Clustering Higher Order Data: 
Finite Mixtures of Multidimensional Arrays

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Abstract

An approach for clustering multi-way data is introduced based on a finite mixture of multidimensional arrays. Attention to the use of multidimensional arrays for clustering has thus far been limited to two-dimensional arrays, i.e., matrices or order-two tensors. Accordingly, this is the first paper to develop an approach for clustering $d$-dimensional arrays for $d > 2$ or, in other words, for clustering using order-$d$ tensors.

Keywords: Finite mixture model; higher-order data; model-based clustering; multidimensional array; tensor.

1 Introduction

There have been many examples of clustering multivariate (i.e., two-way) data using finite mixture models (see, e.g., reviews by [Fraley and Raftery, 2002] [Bouveyron and Brunet-Saumard, 2014] [McNicholas, 2016b]). More recently, there have been some notable examples of clustering three-way data using finite mixtures of matrix-variate distributions (e.g., [Viroli, 2011] [Anderlucci et al., 2015] [Gallaugher and McNicholas, 2018a]). This work on clustering three-way data is timely in the sense that the variety of data that require clustering continues to increase. Furthermore, there is no reason to believe that this need ends with three-way data. An approach for clustering multi-way data is introduced based on a finite mixture of multidimensional arrays. While some might refer to such structures as ‘tensors’, and so write about clustering tensor-variate data, we prefer the nomenclature multidimensional array to avoid confusion with the term ‘tensor’ as used in engineering and physics, e.g., tensor fields.

2 Background

2.1 Multidimensional arrays

Consider data arranged in a multidimensional array, or tensor. Herein, we restrict ourselves to data that can be regarded as the realization of continuous random variables. The number of dimensions a tensor has is referred to as its order. An order-$d$ tensor is equivalent, in our sense, to a $d$-dimensional array—the $d = 2$ structure is a matrix and the $d = 3$ structure can be regarded as a rectangular cuboid. A rectangular cuboid is defined as a three-dimensional box, where all the angles are right angles, all faces are rectangles, and opposite faces are equal [Harris and...
Multidimensional arrays can be partitioned into slices or matrices which are two-dimensional sections of a multidimensional array. This is done by fixing all but two dimensions of the multidimensional array. In general, \((d + 1)\)-way data can be represented using a \(d\)-dimensional array. Now, for clarity, consider the special case \(d = 3\).

### 2.2 Four-way data

Modern data collection technologies, like electronic sensors and cell phones, have created many rich sources of multivariate data. Often, these data can naturally be represented as four-way data, consisting of one three-dimensional array per subject. These three-dimensional arrays can be sliced into matrices, where the rows are typically time points or spatial locations and the columns describe individual measurements. Collections of these matrices can be stacked into three-dimensional arrays, where each frontal slice represents a matrix. Four-way data is a natural way to represent many sources of scientific data across disciplines. For example, four-way data can be a useful way to represent repeated measurements of various attributes over time at different years of a study. This is a common scenario in biostatistics, where multiple physical and health traits (physical activity, blood pressure, enzyme levels, etc.) are routinely measured over short periods of time (e.g., seven days) and these short periods may be repeated over a longer period of time (e.g., annually). Alternatively, four-way data could represent a sequence of still images from a video or measurements on different spatial locations over time.

### 2.3 Multilinear normal distribution

Recall that three-dimensional arrays are cuboids. Suppose there are \(p\), \(q\), \(r\) frontal slices. Let \(X = (x_{ijk}) : p \times q \times r\) be a three-dimensional array. The vectorization of the array \(X\) is defined as follows

\[
\text{vec}(X) = \sum_{i=1}^{p} \sum_{j=1}^{q} \sum_{k=1}^{r} x_{ijk} e_k^3 \otimes e_j^2 \otimes e_i^1, \tag{1}
\]

where \(x_{ijk}\) is \((i, j, k)\)th element of \(X\) and \(e_i^1\), \(e_j^2\) and \(e_k^3\) are unit basis vectors of size \(p\), \(q\) and \(r\), respectively. Assume that \(\text{vec}(X)\) follows a multivariate normal distribution with a double-separable covariance matrix defined as

\[
\Theta \otimes \Psi \otimes \Sigma,
\]

where \(\Theta_{r \times r}\), \(\Psi_{q \times q}\) and \(\Sigma_{p \times p}\) are covariance matrices for each dimension of the three-dimensional array. The double-separable model for \(X\) can be written

\[
\text{vec}(X) = \sum_{ijk} \mu_{ijk} e_k^3 \otimes e_j^2 \otimes e_i^1 + \sum_{ij} \sum_{ij'} \sum_{kk'} \sigma_{ii'} \psi_{jj'} \theta_{kk'} u_{ii'} u_{jj'} u_{kk'} e_k^3 \otimes e_j^2 \otimes e_i^1, \tag{2}
\]

where \(\Theta = \theta \theta^\top\), \(\Psi = \psi \psi^\top\), \(\Sigma = \sigma \sigma^\top\) and the \(u_{ii'} u_{jj'} u_{kk'}\) values are independent and identically distributed \(N(0, 1)\). This model allows the multilinear normal distribution (MLND), denoted \(N_{p,q,r}(\mathcal{M}, \Sigma, \Psi, \Theta)\), to have the following probability density function:

\[
f_{\text{MLND}}(X|\mathcal{M}, \Sigma, \Psi, \Theta) = (2\pi)^{-pqr/2} |\Sigma_i|^{-qr/2} |\Psi_i|^{-pr/2} |\Theta_i|^{-pq/2} \exp \left\{-\frac{1}{2} \text{vec}(X - \mathcal{M})^\top (\Theta \otimes \Psi \otimes \Sigma)^{-1} \text{vec}(X - \mathcal{M}) \right\}, \tag{3}
\]

where \(\mathcal{M}\) is a \(p \times q \times r\) mean array.
2.4 Finite mixture models

Clustering based on mixture models, known as model-based clustering, assumes a random variable \( X \) originates from a population of \( G \) sub-populations. In such a scenario, i.e., clustering, it is not known from which of the \( G \) sub-populations \( X \) arises. If the number of sub-populations is finite, the density of \( X \) is given by

\[
    f(x | \kappa) = \sum_{g=1}^{G} \pi_g f_g(x | \theta_g),
\]

(4)

where the \( \pi_g > 0 \) is the \( g \)th mixing proportion with \( \sum_{g=1}^{G} \pi_g = 1 \), \( f_g(x | \theta_g) \) is the \( g \)th component density with parameters \( \theta_g \), and \( \kappa = \{ \pi_g, \theta_g \}_{g=1}^{G} \) denotes all parameters of the mixture model. Detailed accounts of finite mixture models and their application for clustering can be found in McLachlan and Peel (2000) and McNicholas (2016a). For a mixture of three-dimensional arrays, the density of \( X \) is

\[
    f(X | \vartheta) = \sum_{g=1}^{G} \pi_g f_{\text{MLND}}(X | M_g, \Sigma_g, \Psi_g, \Theta_g),
\]

(5)

where \( \vartheta = \{ \pi_g, M_g, \Sigma_g, \Psi_g, \Theta_g \}_{g=1}^{G} \) represents the parameters of this mixture of MLNDs, each of which has the same interpretation as before. One can interpret \( \pi_g \) as the \textit{a priori} probability that the \( i \)th array \( X_i \) belongs to the \( g \)th component of the mixture.

3 Methodology

3.1 Matricizations

For simplicity of notation, remain with the case \( d = 3 \). We can matricize the three modes of the multidimensional array \( X \) (Kolda and Bader, 2009), which unfolds it to create a matrix for each mode. The matricizations for the first two modes are given by \( qr \times p \) dimensional

\[
    X = \sum_{ijk} x_{ijk} (e_k^3 \otimes e_j^2)(e_i^1)^\top
\]

and \( pr \times q \) dimensional

\[
    Y = \sum_{ijk} x_{ijk} (e_i^1 \otimes e_k^3)(e_j^2)^\top,
\]

respectively. Using these matricizations, we can decompose the expression

\[
    \text{vec}(X)^\top (\Theta \otimes \Psi \otimes \Sigma)^{-1} \text{vec}(X)
\]

into a trace. Denoting \( \tilde{X} = X - M_X \), where the matrix \( M_X \) is a \( qr \times p \) matricization of the mean multidimensional array, we can show the trace is

\[
    \text{vec}(\tilde{X})^\top (\Sigma \otimes \Theta \otimes \Psi)^{-1} \text{vec}(\tilde{X}) = \text{tr}\{\Sigma^{-1} \tilde{X}^\top (\Theta \otimes \Psi)^{-1} \tilde{X}\}.
\]

(6)

Noting that the identity matrix \( I_q = \sum_{j=1}^{q} e_j^2(e_j^2)^\top \) and that \( \Psi^{-\frac{1}{2}} \) is the Cholesky decomposition of \( \Psi^{-1} \), we can re-express the Kronecker product in (6) as follows:

\[
    \text{vec}(\tilde{X})^\top (\Sigma \otimes \Theta \otimes \Psi)^{-1} \text{vec}(\tilde{X}) = \sum_{j=1}^{q} \text{tr}\{\Sigma^{-1} X_j^\top \Theta^{-1} X_j\},
\]

(7)
where \( \mathbf{X}_j = (\mathbf{I}_r \otimes (\mathbf{e}_j^3)^\top \mathbf{\Psi}^{-\frac{1}{2}}) \mathbf{\bar{X}} \). A similar trace can be derived using matricizations for \( \mathbf{Y} \), to give

\[
\text{vec}(\mathbf{\bar{Y}})^\top (\mathbf{\Psi} \otimes \mathbf{\Sigma} \otimes \mathbf{\Theta})^{-1}\text{vec}(\mathbf{\bar{Y}}) = \sum_{k=1}^r \text{tr}\{\mathbf{\Psi}^{-1}\mathbf{Y}_k^\top \mathbf{\Sigma}^{-1}\mathbf{Y}_k\},
\]

where \( \mathbf{Y}_k = (\mathbf{I}_p \otimes (\mathbf{e}_k^3)^\top \mathbf{\Theta}^{-\frac{1}{2}}) \mathbf{\bar{Y}} \), \( \mathbf{\bar{Y}} = \mathbf{Y} - \mathbf{M}_Y \) and \( \mathbf{M}_Y \) is a \( pr \times q \) matricization of the mean array.

### 3.2 Likelihoods

Given a sample of \( N \) iid random three-dimensional arrays \( \mathbf{X}_1, \mathbf{X}_2, \ldots, \mathbf{X}_N \), the complete-data likelihood is given by

\[
\mathcal{L}_c(\vartheta) = \prod_{g=1}^G \prod_{i=1}^N \left[ \pi_g f_{\text{MLND}}(\mathbf{X}_i \mid \mathbf{\Theta}_g) \right]^{z_{ig}},
\]

where \( z_{ig} = 1 \) if \( \mathbf{X}_i \) belongs to component \( g \) and \( z_{ig} = 0 \) otherwise. Note that \( z_i = (z_{i1}, \ldots, z_{iG})' \) is considered a realization of a multinomial random variable with one draw on \( G \) categories and probabilities given by \( \pi_1, \ldots, \pi_G \). Taking the natural logarithm of the complete-data likelihood log-likelihood, we get

\[
\log \mathcal{L}_c(\vartheta) = \sum_{g=1}^G \sum_{i=1}^N z_{ig} \left[ \log \pi_g + \log f_{\text{MLND}}(\mathbf{X}_i \mid \mathbf{\Theta}_g) \right]
\]

(9)

We can further expand the complete-data log-likelihood as

\[
\log \mathcal{L}_c(\vartheta) = -\frac{Npr}{2} \log 2\pi + \sum_{g=1}^G n_g \log \pi_g \quad \text{and} \quad \sum_{g=1}^G \frac{qr}{2} n_g \log |\mathbf{\Sigma}_g| - \frac{pr}{2} \sum_{g=1}^G n_g \log |\mathbf{\Psi}_g| - \frac{pq}{2} \sum_{g=1}^G n_g \log |\mathbf{\Theta}_g| - \frac{1}{2} \sum_{g=1}^G \sum_{i=1}^N z_{ig} \text{tr}\left[\mathbf{\Sigma}_g^{-1}\mathbf{X}_{ig}^\top (\mathbf{\Theta}_g \otimes \mathbf{\Psi}_g)^{-1}\mathbf{X}_{ig}\right],
\]

(10)

where \( n_g = \sum_{i=1}^N z_{ig} \). Depending on the matricization we use, the final term in (10) can be expressed as either

\[
-\frac{1}{2} \sum_{g=1}^G \sum_{i=1}^N \sum_{j=1}^q z_{ig} \text{tr}\left[\mathbf{\Sigma}_g^{-1}\mathbf{X}_{ijg}^\top (\mathbf{\Theta}_g \otimes \mathbf{\Psi}_g)^{-1}\mathbf{X}_{ijg}\right]
\]

(11)

or

\[
-\frac{1}{2} \sum_{g=1}^G \sum_{i=1}^N \sum_{k=1}^r z_{ig} \text{tr}\left[\mathbf{\Psi}_g^{-1}\mathbf{Y}_{ikg}^\top \mathbf{\Sigma}_g^{-1}\mathbf{Y}_{ikg}\right].
\]

(12)

### 3.3 Parameter Estimation

#### 3.3.1 E- and M-steps

The parameters of the models described herein are all estimated by the method of maximum likelihood (ML). The ML estimates are found using the expectation-maximization (EM) algorithm, a two-step iterative algorithm used to calculate the parameter estimates in the presence of missing data [Dempster et al., 1977]. In the E-step, the expected value of the complete-data log-likelihood,
$Q$, is computed conditional on the current parameter estimates. In the M-step, $Q$ is maximized resulting in new, or updated, parameter estimates. The E- and M-steps are iterated until some stopping rule is satisfied (Section 3.3.2).

In our case, the E-step amounts to replacing the $z_{ig}$ values in (10) by the expectations

$$z_{ig} = \frac{\hat{\pi}_g f_{\text{MLND}}(X_i \mid \mathbf{M}_g, \Sigma_g, \Psi_g, \Theta_g)}{\sum_{h=1}^{G} \hat{\pi}_h f_{\text{MLND}}(X_i \mid \mathbf{M}_h, \Sigma_h, \Psi_h, \Theta_h)},$$

(13)

for $i = 1, \ldots, N$ and $g = 1, \ldots, G$. The M-step update for $\pi_g$ is given by $\hat{\pi}_g = \frac{n_g}{N}$. The M-step updates are available in closed form for $\mathbf{M}_g, \Sigma_g, \Psi_g$, and $\Theta_g$, and essentially follow from taking respective first derivatives of $Q$ and setting the resulting expressions to zero. The respective M-step updates for $\Sigma_g$ and $\Theta_g$ involve taking the first derivative of the $Q$ function that uses (11) as its final term. The updates are

$$\hat{\Sigma}_g = \frac{1}{\sqrt{qrn_g}} \sum_{i=1}^{N} \hat{z}_{ig} \sum_{j=1}^{q} (X'_{ijg} \Theta^{-1}_g X_{ijg})$$

(14)

and

$$\hat{\Theta}_g = \frac{1}{pqn_g} \sum_{i=1}^{N} \hat{z}_{ig} \sum_{j=1}^{q} (X_{ijg} \Sigma^{-1}_g X'_{ijg})$$

(15)

respectively. The update for $\Psi_g$ uses the $Q$ function that adopts (12) for its final term. The update is

$$\hat{\Psi}_g = \frac{1}{prn_g} \sum_{i=1}^{N} \hat{z}_{ig} \sum_{k=1}^{r} (Y'_{ikg} \Sigma^{-1}_g Y_{ikg})$$

(16)

The M-step update for the mean array $\mathbf{M}$, uses the $Q$ function equivalent to (10) and is given by

$$\hat{\mathbf{M}}_g = \frac{1}{n_g} \sum_{i=1}^{N} \hat{z}_{ig} \mathbf{X}_i,$$

(17)

where $\hat{\mathbf{M}}_g$ and $\mathbf{X}_i$ are $qr \times p$ matricizations of the estimated mean three-dimensional array, $\hat{\mathbf{M}}_g$ and the sample data arrays, $\mathbf{X}_i$ respectfully.

### 3.3.2 Stopping Rule

To stop our EM algorithms, we use a criterion based on the Aitken acceleration (Aitken, 1926). At iteration $t$ of the EM algorithm, the Aitken acceleration is

$$a^{(t)} = \frac{l^{(t+1)} - l^{(t)}}{l^{(t)} - l^{(t-1)}},$$

(18)

where $l^{(t)}$ is the (observed) log-likelihood at iteration $t$. Böhmig et al. (1994) use $a^{(t)}$ to calculate an asymptotic estimate of the log-likelihood at iteration $t + 1$:}

$$l^{\infty (t+1)} = l^{(t)} + \frac{1}{1 - a^{(t)}} (l^{(t+1)} - l^{(t)}).$$

(19)

We stop the EM algorithm when $l^{\infty (t+1)} - l^{(t)} < \epsilon$ (McNicholas et al., 2010).
3.4 Model Selection

The number of groups $G$ in a clustering problem is rarely known \textit{a priori}. Often, the parameters of a mixture model are estimated for different values of $G$ and some criterion is then used to select $G$. The most common choice for this criteria is the Bayesian information criteria (BIC; [Schwarz] 1978), which can be written

$$
\text{BIC} = 2l(\hat{\vartheta}) - \rho \log N, \quad (20)
$$

where $l(\hat{\vartheta})$ is the maximized log-likelihood, $\rho$ is the number of free parameters in the model and $N$ is the number of observations. For our finite mixture of multilinear normal distributions,

$$
\rho = (G - 1) + Gpqr + \frac{G}{2} \left[ p(p - 1) + q(q - 1) + r(r - 1) \right]. \quad (21)
$$

3.5 Identifiability

The covariance parameters in the Kronecker product are unique up to a strictly positive multiplicative constant. This is related to the fact that

$$
\Theta \otimes \Psi \otimes \Sigma = \left( \frac{1}{ab} \Theta \right) \otimes (a \Psi) \otimes (b \Sigma), \quad (22)
$$

for $a > 0$ and $b > 0$. Setting $a = 1/\psi_{11}$ and $b = 1/\sigma_{11}$ results in the first element of $\Psi$ and $\Sigma$, respectively, being equal to one which gives a unique parameterization. This constraint is imposed once the EM algorithm has converged.

3.6 Implementation

We have used version 1.1.0 of the Julia language ([Bezanson et al.] 2017; [McNicholas and Tait] 2019) to implement the finite mixture of MLNDs described herein. Typically data scientists choose the R language ([R Core Team] 2018) to implement their algorithms. We have deviated from the norm here because, for our purposes, Julia offers a number of advantages over R. Julia is a language specifically designed for numerical computing. It is a dynamic language which checks data types, modifies objects and functions at run-time and not compile time, making the users programming experience similar to R. Despite this, it has performance approaching statically typed languages like C and FORTRAN. Julia is perhaps a more desirable choice than R when fast run time speed is required, when implementing an algorithm from scratch, or when a parallel or distributed implementation is desired. The figures herein we made using Julia, using version 1.0.1 of the Gadfly visualization package ([Jones et al.] 2018).

4 Simulation

To verify the effectiveness of our proposed model, we undertake two simulation studies. The simulated data are generated using the following equation:

$$
\text{vec}(X) = \text{vec}(M) + (\Theta \otimes \Psi \otimes \Sigma)^{\frac{1}{2}} u, \quad (23)
$$

where the Cholesky decomposition of the Kronecker product of the covariance matrices is combined with $u$, a vector of iid $N(0,1)$ random numbers. A signal-to-noise ratio of four was applied
to the simulated data prior to analysis. The covariance parameters are generated by specifying a diagonal matrix of eigenvalues and a random orthogonal matrix and combining them as you would in an eigen-decomposition of the covariance matrix. The orthogonal matrix is created by generating $n^2$ iid $N(0,1)$ random values and orthogonalizing the $n \times n$ matrix with the QR decomposition. We restrict the condition number of these covariance matrices to be between 0.5 and 10. Additionally, the covariance matrix entries were scaled to resemble the entries obtained after applying the identifiability constraint. The EM algorithm used to generate the results was initialized with identity matrices for all the covariance matrix parameters. The values of $\hat{z}_{ig}$ are initialized randomly.

We examine the results of the simulation study in two ways. First, we determine how close the estimated model parameters are to the true parameters. We did this using a measure of relative error defined as follows:

$$\text{Relative Error} = \frac{\|\hat{\Delta} - \Delta\|_F}{\|\Delta\|_F},$$

where $\|\ast\|_F$ is the Frobenius norm of a matrix, $\hat{\Delta}$ is the estimated parameter value, and $\Delta$ is the true parameter value used to generate the simulated data. The smaller this ratio is, the less error is present in the model’s parameter estimates.

The group labels produced by the finite mixture model were compared to the simulated group labels via the adjusted Rand index (ARI; Hubert and Arabie, 1985). The Rand index is the ratio of the pair agreements to the total number of pairs (Rand, 1971). Chance agreement can enlarge the RI, making it difficult to interpret. The ARI corrects the Rand index for chance; it have an expected value of zero under random classification and retains the property of being equal to 1 when there is complete class agreement.

In the first simulation, we generate 150 three dimensional arrays from the MLND with $p = q = r = 4$. We used a two group model, where 75 observations were generated for each group. The groups have different mean array and covariance parameters. We repeated this process 250 times and ran our model for $G = 2, 3, 4$. Across the 250 data sets, the BIC always selected a $G = 2$ component solution with perfect classification and the EM algorithm converged on average in 5.6 iterations (Table 1).

| Metric   | Mean  | SD  |
|----------|-------|-----|
| BIC      | $-29295.1$ | 160.60 |
| Iterations | 5.6   | 2.36 |
| ARI      | 1     | 0   |

Table 1: Summary of results for the first simulation study, i.e., with $p = q = r = 4$. The mean multidimensional arrays are being estimated very precisely. The relative errors are visualized in Figure 1 a violin plot visualizing the distribution of the parameters relative errors between the two cluster groups. The errors are very small, well bellow 0.15 for both groups and bellow 0.05 for group 2.
Figures 1, 2, 3 and 4 illustrate the relative error in the covariance parameters. The errors for all the estimated covariance parameters are well below 1, indicating their close similarity to the true parameters. Group 1 tends to have larger errors in its $\Sigma$ and $\Theta$ parameters, which is likely due to the smaller Frobenius norms of the true group 1 $\Sigma$ and $\Theta$ matrices relative to their group 2 counterparts.

Figure 1: Relative errors for $M_g$ arrays from the first simulation study.

Figure 2: Relative errors for $\Sigma_g$ matrices from the first simulation study.
In the second simulation, we generate 50 three dimensional arrays from the MLND with \( p = q = r = 24 \). We used a two group model, where 25 observations were generated for each group. The groups have different mean arrays and covariance parameters. We repeated this process 150 times. Similarly to the first simulation, the finite mixture model always selected a two group solution as having the lowest BIC, the EM algorithm always converged in just three iterations, and labels produced by the model agreed perfectly with the labels from the simulated data (Table 4).
Table 2: Summary of results for the second simulation study, i.e., with $p = q = r = 24$.

| Metric   | Mean       | SD         |
|----------|------------|------------|
| BIC      | $-2.26 \times 10^6$ | $1.32 \times 10^5$ |
| Iterations | 3          | 0          |
| ARI      | 1          | 0          |

The relative error in the model parameters are visualized with empirical cumulative distribution function plots. They allow us to see what fraction of the relative errors are below a given value. Figure 5 indicates that the group 2 mean arrays are being estimated precisely. Nearly 90% of the group 1 mean array errors are under 1, with the overall distribution being more right skewed than group 2.

![Relative Error](image)

**Figure 5:** Relative errors for $M_g$ arrays from the second simulation study.

Figures 6, 7 and 8 illustrate the relative error in the covariance parameters. The relative errors in the $\Sigma$ and $\Theta$ parameters tend to have heavy right tails, with 80 to 90% of the values being below one. Given the increased dimensionality of the cuboids, applying some kind of regularization to these two covariance matrices could be beneficial. Despite the parameters heavy tailed error distributions, the model was able to perfectly recreate the data labels, a common goal of clustering in data science applications.
Figure 6: Relative errors for $\Sigma_g$ matrices from the second simulation study.

Figure 7: Relative errors for $\Psi_g$ matrices from the second simulation study.
5 Discussion

A finite mixture of multidimensional arrays approach has been introduced for clustering multi-way data. This work could be extended in several directions. For one, parsimony could be introduced by eigenvalue decomposition of the covariance matrices along the lines proposed by Banfield and Raftery (1993), Celeux and Govaert (1995) and Browne and McNicholas (2014). The approach of McNicholas and Murphy (2010) could be used to model longitudinal data directly by using a modified Cholesky decomposition on the relevant covariance matrix or matrices. A finite mixture of multidimensional array factor analyzers will be developed, and can be viewed as an extension of the work of Tang et al. (2013) and Gallaugher and McNicholas (2018b). Finally, one could consider a departure from the MLND and consider non-normal alternatives, either directly in an analogous fashion to the matrix variate work of Gallaugher and McNicholas (2017, 2018a) or via transformation in an analogous fashion to the work of Melnykov and Zhu (2018).

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