = 90$  and  $S = 2$ . Each database is simulated using 60 dyads. As for the case with only one degree of freedom, the database is generated with the interaction of the transition matrix for the women and the men. The outcomes are very similar to the one obtained with only one degree of freedom.

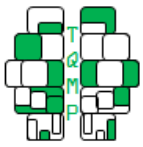
**Analysis.** Figure 4 shows the map from the MDS. There are essentially two groups with a few points further apart. Following a similar rationale as with one degree of freedom, we can assume that the data will segregate into two main groups.

Both the dendrogram, shown in Figure 5, and the algorithmic assessment of the optimal number of clusters lead

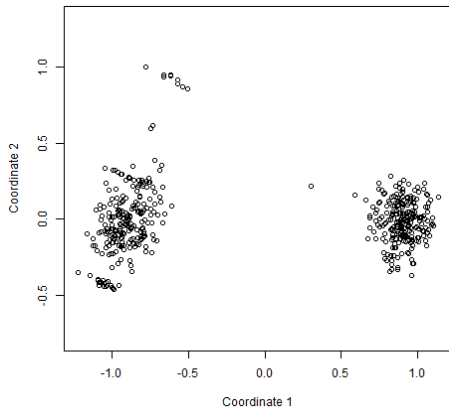
to the same conclusion: The data can be divided into two clusters. To advance the analysis and determine the cluster allocation for each individual, it is necessary to create a database with all this information. Once this step is accomplished, it is possible to color the map obtained with the MDS and analyze the constitution of the clusters according to the transition probabilities.

Figure 6 highlights that the clustering analysis has grouped the individuals according to their position without any overlap. Table 2 shows that the constitution of the probabilities transition matrix is decisive for clustering membership. Cluster 1 contains individuals with a transition matrix like Equation 5, whereas individuals with a transition matrix like Equation 6 are found in the second cluster.

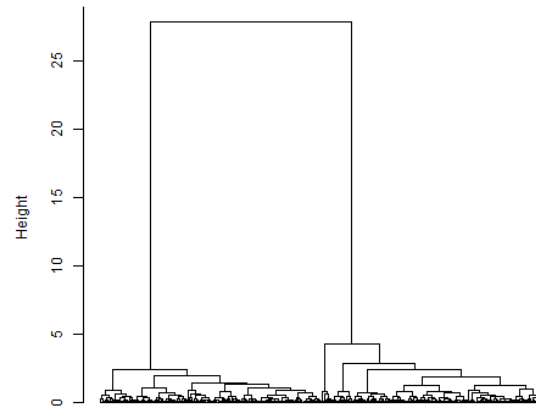




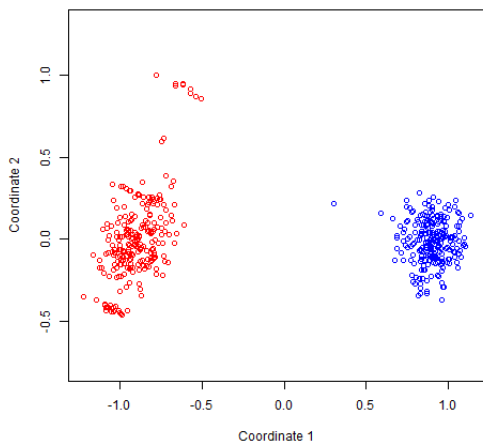
**Figure 4** ■ Multidimensional scaling map for partner-only interaction pattern for the case with two degrees of freedom.



**Figure 5** ■ Dendrogram obtained during hierarchical clustering for partner-only interaction pattern with two degrees of freedom



**Figure 6** ■ Clusters obtained from hierarchical clustering represented on the multidimensional scaling map for partner-only interaction pattern with two degrees of freedom



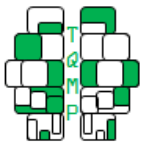
### Lessons from Validation

Our starting point was the hypothesis that individuals, despite adopting the same interaction pattern, might exhibit variations in behavior. These differences are reflected in the transition probabilities that constitute the transition matrix. The proposed analyses have demonstrated that the clustering of individuals depends on the probabilities of transition, even if these individuals share the same interaction's pattern. Whereas the structure of the transition matrix provides insights into interaction pattern the individuals adopt, the transition probabilities in the matrix allows for the grouping together individuals who behave in the same way. These analyses are therefore complementary. Several approaches can be used, depending on the

research questions or the results obtained. The clustering analysis can be conducted on the entire database or on a subsection exhibiting a particular type. Comparable findings can be drawn if an individual adopts any of the alternative interaction patterns.

Once individuals have been assigned to clusters, it is important to understand which transition matrix groups these individuals together. Various techniques can be employed for this purpose, such as identifying the transition matrix of the individual situated at the cluster's center or computing an average transition matrix derived from the transition matrices of all individuals in the cluster (Hastie et al., 2009). In this work, we use the average transition matrix to understand individuals behavior.

Similar results can be obtained with the other patterns



**Table 2** ■ Table of cluster membership with respect to the structure of the transition probabilities when both members of the dyad have a partner-only interaction pattern with a transition matrix with two degrees of freedom

	$p_{1fm} = 0.9$	$p_{1fm} = 0.9$	$p_{1fm} = 0.1$	$p_{1fm} = 0.1$
	$p_{2fm} = 0.7$	$p_{2fm} = 0.7$	$p_{2fm} = 0.3$	$p_{2fm} = 0.3$
	$p_{1sm} = 0.9$	$p_{1sm} = 0.1$	$p_{1sm} = 0.9$	$p_{1sm} = 0.1$
	$p_{2sm} = 0.7$	$p_{2sm} = 0.3$	$p_{2sm} = 0.7$	$p_{2sm} = 0.3$
Cluster 1	120	60	60	0
Cluster 2	0	60	60	120

of interaction. The transition matrices with one degree of freedom for the APM and APM can be found in the Appendix. We also provide comments explaining how to adapt them based on the degrees of freedom.

In this part, we employed a simulation case in which individuals' interaction patterns were known. In actual research analysis, these patterns are unknown and must be identified. The forthcoming illustration outlines the practical application of our methodology: first identifying the interaction patterns and then analyzing the groupings of individuals.

**Illustration**

**Database**

The database contains  $n = 120$  heterosexual dyads who answered the question *Did you have sexual desire yesterday* with two possible answers either *yes* or *no* for 90 consecutive days. We recoded the responses as follows: *yes* is recoded as 1, and *no* is recoded as 2. The aim of our analysis is to model these data using L-APIM and Markov chains. Initially, the aim will be to identify the interaction pattern adopted by the individuals in this database and, secondly, to analyze how the individuals group together.

**Analysis**

We identify the type by conducting a LRT (Bollenrucher et al., 2023). The underlying aim was to identify whether individuals are focused on themselves, their partner, or both when they respond. This table summarizes the information obtained from the test:

AM	APM	PM	IM
114	37	56	33

The majority of people in the database seem to adopt a behavior that is focused solely on themselves. In other words, they exhibit an AM interaction pattern. This was followed by partner-oriented behavior and behavior based on interaction between the two. We noted that some individuals follow an IM pattern of interaction. This means that these are individuals who have the same probability of transition regardless of their state at the previous time and of their

partner state. In other words, they behave as if the previous time did not affect their response at time  $t$ .

The visual representation of individuals through MDS, shown in Figure 7a, reveals the presence of three primary groups. Whereas two of these groups are relatively compact, the third appears more scattered, suggesting the possibility of further division into subgroups. This hypothesis is close to that of four clusters that could be made by analyzing the dendrogram in Figure 7b. The use of algorithmic analysis of the optimal number of clusters goes further is proposed to work with five clusters. This corresponds to a separation that can be observed by examining the dendrogram from a top-down perspective. The initial division cleaves the figure into two parts along the first coordinate. Upon closer examination of the right branch of the dendrogram, we found the two clusters on the left, whereas the left branch of the dendrogram reveals the separation of the cluster on the right into three distinct groups. Figure 7c shows that clustering distributes individuals according to their position on this map. Notably, there is no overlap of points in the blue and pink clusters, in contrast to the other three clusters, in which some overlap is evident. Given that clustering relies on transition probabilities, it is possible to assume that individuals belonging to the pink and blue clusters exhibit transition probabilities that differ significantly from those in the other clusters. On the other hand, the red, purple, and green clusters are more likely to contain individuals with transition probabilities that closely resemble each other.

Analysis of the distribution of interaction patterns in the clusters reveals distinct patterns. Clusters 1 and 5 predominantly consist of individuals with a self-oriented interaction, whereas Cluster 3 is primarily composed of individuals displaying a partner-oriented interaction. Individuals who exhibit APM are primarily concentrated in Cluster 3, whereas the IM is more prevalent in Cluster 4. Based on this distribution, we can assume that the average transition matrices within clusters are likely to exhibit a structure closely related to the predominant interaction type found in each cluster. Additionally, it is expected that two of the clusters will have transition matrices characteristic of the AM. Furthermore, the transition matrix of Cluster 4 should demon-

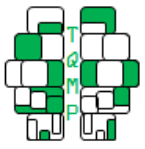
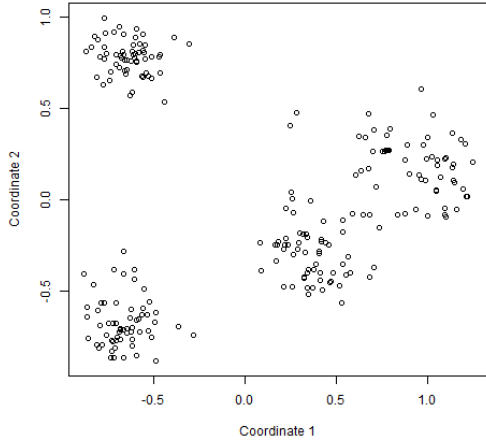
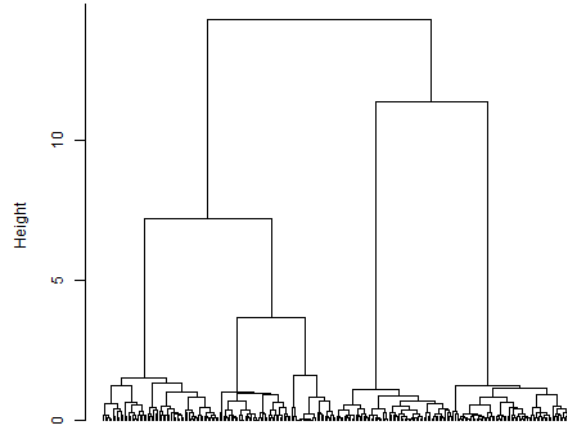


Figure 7 ■ Multidimensional scaling map for partner-only interaction pattern with different probabilities transition matrix

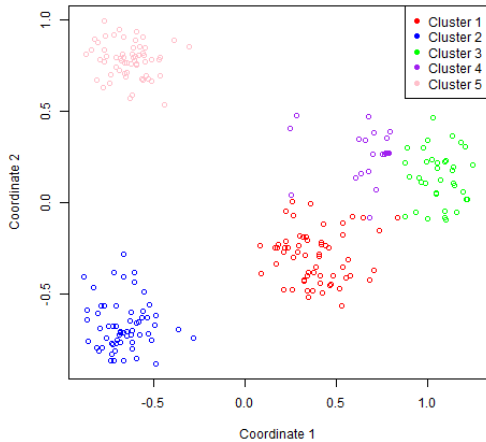
(a) Map from the multidimensional scaling



(b) Dendrogram from the hierarchical clustering



(c) Map from the multidimensional scaling colored with respect to the clusters



strate small variations in its columns, indicating a case in which the probabilities of transition are not related to the previous state.

Equations 9 to 13 are the average transition matrices, with in green the probabilities p when the degree of freedom is one or pj when they are two. Equations 9 to 13 represent the average probabilities transition matrices for each cluster. The purpose of analyzing these matrices is to gain insights into the behavior of individuals in these clusters. In the case of the first and fifth clusters, both exhibit an actor-only structure. In the first cluster's matrix, we observe that if an individual responded affirmatively in the previous state, there is a higher probability of them responding positively at time t + 1 and conversely for negative responses. We can approximate the probability, p, to be around 0.7, resulting in a matrix with one degree of free-

dom. Cluster 5 also exhibits an actor-only structure, as anticipated. However, the individuals in this cluster behave differently from those in cluster 1. This matrix has two degrees of freedom with p1 at 0.2 and p2 at 0.1. Notably, if individuals answered positively at time t, they have a high probability of responding negatively at time t + 1 and vice versa if they answered negatively at time t. Analyzing these two matrices highlights the point we previously raised: Individuals of the same interaction type can have distinct behaviors within that pattern. Cluster matrix 2 is the only one with a partner-only structure. It possesses only one degree of freedom, with p equal to 0.1, resulting in clearly separated transition probabilities. Cluster 3 represents an actor-partner matrix with one degree of freedom. In this case, individuals in the cluster tend to respond positively at time t + 1 if they answered affirmatively at time t, ex-



**Table 3** ■ Table with cluster’s effective with respect to each pattern of pattern of interaction

	AM	APM	PM	IM
Cluster 1	50	2	0	8
Cluster 2	0	6	54	0
Cluster 3	6	27	2	2
Cluster 4	0	0	0	23
Cluster 5	58	2	0	0

cept when both individuals answered negatively, in which case the predominant response at time  $t + 1$  is negative. The structure of matrix 4 closely resembles that of matrix 3, except that the transition probabilities in case (2, 2) are less distinct, which is why this type is identified as independent.

The analysis of interaction types and the average transition matrices resulting from clustering enabled us to identify several types of behavior in the sample of dyads. It becomes evident that the sample includes representations of the three main types of interaction as well as the less common independence type. Those exhibiting actor-only behavior tend to display two distinct behavioral tendencies whereas individuals with partner-only behavior exhibit similar patterns of behavior. In contrast, individuals with an actor-partner pattern have two different tendencies when both individuals answer *no* to the question asked.

**Conclusion and Further Directions**

By applying Markov chains modeling to examine dyadic sequences modeled by L-APIM, it is possible to identify the types of interaction pattern each individual adopts. However, the assignment of types does not offer a complete understanding of individual behavior. Therefore, it is necessary to investigate the similarities among individuals in a dyadic sample. Our article provides a comprehensive explanation of how multidimensional scaling and clustering analysis can be used to represent and identify group of individuals that shared similar behavior. In addition, we

include a step-by-step tutorial in **R** language to allow for the practical application of the complete methodology. The methodology proposed for the analysis of dyadic categorical sequences modeled with L-APIM can be succinctly outlined as follows:

1. Identification of interaction types using the LRT test.
2. Computation of transition probabilities and creation of a distance matrix.
3. Visualization of individuals in a 2D map through multidimensional scaling.
4. Hierarchical clustering and determination of the optimal number of clusters utilizing the algorithm the `NbClust` library provides.
5. Coloring the map based on clustering results, cluster analysis, and computation of average transition matrices.

We theoretically elaborated on these steps in the validation and illustrative sections, and the corresponding codes we provide in the Appendix.

The proposed methodology needs to be applied to empirical data from dyadic studies based on observational coding or questionnaires. Furthermore, when a survey is administered, it is generally common for individuals to be asked several questions. Consequently, our methodology needs to be developed further to consider the behavior of several individuals in response to several questions and to understand what type of analysis and conclusions can be obtained.

$$TP_{Cluster1} = \begin{matrix} & & 1 & 2 \\ \begin{matrix} (1, 1) \\ (1, 2) \\ (2, 1) \\ (2, 2) \end{matrix} & \begin{pmatrix} 0.693 & 0.307 \\ 0.671 & 0.329 \\ 0.322 & 0.678 \\ 0.322 & 0.678 \end{pmatrix} \end{matrix} \quad (9)$$

$$TP_{Cluster2} = \begin{matrix} & & 1 & 2 \\ \begin{matrix} (1, 1) \\ (1, 2) \\ (2, 1) \\ (2, 2) \end{matrix} & \begin{pmatrix} 0.110 & 0.890 \\ 0.882 & 0.118 \\ 0.118 & 0.882 \\ 0.891 & 0.109 \end{pmatrix} \end{matrix} \quad (10)$$

$$TP_{Cluster3} = \begin{matrix} & & 1 & 2 \\ \begin{matrix} (1, 1) \\ (1, 2) \\ (2, 1) \\ (2, 2) \end{matrix} & \begin{pmatrix} 0.892 & 0.108 \\ 0.895 & 0.105 \\ 0.874 & 0.126 \\ 0.083 & 0.917 \end{pmatrix} \end{matrix} \quad (11)$$

$$TP_{Cluster4} = \begin{matrix} & & 1 & 2 \\ \begin{matrix} (1, 1) \\ (1, 2) \\ (2, 1) \\ (2, 2) \end{matrix} & \begin{pmatrix} 0.902 & 0.098 \\ 0.922 & 0.078 \\ 0.936 & 0.064 \\ 0.565 & 0.435 \end{pmatrix} \end{matrix} \quad (12)$$

$$TP_{Cluster5} = \begin{matrix} & & 1 & 2 \\ \begin{matrix} (1, 1) \\ (1, 2) \\ (2, 1) \\ (2, 2) \end{matrix} & \begin{pmatrix} 0.195 & 0.805 \\ 0.193 & 0.807 \\ 0.889 & 0.111 \\ 0.906 & 0.094 \end{pmatrix} \end{matrix} \quad (13)$$



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Appendix

**Transition matrix with one degree of freedom for the actor-only pattern of interaction.** Equation A.1 represents the transition matrix with the actor-only pattern of interaction using the conditional transition probabilities. Equation A.2 is the same equation without the conditional probabilities and with only one degree of freedom. As for the partner-only case, a transition matrix can be written with two degrees of freedom.

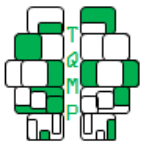
$$TP^{AM} = \begin{matrix} & \begin{matrix} 1 & 2 \end{matrix} \\ \begin{matrix} (1, 1) \\ (1, 2) \\ (2, 1) \\ (2, 2) \end{matrix} & \begin{pmatrix} p_{1|1\cdot} & p_{2|1\cdot} \\ p_{1|1\cdot} & p_{2|1\cdot} \\ p_{1|2\cdot} & p_{2|2\cdot} \\ p_{1|2\cdot} & p_{2|2\cdot} \end{pmatrix} \end{matrix} \quad (A.1)$$

$$TP_{df=1}^{AM} = \begin{matrix} & \begin{matrix} 1 & 2 \end{matrix} \\ \begin{matrix} (1, 1) \\ (1, 2) \\ (2, 1) \\ (2, 2) \end{matrix} & \begin{pmatrix} p & q \\ p & q \\ q & p \\ q & p \end{pmatrix} \end{matrix} \quad (A.2)$$

**Transition matrix with one degree of freedom for the actor-partner pattern of interaction.** Equation A.3 represents the transition matrix with the actor-partner pattern of interaction using the conditional transition probabilities. In contrast to the actor-only and partner-only cases, the equation for the actor-partner interaction pattern can be expressed in various forms without conditional probability and with one degree of freedom. Equations A.4 or A.8 depict the various possibilities, and each of these transition matrices can be formulated with different degrees of freedom.

$$TP^{APM} = \begin{matrix} & \begin{matrix} 1 & 2 \end{matrix} \\ \begin{matrix} (1, 1) \\ (1, 2) \\ (2, 1) \\ (2, 2) \end{matrix} & \begin{pmatrix} p_{1|11} & p_{2|11} \\ p_{1|12} & p_{2|12} \\ p_{1|21} & p_{2|21} \\ p_{1|22} & p_{2|22} \end{pmatrix} \end{matrix} \quad (A.3)$$

$$TP_{df=1}^{APM} = \begin{matrix} & \begin{matrix} 1 & 2 \end{matrix} \\ \begin{matrix} (1, 1) \\ (1, 2) \\ (2, 1) \\ (2, 2) \end{matrix} & \begin{pmatrix} p & q \\ p & q \\ p & q \\ q & p \end{pmatrix} \end{matrix} \quad (A.4)$$



$$TP_{df=1}^{APM} = \begin{matrix} & & 1 & 2 \\ \begin{matrix} (1,1) \\ (1,2) \\ (2,1) \\ (2,2) \end{matrix} & \begin{pmatrix} p & q \\ p & q \\ q & p \\ p & q \end{pmatrix} \end{matrix} \quad (\text{A.5})$$

$$TP_{df=1}^{APM} = \begin{matrix} & & 1 & 2 \\ \begin{matrix} (1,1) \\ (1,2) \\ (2,1) \\ (2,2) \end{matrix} & \begin{pmatrix} p & q \\ q & p \\ q & p \\ q & p \end{pmatrix} \end{matrix} \quad (\text{A.6})$$

$$TP_{df=1}^{APM} = \begin{matrix} & & 1 & 2 \\ \begin{matrix} (1,1) \\ (1,2) \\ (2,1) \\ (2,2) \end{matrix} & \begin{pmatrix} p & q \\ q & p \\ p & q \\ p & q \end{pmatrix} \end{matrix} \quad (\text{A.7})$$

$$TP_{df=1}^{APM} = \begin{matrix} & & 1 & 2 \\ \begin{matrix} (1,1) \\ (1,2) \\ (2,1) \\ (2,2) \end{matrix} & \begin{pmatrix} p & q \\ q & p \\ q & p \\ p & q \end{pmatrix} \end{matrix} \quad (\text{A.8})$$

**Comments on code 1: identification of the interaction pattern** This code corresponds to the initial step mentioned in the methodology summary, which focuses on type identification. The `FunctionsFiles` file is a **R** file containing all the functions needed to analyze categorical dyadic sequences with Markov chains. Following the loading of this file, the database must be loaded as well. Subsequently, the interaction type is detected and stored in a vector, which is then appended to the database. The grouped data can be used to assess the count of individuals falling into each identified pattern type.

**Listing 1: Identification of the interaction pattern**

```
source("FunctionsDyadicMarkov.R")
load(data.RData)
typeTest <- vector()
for(i in unique(data$dyad)) {
  fm <- as.numeric(data[data$dyad==i & data$members=="FM",1:90])
  sm <- as.numeric(data[data$dyad==i & data$members=="SM",1:90])
  fm.test <- intType(states = s, FM = fm, SM = sm, alpha = 0.05)
  sm.test <- intType(states = s, FM = sm, SM = fm, alpha = 0.05)
  typeTest <- append(typeTest, c(fm.test$type, sm.test$type))
}
data$typeTest <- typeTest
table(data$typeTest)
```

**Comments on code 2: extraction of the probabilities and computation of the distance matrix.** Based on the dataset, the transition probability vector of each individual is extracted directly from its matrix, which is initially estimated from the count matrix. The `dist` function is the function used to calculate the Euclidean distance between matrices.

**Listing 2: Probabilities transition matrix and distance matrix**

```
Prob <- NULL
for(d in 1:(nrow(data)/2)) {
  p1 <- c(mleEstimation(countEmp(s, as.numeric(unlist(data[(2*d - 1), 1:tm])),
    as.numeric(unlist(data[(2*d), 1:tm])))))
  p2 <- c(mleEstimation(countEmp(s, as.numeric(unlist(data[(2*d), 1:tm])),
    as.numeric(unlist(data[(2*d - 1), 1:tm])))))
  Prob <- rbind(rbind(Prob, p1), p2)
}
dissMat <- dist(as.data.frame(Prob))
```





**Comments on code 3: multidimensional scaling map.** The multidimensional scaling is computed directly on the distance matrix with the classic function `cmdscale`. The coordinates are extracted from the object. Then, the plot can be made. This plot represents the individuals on a map.

**Listing 3: Multidimensional scaling map**

```
cmd <- cmdscale(dissMat, eig = TRUE, k = 2)
x <- cmd$points[,1]
y <- cmd$points[,2]
plot(x, y, xlab = "Coordinate 1", ylab = "Coordinate 2", asp = 1)
```

**Comments on code 4: clustering.** The `hclust` function is used to obtain the hierarchical clustering dendrogram. Subsequently, the tree is cut according to the number of clusters required. To calculate the optimal number of clusters, the `NbClust` library needs to be loaded. This library includes an algorithm designed to identify the optimal number of clusters. As mentioned previously, the function can consider several linking methods and optimality indices. The references given for this library may be useful for modifying these arguments. Finally, the cluster membership vector is added to the database to facilitate analysis.

**Listing 4: Number of clusters**

```
library(NbClust)
optimalClust <- NbClust(as.data.frame(Prob), dist(as.data.frame(Prob)),
  method = "euclidean", distance = NULL, method = "ward.D2", index = "ch")
optimalClust$Best.nc[1]
optimalNb <- optimalClust$Best.nc[1]
res <- hclust(dissMat, method = "ward.D2")
plot(res, labels = FALSE, hang = -1, xlab = "Clusters")
clust <- cutree(res, optimalNb)
data <- cbind(data, cluster = clust)
```

**Comments on code 5: clusters analysis and mean transition matrix.** Several analyses need to be conducted once the clustering has been completed. The first step is to introduce color coding based on clusters in the visual map of individuals. This coloring allows to see whether the clusters are well separated from each other or whether there are overlaps. The second step it to assess the distribution of clusters concerning interaction types. This examination is conducted to identify potential patterns associated with various interaction types. The third step is to compute the average transition matrices and to analyze them. The matrices are rounded to three and one digits to facilitate the analysis of the degree of freedom.

**Listing 5: Analysis of the clusters and mean probabilities transition matrix**

```
table(data$cluster, data$typeTest)
plot(x, y, xlab = "Coordinate 1", ylab = "Coordinate 2", asp = 1,
  col = c("red", "blue", "green", "purple", "pink")[data$cluster])
legend(x = "topright",
  legend = c("Cluster 1", "Cluster 2", "Cluster 3", "Cluster 4", "Cluster 5"),
  col = c("red", "blue", "green", "purple", "pink"), pch = 16)
completeData <- cbind(data, as.data.frame(Prob))
meanTPC1 <- matrix(apply(completeData[completeData$cluster==1,
  (ncol(completeData)-8+1):ncol(completeData)], 2, FUN = mean),
  ncol = 2, byrow = FALSE)
meanTPC2 <- matrix(apply(completeData[completeData$cluster==2,
  (ncol(completeData)-8+1):ncol(completeData)], 2, FUN = mean),
  ncol = 2, byrow = FALSE)
```



```
meanTPC3 <- matrix(apply(completeData[completeData$cluster==3,
                        (ncol(completeData)-8+1):ncol(completeData)], 2, FUN = mean),
                  ncol = 2, byrow = FALSE)
meanTPC4 <- matrix(apply(completeData[completeData$cluster==4,
                        (ncol(completeData)-8+1):ncol(completeData)], 2, FUN = mean),
                  ncol = 2, byrow = FALSE)
meanTPC5 <- matrix(apply(completeData[completeData$cluster==5,
                        (ncol(completeData)-8+1):ncol(completeData)], 2, FUN = mean),
                  ncol = 2, byrow = FALSE)

round(meanTPC1, digits = 3)
round(meanTPC2, digits = 3)
round(meanTPC3, digits = 3)
round(meanTPC4, digits = 3)
round(meanTPC5, digits = 3)
```

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