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Canonical Polyadic Decomposition based on joint eigenvalue decomposition

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Abstract

A direct algorithm based on Joint EigenValue Decomposition (JEVD) has been proposed to compute the Canonical Polyadic Decomposition (CPD) of multi-way arrays (tensors). The iterative part of our method is thus limited to the JEVD computation. At this occasion we also propose an original JEVD technique. Most of the iterative CPD algorithms such as ALS have been shown by means of practical studies to suffer from convergence problems (local minima, slow convergence or high computational cost per iteration). On the other hand, direct methods seem in practice to confine these disadvantages but impose some restrictive necessary conditions. In this context, our proposed algorithm involves less restrictive necessary conditions than other recent direct approaches and a limited computational complexity. It has been compared to reference (direct and non-direct) algorithms on synthetic arrays and real spectroscopic data. These numerical examples highlight the main advantages of the proposed methods to solve both the JEVD and CPD problems.

Keywords: multi-way arrays, direct canonical polyadic decomposition, PARAFAC, joint eigenvalue decomposition, fluorescence, over-factoring

1 1. Introduction

In this paper, we mainly propose a direct algorithm for the canonical polyadic decomposition of real or complex-valued tensors (assimilated to multi-way arrays) using the Joint EigenValue Decomposition (JEVD) of a set of non-defective matrices. The present contribution is actually twofold since we jointly propose an algorithm to solve the JEVD problem. Tensor decomposition plays a wider and wider role in numerous application areas such as Psychometric [1], Signal Processing for Biomedical Engineering [2, 3, 4], Sensor array [5, 6, 7], Arithmetic Complexity [8] and Chemometrics [9, 10]. Thanks to its uniqueness properties [11, 12, 13, 14, 15, 16],

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the polyadic decomposition introduced in 1927 by Hitchcock [17] is probably the most popular
 nowadays. In fact, it is now best known as CANonical DECOMPosition (CANDECOMP) [1],
 PARAIlel FACtor analysis (PARAFAC) [18] or CANDECOMP/PARAFAC (CP). In order to
 be consistent and honor the original work we will keep the acronym CPD, which stands for
 Canonical Polyadic Decomposition.

More precisely, a polyadic decomposition of an array is a sum of rank-one terms that yields an exact fit [17]. The CPD is then defined as the minimal polyadic decomposition. The rank of an array may be thus defined as the minimal number of rank-1 tensors needed to achieve the CPD.

Many algorithms have been proposed in order to compute the CPD of multi-way arrays. One 18 of the most famous algorithms, due to its speed and ease of implementation, resorts to an iter-19 ative Alternating Least Squares (ALS) procedure [18]. Other iterative algorithms based on first 20 and second order optimization methods such as gradient, Gauss-Newton, Levenberg-Marquardt 21 or conjugate gradient have also been proposed (see [19] [20, 21, 22] for a full comparison). 22 Recently, a set of iterative algorithms based on a reduced functional has been introduced in 23 [23]. These last algorithms bring qualitative information on the solution but the counter part is a 24 longer computational time. Furthermore, an Enhanced Line Search (ELS) procedure has been 25 proposed in [24] in order to speed up the ALS algorithm. ELS extension to other iterative CPD 26 algorithm and efficiency of the ALS-ELS algorithm has been highlighted in [21]. However, in 27 spite of this refinement, the ALS algorithm suffers from a classical drawback. Indeed, nothing 28 ensures its global convergence and it can be stuck in local minima. More generaly, iterative 29 approaches show convergence problems when several factors of the CPD are correlated. 30

In the meantime, a few direct approaches have been proposed. One can mention the DTLD 31 approach [25]. However it is restricted to three-way arrays and provide poor results [26, 20]. 32 Thereby this kind of solution is generally used as a way of initializing iterative methods. Other 33 direct approaches have been proposed in the literature as well but not yet compared numerically 34 in studies such as the ones mentioned above. These methods rephrase the CPD as the simul-35 taneous diagonalization, by equivalence [27, 28, 29] or congruence [15], of a set of matrices. 36 The CPD problem can also be translated into a simultaneous generalized Schur decomposition, 37 with orthogonal unknowns, as shown in [29]. Direct methods compute the CPD by solving an 38 alternative algebra problem of lower dimensions but they do not provide a solution in terms of 39 least squares contrarily to the ALS and derivative-based techniques. The reformulated problem 40 is usually solved by means of a Jacobi-like procedure. 41

We thus propose here a new formulation of the CPD as a JEVD problem leading to a novel 42 direct solution, named DIAG (DIrect AlGorithm for canonical polyadic decomposition), involv-43 ing less restrictive necessary conditions than the "Closed Form Solution" (CFS) presented in 44 [27, 28]. Recall that the CFS algorithm requires that the rank of the considered CPD array does 45 not exceed two of the dimensions of the array. At this occasion we also propose an original 46 Jacobi-like JEVD algorithm, called JDTM (Joint Diagonalization algorithm based on Target-47 ing hyperbolic Matrices). Numerical examples highlight the main advantages of the proposed 48 methods to solve the JEVD and CPD problems. Note that the DIAG method can be seen as 49 a generalization of the BIOME approach [30] to the case of unsymmetric arrays. JDTM and 50 DIAG have been presented briefly in two separate conference papers [31, 32], respectively. In 51 [32] DIAG was associated to another JEVD algorithm and was called SALT (SemiALgebraic 52 Tensor decomposition). The present paper details theoretical aspects of both algorithms in sec-53 tions 2 and 3, respectively including their extension to the complex case which is not trivial and 54

their computational complexity. In addition subsection 3.5 is dedicated to the comparison of necessary conditions of different CPD algorithms, namely ALS, CFS and DIAG . Numerical results are also emphasized in section 4 which illustrate the main features of the DIAG approach, notably the problem of over-factoring is addressed. Finally a concrete application to fluorescence spectroscopy is proposed in section 5.

60 2. Joint eigenvalue decomposition of non-defective matrices

We use the following consistent notations in the whole paper: vectors, matrices and tensors 61 are denoted by lower case boldface (a), upper case boldface (A) and upper case boldface calli-62 graphic (\mathcal{A}) letters respectively. The *i*-th entry of vector **a** is denoted by a_i while A_{ij} is the (i, j)-63 th component of matrix A. Entry (i_1, \ldots, i_Q) of any Q-order tensor $\mathcal{T} \in \mathbb{R}^{I_1 \times \cdots \times I_Q}$ or $\mathbb{C}^{I_1 \times \cdots \times I_Q}$ 64 (Q > 2) is denoted by $\mathcal{T}_{i_1, \dots, i_Q}$. Outer product, Kronecker product and Khatri-Rao product are 65 denoted by o, \otimes and \odot , respectively. Moore-Penrose matrix inverse, euclidean and frobenius 66 norm are denoted by \sharp , $\|\boldsymbol{E}^{(k)}\|_F$ and $\|.\|_F$, respectively. We define $[x; y]_N = [x; y] \cap \mathbb{N}$. [.] denotes 67 the floor function. Complex modulus and conjugate of any complex z are denoted by |z| and \overline{z} 68 respectively. The imaginary unit is denoted by *i*. 69 Givens and hyperbolic rotation matrices are denoted by G and H, respectively. For instance in 70

the real case, $G(\theta_{ij})$ and $H(\phi_{ij})$ are equal to the identity matrix, at the exception of the elements:

$$G(\theta_{ij})_{ii} = G(\theta_{ij})_{jj} = \cos(\theta_{ij}) \qquad \qquad G(\theta_{ij})_{ij} = -G(\theta_{ij})_{ji} = \sin(\theta_{ij}) \\ H(\phi_{ij})_{ii} = H(\phi_{ij})_{ji} = \cosh(\phi_{ij}) \qquad \qquad H(\phi_{ij})_{ij} = H(\phi_{ij})_{ji} = \sinh(\phi_{ij})$$

The JEVD problem consists in finding an eigenvector matrix A from a set of non-defective matrices $M^{(k)}$ satisfying:

$$\forall k \in [1; K]_{\mathbb{N}}, \ \boldsymbol{M}^{(k)} = \boldsymbol{A} \boldsymbol{D}^{(k)} \boldsymbol{A}^{-1}, \tag{1}$$

where the K diagonal matrices $D^{(k)}$ are unknown. One could solve these EVDs separately, and 74 retain the solution that leads to the best estimate regarding the considered application. However, 75 as explained in [29], it is safer from a numerical point of view to decompose the K matrices 76 $M^{(k)}$ simultaneously, in some optimal sense, especially when the perturbation of these matrices 77 may have caused eigenvalues to cross each other. Indeed, in practice only noisy observations 78 of the K matrices $M^{(k)}$ are clustered and it is well known that, when eigenvalues are close, the 79 eigenvectors in a single EVD may be strongly affected by small perturbations [33]. The reason is 80 that for coinciding eigenvalues only the corresponding eigenspace is defined; different directions 81 in this subspace will emerge as eigenvectors for different infinitesimal perturbations. When this 82 happens for one or more of the matrices in the JEVD problem, the other matrices may still allow 83 to identify the actual eigenvectors. This follows theorem proved in [29]: 84

Theorem 1. The JEVD is unique up to a permutation and a scaling of the columns of A if and only if all the columns of the $K \times N$ matrix E, whose (k, n)-th component $E_{k,n}$ is equal to $D_{n,n}^{(k)}$, are not proportional.

⁸⁸ Note that in order to ensure uniqueness of the JEVD up to permutation and scale indeterminacies, ⁸⁹ we will assume in the sequel that the *K* involved diagonal matrices $D^{(k)}$ fulfil the condition given ⁹⁰ in Theorem 1.

Few papers have proposed numerical solutions to the JEVD problem. All of them adapted Jacobi's principle to the search for a non-singular and non-necessarily orthogonal eigenmatrix *A* ⁹³ by using a suitable factorization, which is not reduced to the product of Givens matrices. This
 ⁹⁴ domination of Jacobi-like methods is due to their good convergence properties [34].

Two main kinds of Jacobi-like algorithms have been developed in this context, based on dif-95 ferent matrix factorizations. Originally, several authors had recourse to the QR factorization of A 96 in order to compute the different sets of eigenvalues [35, 36]. Arguing that these QR-algorithms 97 suffer from convergence problems, Fu and Gao proposed an effective sh-rt algorithm [37] based 98 on the polar decomposition. Indeed the polar decomposition has been used favourably for eigenqq value decomposition purpose since a long time [38, 39, 34] and also for joint diagonalization 100 by congruence [40]. Then the JUST algorithm was introduced in [41] as a variation of the sh-rt 101 approach for which the iterative computation of the hyperbolic matrix is made by minimizing an 102 alternative criterion. We propose here a third criterion and an appropriate optimization method, 103 giving birth to the JDTM algorithm. Another JEVD approach based on LU factorization and 104 called JET was introduced in [32] for real-valued matrices. 105

The real case is addressed in the three following subsections. The extension to the complex case
 is described in subsection 2.4. JDTM algorithm has been compared to JUST and sh-rt algorithms
 in various situations involving real matrices. Significant numerical results are given in section
 4.1.

110

111 2.1. A Jacobi-like process

In this subsection, all matrices are square matrices of order N. Polar matrix decomposition 112 states that any non-singular real matrix can be factorized into the product of an orthogonal matrix 113 Q and a symmetric positive semidefinite matrix S. It is well known that Q can be decomposed 114 into a product of Givens rotation matrices $G(\theta_{ij})$ and a unitary diagonal matrix. In the same way, 115 it has been shown that S can be decomposed into a product of hyperbolic rotation matrices $H(\phi_{ij})$ 116 and diagonal matrices [40]. Thereby, due to the indeterminacies of the JEVD problem mentioned 117 in theorem 1 and taking into account that diagonal, hyperbolic and Givens matrices commute, 118 the matrix A solving the JEVD problem given by (1) can be chosen as a product of Givens and 119 hyperbolic rotation matrices: 120

$$\mathbf{A} = \prod_{i=1}^{N-1} \prod_{j=i+1}^{N} \boldsymbol{G}(\theta_{ij}) \boldsymbol{H}(\phi_{ij}).$$
(2)

Inserting (2) into (1) and using the fact that $H(\phi_{ij})^{-1} = H(-\phi_{ij})$ we get:

$$\forall k \in [1; K]_{\mathbb{N}}, \ \boldsymbol{D}^{(k)} = \left(\prod_{i=1}^{N-1} \prod_{j=i+1}^{N} \boldsymbol{G}(\theta_{ij})^{\mathsf{T}} \boldsymbol{H}(-\phi_{ij})\right) \boldsymbol{M}^{(k)} \left(\prod_{i=1}^{N-1} \prod_{j=i+1}^{N} \boldsymbol{G}(\theta_{ij}) \boldsymbol{H}(\phi_{ij})\right), \tag{3}$$

¹²² but we prefer the simpler formulation:

$$\forall k \in [1; K]_{\mathbb{N}}, \ \boldsymbol{D}^{(k)} = \left(\prod_{m=1}^{M} \boldsymbol{H}(-\phi_m)\boldsymbol{G}(\theta_m)^{\mathsf{T}}\right)\boldsymbol{M}^{(k)}\left(\prod_{m=1}^{M} \boldsymbol{G}(\theta_m)\boldsymbol{H}(\phi_m)\right), \tag{4}$$

where each integer *m* of $[1; M]_N$ stands for a couple (i, j) with $1 \le i < j \le N$. It is worth mentioning that any Givens or hyperbolic matrix is defined by only one parameter (angle). Therefore, ideally we have to find a set of M = N(N - 1)/2 couples of parameters $\{(\theta_{ij}, \phi_{ij})\}_{1 \le i < j \le N}$ in order to get (1). Instead of simultaneously identifying these *M* couples of parameters, a Jacobi-like ¹²⁷ procedure will repeat sequences of 2*M* successive optimizations until convergence. Each opti-¹²⁸ mization is performed with respect to only one parameter. A sequence of 2*M* optimizations is ¹²⁹ generally called a sweep. As a result, $N_s M$ couples of Givens and hyperbolic matrices are used ¹³⁰ in practice to identify A, where N_s is the number of sweeps. We thus look for a matrix A of the ¹³¹ form $A = \prod_{n_s=1}^{N_s} \prod_{m=1}^M G(\theta_m^{n_s}) H(\phi_m^{n_s})$. The idea is to iteratively diagonalize the $M^{(k)}$ matrices by ¹³² sequentially optimizing with respect to $\theta_m^{n_s}$ and $\phi_m^{n_s}$ for each value of m and n_s . Hence the first ¹³³ sweep ($n_s = 1$) consists on the following transformations:

$$\forall k \in [1; K]_{\mathbb{N}}, \ N^{(k,1,1)} = \boldsymbol{G}(\boldsymbol{\theta}_1^1)^{\mathsf{T}} \boldsymbol{M}^{(k)} \boldsymbol{G}(\boldsymbol{\theta}_1^1), \tag{5}$$

$$\forall (k,m) \in [1;K]_{\mathbb{N}} \times [1;M]_{\mathbb{N}}, \ \boldsymbol{M}^{(k,m,1)} = \boldsymbol{H}(-\phi_m^1) \boldsymbol{N}^{(k,m,1)} \boldsymbol{H}(\phi_m^1).$$
(6)

$$\forall (k,m) \in [1;K]_{\mathbb{N}} \times [2;M]_{\mathbb{N}} N^{(k,m,1)} = G(\theta_m^1)^{\mathsf{T}} M^{(k,m-1,1)} G(\theta_m^1)$$
(7)

Then the following sweeps $(1 < n_s \le N_s)$ follow the same scheme:

$$\forall (k, n_s) \in [1; K]_{\mathbb{N}} \times [2; N_s]_{\mathbb{N}}, \ N^{(k, 1, n_s)} = G(\theta_1^{n_s})^{\mathsf{T}} M^{(k, M, n_s - 1)} G(\theta_1^{n_s}), \quad (8)$$

$$\forall (k, m, n_s) \in [1; K]_{\mathbb{N}} \times \in [1; M]_{\mathbb{N}} \times [2; N_s]_{\mathbb{N}}, \ M^{(k, m, n_s)} = H(-\phi_m^{n_s}) N^{(k, m, n_s)} H(\phi_m^{n_s}).$$
(9)

$$\forall (k, m, n_s) \in [1; K]_{\mathbb{N}} \times \in [2; M]_{\mathbb{N}} \times [2; N_s]_{\mathbb{N}}, \ N^{(k, m, n_s)} = G(\theta_m^{n_s})^{\mathsf{T}} \boldsymbol{M}^{(k, m-1, n_s)} \boldsymbol{G}(\theta_m^{n_s}), \ (10)$$

Thereby, the optimal corresponding Givens and hyperbolic matrices are sequentially computed in order to get *K* diagonal matrices $M^{(k,M,N_s)}$ at the end of the process.

137 2.2. Optimization of matrix angles

¹³⁸ A natural criterion to compute the optimal (m, n_s) -th Givens angle $\theta_m^{n_s}$ is thus to minimize the ¹³⁹ sum of the euclidean norms of the off-diagonal terms of the *K* matrices $N^{(k,m,n_s)}$:

$$\zeta_G(\theta_m^{n_s}) = \sum_{k=1}^K \sum_{\substack{p=1,q=1\\p\neq q}}^{N,N} \left(N_{pq}^{(k,m,n_s)} \right)^2.$$
(11)

This criterion is the generalization of the original Jacobi criterion to the joint diagonalization context. Since Givens matrices are orthogonal, the same definition of $N^{(k,m,n_s)}$ holds in both the joint diagonalization by congruence and JEVD cases and thus the same optimization algorithms can be used. For instance, our proposed algorithm resorts to the same approach as the JAD algorithm described in [42] whereas the sh-rt and JUST algorithms use their own minimization scheme.

Once the optimal Givens matrix $G(\theta_m^{n_s})$ is computed, different criteria can be used for the 146 optimal computation of $H(\phi_m^{n_s})$. This is the main difference between the three JEVD algorithms. 147 The sh-rt method aims at minimizing the Frobenius norm of $\boldsymbol{M}^{(h,m,n_s)}$ where *h* is found such that $\left|M_{ii}^{(h,m,n_s)} - M_{jj}^{(h,m,n_s)}\right| = \max_{1 \le k \le K} \left|M_{ii}^{(k,m,n_s)} - M_{jj}^{(k,m,n_s)}\right|$, whereas the JUST algorithm resorts to criterion (11) by replacing $N^{(k,m,n_s)}$ by $M^{(k,m,n_s)}$. Instead of minimizing all the (off-diagonal) 148 149 150 entries, we propose to target two particular off-diagonal entries of $M^{(k,m,n_s)}$: if *m* corresponds to the $(i, j)_{i < j}$ couple, we simply aim at computing the optimal $M_{ij}^{(k,m,n_s)}$ and $M_{ji}^{(k,m,n_s)}$ components by 151 152 using a "targeting" hyperbolic matrix. It is noteworthy that the transformation (9) affects the *i*-th 153 and j-th rows and the i-th and j-th columns of M^{k,m,n_s} but only the (i, j) and the (j, i) components 154 are twice affected by the hyperbolic matrix and its inverse. Hence our choice to focus on the latter. 155

Therefore, our Joint Diagonalization algorithm based on Targeting hyperbolic Matrices (JDTM) resorts to the following alternative criterion ζ_{H}^{JDTM} for the computation of the hyperbolic matrix:

$$\zeta_{H}^{JDTM}(\phi_{m}^{n_{s}}) = \sum_{k=1}^{K} \left(M_{ij}^{(k,m,n_{s})} \right)^{2} + \left(M_{ji}^{(k,m,n_{s})} \right)^{2},$$
(12)

Targeting some components was originally proposed by Souloumiac in a different context [40].
 In the case of Givens matrices we showed that the optimizations of criteria (11) and (12) were

¹⁶⁰ mathematically equivalent.

Now, let us look at the components of $M^{(k,m,n_s)}$. As previously mentioned, we only consider the (i, j)-th and (j, i)-th components which are given by:

$$M_{ij}^{(k,m,n_s)} = \left(N_{ii}^{(k,m,n_s)} - N_{jj}^{(k,m,n_s)}\right) \frac{\sinh(2\phi_m^{n_s})}{2} + N_{ij}^{(k,m,n_s)}\cosh(\phi_m^{n_s})^2 - N_{ji}^{(k,m,n_s)}\sinh(\phi_m^{n_s})^2, \quad (13)$$

163

$$M_{ji}^{(k,m,n_s)} = \left(N_{jj}^{(k,m,n_s)} - N_{ii}^{(k,m,n_s)}\right) \frac{\sinh(2\phi_m^{n_s})}{2} - N_{ij}^{(k,m,n_s)}\sinh(\phi_m^{n_s})^2 + N_{ji}^{(k,m,n_s)}\cosh(\phi_m^{n_s})^2.$$
(14)

¹⁶⁴ Furthermore we can write that:

$$\left(M_{ij}^{(k,m,n_s)}\right)^2 + \left(M_{ji}^{(k,m,n_s)}\right)^2 = \frac{\left(M_{ij}^{(k,m,n_s)} + M_{ji}^{(k,m,n_s)}\right)^2}{2} + \frac{\left(M_{ij}^{(k,m,n_s)} - M_{ji}^{(k,m,n_s)}\right)^2}{2}.$$
(15)

The first term of the right-hand side does not depend on $\phi_m^{n_s}$. Indeed, we derive from (13) and (14) the following equality:

$$\frac{\left(M_{ij}^{(k,m,n_s)} + M_{ji}^{(k,m,n_s)}\right)^2}{2} = \frac{\left(N_{ij}^{(k,m,n_s)} + N_{ji}^{(k,m,n_s)}\right)^2}{2}.$$
(16)

¹⁶⁷ Thereby minimizing ζ_H^{JTDM} is equivalent to minimize the λ function defined by:

$$\lambda(\phi_m^{n_s}) = \sum_{k=1}^K \left(M_{ij}^{(k,m,n_s)} - M_{ji}^{(k,m,n_s)} \right)^2.$$
(17)

We denote by $\mathbf{y}^{(m,n_s)}$ the column vector of \mathbb{R}^K defined by $y_k^{(m,n_s)} = M_{ij}^{(k,m,n_s)} - M_{ji}^{(k,m,n_s)}$, so that $\lambda(\phi_m^{n_s}) = \mathbf{y}^{(m,n_s)^{\mathsf{T}}} \mathbf{y}^{(m,n_s)}$. It is easily shown that the system of linear equations (13) and (14) can be rewritten such that:

$$\boldsymbol{y}^{(m,n_s)} = \boldsymbol{W}^{(m,n_s)} \boldsymbol{x}(\boldsymbol{\phi}_m^{n_s}), \tag{18}$$

171 with:

$$\boldsymbol{W}^{(m,n_s)} = \begin{bmatrix} N_{ii}^{(1,m,n_s)} - N_{jj}^{(1,m,n_s)} & N_{ij}^{(1,m,n_s)} - N_{ji}^{(1,m,n_s)} \\ \vdots & \vdots \\ N_{ii}^{(K,m,n_s)} - N_{jj}^{(K,m,n_s)} & N_{ij}^{(K,m,n_s)} - N_{ji}^{(K,m,n_s)} \end{bmatrix} ; \quad \boldsymbol{x}(\phi_m^{n_s}) = \begin{bmatrix} \sinh(2\phi_m^{n_s}) \\ \cosh(2\phi_m^{n_s}) \\ \cosh(2\phi_m^{n_s}) \end{bmatrix}.$$

Now defining the diagonal 2 × 2 matrix J such that $J_{11} = -J_{22} = -1$ and observing that $\mathbf{x}(\phi_m^{n_s})^{\mathsf{T}} J \mathbf{x}(\phi_m^{n_s}) = 1$, we have thus to minimize the quantity $\mathbf{x}(\phi_m^{n_s})^{\mathsf{T}} W^{(m,n_s)\mathsf{T}} W^{(m,n_s)\mathsf{T}} \mathbf{x}(\phi_m^{n_s})$ under the constraint that $\mathbf{x}(\phi_m^{n_s})^{\mathsf{T}} \mathbf{J} \mathbf{x}(\phi_m^{n_s}) = 1$. This can be done using the Lagrange multipliers strategy. Thereby, we have to minimize the *L* function given by:

$$L(\boldsymbol{x}(\phi_m^{n_s}), \boldsymbol{\mu}(\phi_m^{n_s})) = \boldsymbol{x}(\phi_m^{n_s})^{\mathsf{T}} \boldsymbol{W}^{(m,n_s)\mathsf{T}} \boldsymbol{W}^{(m,n_s)} \boldsymbol{x}(\phi_m^{n_s}) - \boldsymbol{\mu}(\phi_m^{n_s}) \boldsymbol{x}(\phi_m^{n_s})^{\mathsf{T}} \boldsymbol{J} \boldsymbol{x}(\phi_m^{n_s}).$$
(19)

¹⁷⁶ Differentiation with respect to $\mathbf{x}(\phi_m^{n_s})$ leads to:

$$\boldsymbol{W}^{(m,n_s)^{\mathsf{T}}}\boldsymbol{W}^{(m,n_s)}\boldsymbol{x}(\boldsymbol{\phi}_m^{n_s}) = \boldsymbol{\mu}(\boldsymbol{\phi}_m^{n_s})\boldsymbol{J}\boldsymbol{x}(\boldsymbol{\phi}_m^{n_s}).$$
(20)

177 Since $J^{-1} = J$ we have:

$$\boldsymbol{J}\boldsymbol{W}^{(m,n_s)^{\mathsf{T}}}\boldsymbol{W}^{(m,n_s)}\boldsymbol{x}(\phi_m^{n_s}) = \mu(\phi_m^{n_s})\boldsymbol{x}(\phi_m^{n_s}).$$
(21)

Thus, $\mu(\phi_m^{n_s})$ and $\mathbf{x}(\phi_m^{n_s})$ are associated eigenvalue and eigenvector of matrix $\mathbf{J}\mathbf{W}^{(m,n_s)}\mathbf{W}^{(m,n_s)}$. More particularly, we have the following lemma:

Lemma 1. If the columns of $W^{(m,n_s)}$ are different then $JW^{(m,n_s)}W^{(m,n_s)}$ has two nonzero eigenvalues of opposite sign and $\mathbf{x}(\phi_m^{n_s})$ is the eigenvector associated to the positive eigenvalue.

- **Proof 1.** Let w_1 and w_2 be the column vectors of matrix $W^{(m,n_s)}$. Both belong to \mathbb{R}^K , equipped
- with the Euclidean norm and we define $a = w_1^{\mathsf{T}} w_1$, $b = w_1^{\mathsf{T}} w_2$ and $c = w_2^{\mathsf{T}} w_2$. Hence a, b and c
- denote the squared euclidean norm of w_1 , the scalar product between w_1 and w_2 and the squared
- 185 Euclidean norm of w_2 respectively. Hence,

$$\boldsymbol{J}\boldsymbol{W}^{(m,n_s)\mathsf{T}}\boldsymbol{W}^{(m,n_s)} = \begin{bmatrix} -a & -b \\ b & c \end{bmatrix}$$

186 The characteristic polynomial is then:

$$P(\alpha) = \alpha^2 + (a - c)\alpha + (b^2 - ca)$$
⁽²²⁾

187 and the discriminant is:

$$\Delta = (a-c)^2 - 4b^2 + 4ca$$

= $(a+c-2b)(a+c+2b)$
= $||\mathbf{w}_1 - \mathbf{w}_2||^2 ||\mathbf{w}_1 + \mathbf{w}_2||^2$

Thereby, since $\mathbf{w}_1 \neq \mathbf{w}_2$, $\Delta > 0$ and $\mathbf{JW}^{(m,n_s)} \mathbf{W}^{(m,n_s)}$ is diagonalizable and admits two distinct eigenvalues α_1 and α_2 . Then we have:

$$\alpha_1 \alpha_2 = \frac{(a-c)^2 - \Delta}{4a^2}$$
$$= \frac{b^2 - ac}{a^2}$$

- ¹⁹⁰ The Cauchy-Schwartz inequality gives $b^2 < ac$ hence $\alpha_1 \alpha_2 < 0$.
- ¹⁹¹ We now demonstrate the second part of the lemma. Multiplying (21) by $\mathbf{x}(\phi_m^{n_s})^{\mathsf{T}} \mathbf{J}$ yields:

$$\mathbf{x}(\phi_m^{n_s})^{\mathsf{T}} \mathbf{W}^{(m,n_s)^{\mathsf{T}}} \mathbf{W}^{(m,n_s)} \mathbf{x}(\phi_m^{n_s}) = \mu(\phi_m^{n_s}) \mathbf{x}(\phi_m^{n_s})^{\mathsf{T}} \mathbf{J} \mathbf{x}(\phi_m^{n_s}),$$

$$= \mu(\phi_m^{n_s}).$$
(23)

¹⁹² The quadratic form $\mathbf{x}(\phi_m^{n_s})^{\mathsf{T}} \mathbf{W}^{(m,n_s)\mathsf{T}} \mathbf{W}^{(m,n_s)} \mathbf{x}(\phi_m^{n_s})$ is positive thus $\mu(\phi_m^{n_s})$ is positive too.

- ¹⁹³ Hence the previous lemma allows us to easily compute $\mathbf{x}(\phi_m^{n_s})$ from $W^{(m,n_s)}$ and $\phi_m^{n_s}$ is deduced
- ¹⁹⁴ from the definition of $\boldsymbol{x}(\phi_m^{n_s})$:

$$\phi_m^{n_s} = \frac{1}{2} \operatorname{atanh} \left(\frac{x(\phi_m^{n_s})_1}{x(\phi_m^{n_s})_2} \right).$$
(24)

Algorithm 1 summarizes the proposed method.

Algorithm 1: Summary of the JDTM algorithm

- 1: Define a threshold ε and a maximal number of sweep N_s^{max}
- 2: Initialize A with the identity matrix;

3:
$$n_s = 1;$$

- 4: while $\sum_{k} \sum_{p \neq q} (M_{p,q}^{(k)})^2 > \varepsilon$ and $n_s \leq N_s^{max}$ do
- 5: m = 1;

6: **for** i = 1 to N - 1 **do**

- 7: **for** j = i + 1 to *N* **do**
- 8: Compute the optimal angle $\theta_m^{n_s}$ corresponding to the couple (i, j) and build $G(\theta_m^{n_s})$;
- 9: Replace the *K* matrices $\boldsymbol{M}^{(k)}$ by $\boldsymbol{G}(\theta_m^{n_s})^{\mathsf{T}} \boldsymbol{M}^{(k)} \boldsymbol{G}(\theta_m^{n_s})$;
- 10: Compute the optimal angle $\phi_m^{n_s}$ corresponding to the couple (i, j) and build $H(\phi_m^{n_s})$;
- 11: Replace the K matrices $M^{(k)}$ by $H(-\phi_m^{n_s})M^{(k)}H(\phi_m^{n_s})$;
- 12: Replace A by $AG(\theta_m^{n_s})H(\phi_m^{n_s})$;
- 13: m = m + 1;
- 14: **end for**
- 15: **end for**
- 16: $n_s = n_s + 1;$
- 17: end while
- 18: $N_s = n_s;$

195

196 2.3. Computational complexity

The computational complexity of an algorithm is given by the number Γ of floating point 197 operations (flop), given in practice by the number of required multiplications. At each sweep, 198 there are N(N - 1)/2 Givens and hyperbolic matrices to compute and as many updates of ma-199 trices $A, M^{(1)}, \dots, M^{(K)}$. Computation of each hyperbolic matrix is dominated by the product 200 $JW^{(m,n_s)T}W^{(m,n_s)}$ which requires 3K multiplications. Givens matrices are computed in a similar 201 way [42] and thus also need 3K multiplications. For each update (line 12 of algorithm 1), matrix 202 A is multiplied by a Givens and a hyperbolic matrix. Both products can be done using a total of 203 8N multiplications. Finaly the update of each matrix $M^{(k)}$ (lines 9 and 11 of algorithm 1) is twice 204 more costly and involves 16N multiplications. Therefore the total computational complexity is: 205

$$\Gamma_{JDTM} = N_s N(N-1)(3K+4N+8KN)$$
(25)

206 2.4. Extension to the complex case

Let's now consider that matrices A and $M^{(1)}, \dots, M^{(K)}$ belong to the complex field. In this case, the JDTM algorithm has to be significantly modified. Indeed, each of the Givens and hyperbolic rotation matrices involved in the polar decomposition of a complex matrix is now defined by two parameters. Similarly to the real case, we only focus on the determination of

- hyperbolic matrices H which makes the specificity of the proposed algorithm. Indeed, G can still be estimated by the classic procedure [42].
- We resort to the following classical parametrization of complex hyperbolic matrices, for each couple $m = (i, j)_{i < j}$ we have:

$$H(\phi_m, \alpha_m)_{ii} = H(\phi_m, \alpha_m)_{jj} = \cosh(\phi_m); \quad H(\phi_m, \alpha_m)_{ij} = \overline{H}(\phi_m, \alpha_m)_{ji} = \sinh(\phi_m) e^{i\alpha_m}$$

Thereby we have to estimate for each matrix the couple (ϕ_{ij}, α_{ij}) that minimizes the new JDTM cost function:

$$\zeta_{HC}^{JDTM}(\phi_m^{n_s}, \alpha_m^{n_s}) = \sum_{k=1}^K |M_{ij}^{(k,m,n_s)}|^2 + |M_{ji}^{(k,m,n_s)}|^2.$$
(26)

²¹⁷ Using the previous parametrization, we obtain:

$$M_{ij}^{(k,m,n_s)} = \left(N_{ii}^{(k,m,n_s)} - N_{jj}^{(k,m,n_s)}\right) \frac{\sinh(2\phi_m^{n_s})}{2} e^{-i\alpha_m^{n_s}} + N_{ij}^{(k,m,n_s)} \cosh(\phi_m^{n_s})^2 - N_{ji}^{(k,m,n_s)} \sinh(\phi_m^{n_s})^2 e^{-2i\alpha_m^{n_s}},$$
(27)

$$M_{ji}^{(k,m,n_s)} = \left(N_{jj}^{(k,m,n_s)} - N_{ii}^{(k,m,n_s)}\right) \frac{\sinh(2\phi_m^{n_s})}{2} e^{i\alpha_m^{n_s}} - N_{ij}^{(k,m,n_s)} \sinh(\phi_m^{n_s})^2 e^{2i\alpha_m^{n_s}} + N_{ji}^{(k,m,n_s)} \cosh(\phi_m^{n_s})^2.$$
(28)

It can be easily shown that minimizing ζ_{HC}^{JDTM} is equivalent to minimizing $\tilde{\zeta}_{HC}^{JDTM}$:

$$\tilde{\zeta}_{HC}^{JDTM}(\phi_m^{n_s}, \alpha_m^{n_s}) = \sum_{k=1}^K |\tilde{M}_{ij}^{(k,m,n_s)} + M_{ji}^{(k,m,n_s)}|^2 + |\tilde{M}_{ij}^{(k,m,n_s)} - M_{ji}^{(k,m,n_s)}|^2,$$
(29)

220 where:

$$\tilde{M}_{ij}^{(k,m,n_s)} = \left(N_{ii}^{(k,m,n_s)} - N_{jj}^{(k,m,n_s)}\right) \frac{\sinh(2\phi_m^{n_s})}{2} e^{ia_m^{n_s}} + N_{ij}^{(k,m,n_s)} \cosh(\phi_m^{n_s})^2 e^{2ia_m^{n_s}} - N_{ji}^{(k,m,n_s)} \sinh(\phi_m^{n_s})^2.$$
(30)

After some straightforward computations, (28), (29) and (30) yield:

222 223

which can be rewritten as a function of $4\phi_m^{n_s}$ and $\alpha_m^{n_s}$:

$$\begin{split} \tilde{\zeta}_{HC}^{JDTM}(4\phi_{m}^{n_{s}},\alpha_{m}^{n_{s}}) &= \frac{1}{2}\sum_{k=1}^{K} \left(\left| N_{ij}^{(k,m,n_{s})} \right|^{2} + \left| N_{ji}^{(k,m,n_{s})} \right|^{2} \right) \left(\cosh(4\phi_{m}^{n_{s}}) + 1 \right) \\ &+ \left(\left| N_{ii}^{(k,m,n_{s})} - N_{jj}^{(k,m,n_{s})} \right|^{2} - \left(N_{ij}^{(k,m,n_{s})} \overline{N}_{ji}^{(k,m,n_{s})} e^{2i\alpha_{m}^{n_{s}}} + N_{ij}^{(k,m,n_{s})} \overline{N}_{ij}^{(k,m,n_{s})} e^{-2i\alpha_{m}^{n_{s}}} \right) \right) \left(\cosh(4\phi_{m}^{n_{s}}) - 1 \right) \\ &+ \left(\overline{\left(N_{ii}^{(k,m,n_{s})} - N_{jj}^{(k,m,n_{s})} \right)} N_{ij}^{(k,m,n_{s})} - \left(N_{ii}^{(k,m,n_{s})} - N_{jj}^{(k,m,n_{s})} \right) \overline{N}_{ji}^{(k,m,n_{s})} \right) e^{i\alpha_{m}^{n_{s}}} \sinh(4\phi_{m}^{n_{s}}) \\ &+ \left(\left(N_{ii}^{(k,m,n_{s})} - N_{jj}^{(k,m,n_{s})} \right) \overline{N}_{ij}^{(k,m,n_{s})} - N_{ji}^{(k,m,n_{s})} - N_{jj}^{(k,m,n_{s})} - N_{jj}^{(k,m,n_{s})} \right) \right) e^{-i\alpha_{m}^{n_{s}}} \sinh(4\phi_{m}^{n_{s}}). \end{split}$$

$$\tag{32}$$

224

Differentiating (32) with respect to $4\phi_m^{n_s}$ and $\alpha_m^{n_s}$ alternatively, then defining $t_m^{n_s} = \tanh(2\phi_m^{n_s})$ and $z_m^{n_s} = e^{i\alpha_m^{n_s}}$, it can be shown after few more trivial computations that the solution couple which minimizes $\tilde{\zeta}_{HC}^{JDTM}$ is also a solution of the following polynomial system:

$$P_0(z_m^{n_s}) + (2P_1(z_m^{n_s})t_m^{n_s} + P_0(z_m^{n_s})t_m^{n_s})t_m^{n_s} = 0$$

$$(Q_1(z_m^{n_s})t_m^{n_s} - Q_0(z_m^{n_s}))t_m^{n_s} = 0$$

$$(33)$$

225 with:

$$P_{0}(z) = \sum_{k=1}^{K} \left(\overline{\left(N_{ii}^{(k,m,n_{s})} - N_{jj}^{(k,m,n_{s})}\right)} N_{ij}^{(k,m,n_{s})} - \left(N_{ii}^{(k,m,n_{s})} - N_{jj}^{(k,m,n_{s})}\right) \overline{N}_{ji}^{(k,m,n_{s})}\right) z^{3} + \left(\left(N_{ii}^{(k,m,n_{s})} - N_{jj}^{(k,m,n_{s})}\right) \overline{N}_{ij}^{(k,m,n_{s})} - N_{ji}^{(k,m,n_{s})} - N_{ji}^{(k,m,n_{s})} - N_{jj}^{(k,m,n_{s})}\right) z^{3} + \left(\left(N_{ii}^{(k,m,n_{s})} - N_{jj}^{(k,m,n_{s})}\right) - N_{ji}^{(k,m,n_{s})} - N_{jj}^{(k,m,n_{s})}\right) z^{2} - \overline{N}_{ij}^{(k,m,n_{s})} N_{ji}^{(k,m,n_{s})} z^{4} + \left(\left|N_{ij}^{(k,m,n_{s})}\right|^{2} + \left|N_{ji}^{(k,m,n_{s})}\right|^{2} + \left|N_{ii}^{(k,m,n_{s})} - N_{jj}^{(k,m,n_{s})}\right|^{2} \right) z^{2} - \overline{N}_{ij}^{(k,m,n_{s})} N_{ji}^{(k,m,n_{s})} z^{4} - \left(\left(N_{ii}^{(k,m,n_{s})} - N_{jj}^{(k,m,n_{s})}\right) \overline{N}_{ji}^{(k,m,n_{s})} - N_{jj}^{(k,m,n_{s})}\right) \overline{N}_{ji}^{(k,m,n_{s})} \right) z^{3} - \left(\left(N_{ii}^{(k,m,n_{s})} - N_{jj}^{(k,m,n_{s})}\right) \overline{N}_{ij}^{(k,m,n_{s})} - N_{jj}^{(k,m,n_{s})}\right) \overline{N}_{ji}^{(k,m,n_{s})} - N_{jj}^{(k,m,n_{s})}\right) z^{3} - \left(\left(N_{ii}^{(k,m,n_{s})} - N_{jj}^{(k,m,n_{s})}\right) \overline{N}_{ij}^{(k,m,n_{s})} - N_{ji}^{(k,m,n_{s})} - N_{jj}^{(k,m,n_{s})}\right) \right) z^{4} - \left(\left(N_{ii}^{(k,m,n_{s})} - N_{jj}^{(k,m,n_{s})}\right) N_{ji}^{(k,m,n_{s})} - N_{jj}^{(k,m,n_{s})}\right) N_{ji}^{(k,m,n_{s})}\right) z^{3} - \left(\left(N_{ii}^{(k,m,n_{s})} - N_{jj}^{(k,m,n_{s})}\right) \overline{N}_{ij}^{(k,m,n_{s})} - N_{jj}^{(k,m,n_{s})}\right) N_{ji}^{(k,m,n_{s})} \right) z^{3} - \left(\left(N_{ii}^{(k,m,n_{s})} - N_{jj}^{(k,m,n_{s})}\right) \overline{N}_{ij}^{(k,m,n_{s})} - N_{jj}^{(k,m,n_{s})}\right) z^{4} - \left(N_{ii}^{(k,m,n_{s})} - N_{jj}^{(k,m,n_{s})}\right) z^{4} - \left(N_{ii}^{(k,m,n_{s})} - N_{jj}^{(k,m,n_{s})}\right) z^{4} - \left(N_{ij}^{(k,m,n_{s})} - \left(N_{ij}^{(k,m,n_{s})} - N_{ij}^{(k,m,n_{s})}\right) z^{4} - \left(N_{ij}^{(k,m,n_{s})} - N_{ij}^{(k,m,n_{s})}\right) z^{4} - \left(N_{ij}^{(k,m,n_{s})} - N_{ij}^{(k,m,n_{s})$$

²²⁶ Solution sets are then easily given by:

$$P_0(z_m^{n_s}) = 0 \text{ and } t_m^{n_s} = 0;$$
 (36)

227 Or:

$$P_0(z_m^{n_s})(Q_1(z_m^{n_s}))^2 + 2P_1(z_m^{n_s})Q_0(z_m^{n_s})Q_1(z_m^{n_s}) + P_0(z_m^{n_s})(Q_0(z_m^{n_s}))^2 = 0 \text{ and } t_m^{n_s} = \frac{Q_0(z_m^{n_s})}{Q_1(z_m^{n_s})}.$$
 (37)

228 3. Toward a new direct CPD algorithm: the DIAG method

229 3.1. The Canonical Polyadic Decomposition

²³⁰ CPD states that any *Q*-order tensor (or *Q*-way array) \mathcal{T} of size $I_1 \times \cdots \times I_Q$ can be exactly ²³¹ decomposed into a sum of *Q*-order rank-1 tensors. A *Q*-order rank-1 tensor can be defined as the ²³² outer product between *Q* vectors $\mathbf{x}^{(1)}, \cdots, \mathbf{x}^{(Q)}$. The rank *R* of \mathcal{T} is then the minimal number of ²³³ rank-1 tensors needed to achieve the following decomposition:

$$\mathcal{T} = \sum_{r=1}^{R} \boldsymbol{x}_{r}^{(1)} \circ \cdots \circ \boldsymbol{x}_{r}^{(Q)}.$$
(38)

Usually one also defines Q "loading" (or factor) matrices $X^{(1)}, \dots, X^{(Q)}$ of size $I_1 \times R, \dots$, $I_Q \times R$, respectively, so that $x_r^{(q)}$ is the r^{th} column of $X^{(q)}$ and the CPD is commonly rewritten as:

$$\forall q \in [1; Q]_{\mathbb{N}}, \ \forall i_q \in [1; I_q]_{\mathbb{N}}, \ \mathcal{T}_{i_1 \cdots i_Q} = \sum_{r=1}^R X_{i_1 r}^{(1)} X_{i_2 r}^{(2)} \cdots X_{i_Q r}^{(Q)}.$$
(39)

Our main problem is thus to find for a given tensor \mathcal{T} of given rank R and order Q, the Q factor matrices that solves (39).

238 3.2. Unfolding matrix

It is well known that the CPD can be rewritten in a matrix form. Indeed, the tensor dimensions 239 can be merged in order to store all tensor entries in a single "unfolding" matrix. Obviously, there 240 are many way to merge the tensor dimensions and thus many possible unfolding matrices. As it 241 will be seen, the choice of the unfolding matrix has an impact on the algorithm limitations and 242 performance. Therefore, in order to cover all the possibilities, we introduce a P parameter in 243 order that the P first dimensions are merged into the matrix rows whereas the remaining Q - P244 dimensions are merged into the matrix columns. The corresponding unfolding matrix is denoted 245 by T(P). Note that all the other unfolding matrices can be merely obtained by permuting the 246 tensor dimensions and changing the P value. T(P) entries are linked to \mathcal{T} entries by the following 247 transfer formulas: 248

$$\forall (m,n) \in [1;\pi_1^P]_{\mathbb{N}} \times [1;\pi_{P+1}^Q]_{\mathbb{N}}, \ \boldsymbol{T}(P)_{m,n} = \mathcal{T}_{i_1,\cdots,i_Q}$$
(40)

249 where, $\pi_a^a = I_a, \pi_a^b = I_a I_{a+1} \cdots I_b$ and:

$$\forall m \in [1; \pi_1^P]_{\mathbb{N}}, \quad m = i_1 + \sum_{q=2}^P (i_q - 1)\pi_1^{q-1},$$
(41)

$$\forall n \in [1; \pi_{P+1}^{Q}]_{\mathbb{N}}, \quad n = i_{P+1} + \sum_{q=P+2}^{Q} (i_q - 1) \pi_{P+1}^{q-1}.$$
(42)

²⁵⁰ Then after some computations the CPD equation (39) can be rewritten as:

$$\boldsymbol{T}(P) = \left(\boldsymbol{X}^{(P)} \odot \cdots \odot \boldsymbol{X}^{(1)}\right) \left(\boldsymbol{X}^{(Q)} \odot \cdots \odot \boldsymbol{X}^{(P+1)}\right)^{\mathrm{T}}.$$
(43)

It is worth mentioning that a majority of CPD algorithms such as ALS or CFS resorts to the P = 1 case.

253 3.3. The DIAG algorithm

The algorithm presented here is available both in the real and complex field. We start from equation (43) and we define for a given couple of integers *a* and *b*, *a* < *b*, the matrix $Y_X^{(b,a)}$ by:

$$\boldsymbol{Y}_{\boldsymbol{X}}^{(b,a)} = \boldsymbol{X}^{(b)} \odot \cdots \odot \boldsymbol{X}^{(a)}.$$
(44)

Now, let USV^{H} be the singular value decomposition of T(P) truncated at the order R, assuming that $R \le \min(\pi_1^P, \pi_{P+1}^Q)$ (hypothesis \mathcal{H}_1). Thus there exists an invertible square matrix M of size $R \times R$ such that:

$$Y_{X}^{(P,1)} = UM, \tag{45}$$

$$\boldsymbol{Y}_{\boldsymbol{Y}}^{(\boldsymbol{Q},\boldsymbol{P}+1)_{\mathsf{T}}} = \boldsymbol{M}^{-1}\boldsymbol{S}\boldsymbol{V}^{\mathsf{H}}.$$
(46)

Recalling that $Y_X^{(Q,P+1)} = X^{(Q)} \odot Y_X^{(Q-1,P+1)}$ and using the definition of the Kathri-Rao product, $Y_X^{(Q,P+1)_{\mathsf{T}}}$ can be seen as a row block matrix:

$$\boldsymbol{Y}_{X}^{(Q,P+1)_{\mathsf{T}}} = \left[\boldsymbol{\phi}^{(1)} \boldsymbol{Y}_{X}^{(Q-1,P+1)_{\mathsf{T}}}, \cdots, \boldsymbol{\phi}^{(I_{Q})} \boldsymbol{Y}_{X}^{(Q-1,P+1)_{\mathsf{T}}} \right], \tag{47}$$

where $\phi^{(1)}, \dots, \phi^{(I_Q)}$ are the I_Q diagonal matrices built from the I_Q rows of the matrix X^Q . As a consequence, equations (46) and (47) yield:

$$SV^{\mathsf{H}} = \left[\Gamma^{(1)^{\mathsf{T}}}, \cdots \Gamma^{(l_Q)^{\mathsf{T}}}, \right], \tag{48}$$

263 where :

$$\forall i \in [1; I_Q]_{\mathbb{N}}, \ \boldsymbol{\Gamma}^{(i)} = \boldsymbol{Y}_X^{(Q-1, P+1)} \boldsymbol{\phi}^{(i)} \boldsymbol{M}^{\mathsf{T}}.$$

$$\tag{49}$$

All matrices $\Gamma^{(i)}$ and $Y_X^{(Q-1,P+1)}$ are of size $\pi_{P+1}^{Q-1} \times R$. We assume that *P* is chosen so that P < Q-1and $R \le \pi_{P+1}^{Q-1}$ (hypothesis \mathcal{H}_2) and that they all admit a Moore-Penrose matrix inverse. Then we define:

$$\forall i_1, i_2 \in [1; I_Q]_{\mathbb{N}}^2, \ i_2 > i_1 \ \Theta^{(i_1, i_2)} = \Gamma^{(i_1)\sharp} \Gamma^{(i_2)}.$$
(50)

Now replacing $\Gamma^{(i)}$ by its definition yields:

$$\boldsymbol{\Theta}^{(i_1,i_2)} = \boldsymbol{M}^{-\mathsf{T}} \boldsymbol{\phi}^{(i_1)-1} \boldsymbol{Y}_X^{(Q-1,P+1)\sharp} \boldsymbol{Y}_X^{(Q-1,P+1)} \boldsymbol{\phi}^{(i_2)} \boldsymbol{M}^{\mathsf{T}},$$
(51)

$$= \boldsymbol{M}^{-\mathsf{T}} \boldsymbol{\Lambda}^{(i_1, i_2)} \boldsymbol{M}^{\mathsf{T}}, \tag{52}$$

where $\Lambda^{(i_1,i_2)} = \phi^{(i_1)-1}\phi^{(i_2)}$. Thus, $M^{-\tau}$ performs the JEVD of the known set of matrices $\Theta^{(i_1,i_2)}$. 268 Therefore M^{-T} can be estimated by the JDTM algorithm. Then one can immediately deduce 269 $Y_X^{(P,1)}$ and $Y_X^{(Q,P+1)}$ from (45) and (46). At this stage there are several ways to estimate the factor 270 matrices from $Y_X^{(P,1)}$ and $Y_X^{(Q,P+1)}$. One simple approach is to estimate each column of the first *P* factor matrices from the corresponding column of $Y_X^{(P,1)}$ and each column of the Q-P remaining factor matrices from the corresponding column of $Y_X^{(Q,P+1)}$. Indeed, column *r* of $Y_X^{(P,1)}$ can be 271 272 273 reshaped into an order-P, rank-1 tensor $\boldsymbol{\mathcal{Y}}_{Xr}^{(P,1)}$ whose factor vectors are the r-th columns of matri-274 ces $X^{(1)}, \dots, X^{(P)}$. Thereby a simple rank-1 High-Order SVD (HOSVD, [43]) of $\mathcal{Y}_{Xr}^{(P,1)}$ provides 275 a direct estimation of $\mathbf{x}_r^{(1)}, \dots, \mathbf{x}_r^{(P)}$. In the same way, the column r of $\mathbf{Y}_X^{(Q,P+1)}$ can be reshaped in a (Q - P)-order, rank-1 tensor $\mathbf{\mathcal{Y}}_{X_r}^{(Q,P+1)}$ whose factor vectors are the r-th columns of matrices $\mathbf{X}^{(P+1)} \cdots \mathbf{X}^{(Q)}$. Hence, $\mathbf{x}_r^{(P+1)} \cdots \mathbf{x}_r^{(Q)}$ can be estimated from the rank-1 HOSVD of $\mathbf{\mathcal{Y}}_{X_r}^{(Q,P+1)}$. Fi-276 277 278 nally both operations are repeated for all the r values. The DIAG algorithm is summarized by 279 Algorithm 2. 280

281 3.4. Computational complexity

²⁸² Γ_{DIAG} is clearly dominated by the three following computations. First, the truncated SVD of ²⁸³ the unfolding matrix of size (π_1^P, π_{P+1}^Q) requires $2\pi_{P+1}^Q(\pi_1^P)^2 + 5R^2(\pi_1^P + \pi_{P+1}^Q) - 2(R^3 + (\pi_1^P)^3)/3$ ²⁸⁴ multiplications, assuming that $\pi_{P+1}^Q > \pi_1^P$. Then, the computation of the Θ matrices needs ap-²⁸⁵ proximately $(RI_Q)^2 \pi_{P+1}^{Q-1}$ additional multiplications. Finally the cost of the JEVD procedure is ²⁸⁶ approximated by $8N_s(I_Q)^2 R^3$. Additional computations can be neglected and thus we have:

$$\Gamma_{DIAG} \approx 2\pi_{P+1}^{Q} (\pi_{1}^{P})^{2} + 5R^{2} (\pi_{1}^{P} + \pi_{P+1}^{Q}) - 2(R^{3} + (\pi_{1}^{P})^{3})/3 + (RI_{Q})^{2} \pi_{P+1}^{Q-1} + 8N_{s}(I_{Q})^{2} R^{3}.$$
(53)

Algorithm 2: Summary of the DIAG algorithm

- 1: Choose a value of P and a permutation of the dimensions of \mathcal{T} as described in section 3.6;
- 2: Matricize the (possibly permuted) tensor \mathcal{T} into matrix T(P) according to (40), (41) and (42);
- 3: Compute the SVD USV^{H} of T(P), truncated at rank R;
- 4: Split SV^{H} into I_Q blocks of size $R \times \pi_{P+1}^{Q-1}$ in order to form the I_Q matrices $\Gamma^{(i)}$ given by (49);
- 5: **for** $i_1 = 1$ to $I_Q 1$ **do**
- **for** $i_2 = i_1 + 1$ to I_Q **do** 6:
- Compute $\Theta^{(i_1,i_2)} = \Gamma^{(i_1)\sharp}\Gamma^{(i_2)}$: 7:
- end for 8.
- 9: end for
- 10: Compute matrix $M^{-\tau}$ by JEVD of the set of $\Theta^{(i_1,i_2)}$ matrices; 11: Deduce matrices $Y_X^{(P,1)} = UM$ and $Y_X^{(Q,P+1)} = M^{-1}SV^{H}$;

- 11. Deduce matrices $\mathbf{Y}_{X} = \mathbf{C} \mathbf{W}$ and $\mathbf{Y}_{X} = \mathbf{W}^{-1} \mathbf{S}^{-1} \mathbf{V}^{-1}$, 12. **for** r = 1 to R **do** 13. Build $\mathbf{\mathcal{Y}}_{Xr}^{(P,1)}$ and $\mathbf{\mathcal{Y}}_{Xr}^{(Q,P+1)}$ by reshaping the r-th columns of $\mathbf{Y}_{X}^{(P,1)}$ and $\mathbf{Y}_{X}^{(Q,P+1)}$; 14. Deduce $\mathbf{x}_{r}^{(1)}, \cdots, \mathbf{x}_{r}^{(P)}$ from the rank 1 HOSVD of $\mathbf{\mathcal{Y}}_{Xr}^{(P,1)}$; 15. Deduce $\mathbf{x}_{r}^{(P+1)}, \cdots, \mathbf{x}_{r}^{(Q)}$ the rank 1 HOSVD of $\mathbf{\mathcal{Y}}_{Xr}^{(Q,P+1)}$;

- 16: end for

 Γ_{DIAG} should be compared to the numerical complexity of the ALS algorithm which is approxi-287 mately given by: 288

$$\Gamma_{ALS} \approx N_{ALS} \left(3R\pi_1^Q + 7R^2 \sum_{\substack{q=1\\k\neq q}}^Q \prod_{\substack{k=1\\k\neq q}}^Q I_k \right), \tag{54}$$

However the numerical complexity of the DIAG algorithm is strongly related to the choice of the 289 unfolding matrix and both complexities depend on a large number of parameters. Furthermore 290 N_{ALS} can fluctuate wildly. Therefore at this point it would be very hazardous to draw general con-291 clusions from the previous formulas even in simple cases. Nevertheless we made some extensive 292 flop comparisons between both algorithms by varying Q, R, P and the tensor dimensions. Results 293 are reported in section 4.2.4. It will be shown that in all the considered situations $\Gamma_{DIAG} \leq \Gamma_{ALS}$ 294 and $N_s \ll N_{ALS}$. 295

296

The numerical complexity of the CFS algorithm is very complicated to establish since this 297 algorithm computes several estimations of each factor matrix. However we can easily explain 298 what makes DIAG a cheaper approach. CFS is a three step algorithm. The first step is algebraic 299 and performs the HOSVD of the tensor. In terms of numerical complexity this operation is 300 usually close to the SVD of the unfolding matrix performed in the DIAG algorithm. The second 301 step is the resolution of $Q(Q-1)^2$ JEVDs whereas DIAG requires only one JEVD. Finally, we 302 have to choose the best estimates of the factor matrices among a large number of combinations 303 which is also very time consuming. 304

3.5. Necessary conditions to the identifiability of DIAG, ALS and CFS 305

The CPD algorithms are not always applicable due to their intrinsic restricted conditions. 306 We propose to compare here necessary conditions that ensure identifibility of the ALS, CFS and 307

³⁰⁸ DIAG methods. Let Q, R and I(i) be the tensor order, the CPD rank and the *i*-th dimension of ³⁰⁹ the tensor, respectively. A tensor of order Q and rank R can be canonically decomposed by ALS ³¹⁰ only if:

$$(C_{ALS}): \ \forall \ q \in [1; Q]_{\mathbb{N}}, \ \prod_{\substack{i=1\\i \neq q}}^{Q} I(i) \ge R.$$

$$(55)$$

DIAG conditions are given by hypotheses \mathcal{H}_1 and \mathcal{H}_2 . \mathcal{H}_1 and \mathcal{H}_2 were expounded for a given

order of the tensor dimensions (default order). Actually, By taking into account that the dimen-

³¹³ sions can be permuted we obtain the following more general condition:

$$(C_{DIAG}): \exists P \in [2; Q-1]_{\mathbb{N}}, \exists f_I \text{ a permutation of the } Q \text{ first natural numbers and } \exists q_s > P \text{ such that:} \\ \prod_{i=1}^{P} I(f_I(i)) \ge R \text{ and } \prod_{\substack{i=p+1\\i\neq q}}^{Q} I(f_I(i)) \ge R.$$
(56)

Finally, the condition C_{CFS} for the closed-form solution is given in [28]:

$$(C_{CFS})$$
: $\exists (q_1, q_2) \in [1; Q]^2_{\mathbb{N}}, q_1 \neq q_2 \text{ such that } I(q_1) \ge R \text{ and } I(q_2) \ge R.$ (57)

Proposition 1. C_{DIAG} is more restrictive than C_{ALS} but less restrictive than C_{CFS} :

 $_{316} \quad C_{CFS} \Rightarrow C_{DIAG} \Rightarrow C_{ALS}$

A proof is given in appendix. In practice the DIAG condition implies $P \le Q - 2$ and can be reformulated quite easily for low order tensors ($3 \le Q \le 5$):

Third order tensors, Q = 3. Here we have necessarily P = 1 hence C_{DIAG} becomes simply: at least two of the tensor dimensions are greater or equal to the CPD rank R. Thereby at order 3 (and only at order 3) C_{DIAG} and C_{CFS} are equivalent.

- Fourth order tensors, Q = 4. Here we can choose either P = 1 or P = 2 but the condition remains the same in both cases and is simply: at least one tensor dimension is greater than R and at least one product of two of the remaining dimensions is also greater than R.
- Fifth order tensors, Q = 5. Here $1 \le P \le 3$:

326	٠	if we choose $P = 1$ or $P = 3$ then C_{DIAG} becomes: at least one tensor dimension is
327		greater than R and at least one product of three of the remaining dimensions is also
328		greater than R.

• if we choose P = 2 then C_{DIAG} becomes: at least one product between two tensor dimensions and another product between two of the remaining dimensions are greater than R.

332 3.6. Choice of the unfolding matrix

An obvious criterion is the residual error between \mathcal{T} and the reconstructed tensor built from the estimated factor matrices. However it would be very time consuming to test several possibilities. As a consequence the choice of the more appropriate unfolding matrix should be related to hypothesis \mathcal{H}_1 and \mathcal{H}_2 . Indeed, one has to choose a permutation of the tensor dimensions and a *P* value that ensure both hypotheses. Otherwise, the DIAG algorithm is not suitable as it is explained in the previous section. Recall notably that the DIAG algorithm implies $P \leq Q - 2$.

Indeed, at order 3 we have necessarily P = 1. At order 4 we have two possible values (1 and 339 2) and so on. Therefore if one wants to maximize the value of the highest possible rank then 340 one should maximize $\min(\pi_1^{q-1}, \pi_{P+1}^{q-1})$, hence choose T(p) as squared as possible. In practice 341 we observed that this recommendation is always a good option even if all tensor dimensions are 342 greater than the rank. Apart from that one should note that the number of matrices to be jointly 343 diagonalized is directly related to the squared dimension of the last mode and thus the numerical 344 complexity of the JEVD step. Therefore in the case of a tensor with one very large dimension 345 we do not recommend to put it at the end (if possible). More generally, we recommend to take 346 into consideration the overall complexity of the DIAG algorithm given by equation (53) and to 347 consider that with the JDTM algorithm the number of sweeps (N_s) exceeds very rarely 10. In 348 section 4.2.4 we give several significant numerical examples of DIAG complexity for various 349 tensor dimensions and unfolding matrices. 350

351 4. Numerical simulations

The proposed algorithms are first validated on synthesized data sets. We first focus the JEVD sub-problem for which we compare JDTM performances to these of other JEVD algorithms. Then we compare the DIAG approach with CFS, an other direct algorithm and ALS-ELS which is a reference iterative method, with respect to several scenarios. The last subsection is dedicated to a particular tensor family for which iterative algorithms consistently fail to find the CPD.

357 4.1. Performance comparison of the JDTM algorithm

The performance of the JDTM algorithm is studied and compared to that of the JET, sh-rt and JUST methods by varying the number K of matrices to be jointly diagonalized, the Signalto-Noise Ratio (SNR) and the matrix dimensions N. The matrix set to be jointly diagonalized is built according to the following model:

$$\forall k \in [1; K]_{\mathbb{N}}, \ \boldsymbol{M}^{(k)} = \frac{\widetilde{\boldsymbol{M}}^{(k)}}{\|\widetilde{\boldsymbol{M}}^{(k)}\|_{F}} + \sigma \frac{\boldsymbol{E}^{(k)}}{\|\boldsymbol{E}^{(k)}\|_{F}} \text{ with } \widetilde{\boldsymbol{M}}^{(k)} = \boldsymbol{A} \boldsymbol{D}^{(k)} \boldsymbol{A}^{-1}.$$
(58)

Entries of A, $D^{(k)}$ and $E^{(k)}$ are drawn randomly according to a standard normal distribution. The scalar parameter σ allows us to regulate the power of the Gaussian additive noise $E^{(k)}$. The SNR is then equal to $-20 \log_{10}(\sigma)$. Hence, σ is chosen in order to obtained the desired value of SNR. At the end of each sweep, the squared off-diagonal components of the *K* matrices $M^{(k,M,n_s)}$ are summed and the obtained value is compared to the value computed at the previous sweep. Algorithms are stopped when the relative deviation between two successive values is smaller than 10^{-3} .

After having removed the scaling and permutation indeterminacies we define r_A as the relative root squared error between the true eigenvector matrix and its estimate \widehat{A} :

$$r_{A} = \sqrt{\frac{\sum_{i=1}^{N} \sum_{j=1}^{N} \left(A_{i,j} - \widehat{A}_{i,j}\right)^{2}}{\sum_{i=1}^{N} \sum_{j=1}^{N} \left(A_{i,j}\right)^{2}}}.$$
(59)

³⁷¹ Note that in most practical applications and notably in blind source separation, one is only inter-

ested by the estimation of the eigenvector matrix. Hence r_A appears as a relevant JEVD criterion.

Finally the number of sweeps, N_s , required by each algorithm is stored in order to compute the values of the total numerical complexities Γ . Therefore, algorithm results are judged according to three criteria, namely N_s , Γ and r_A .

Each simulation is repeated 100 times with a new draw of the matrices A, $D^{(k)}$ and $E^{(k)}$ at each time. We present here median values of r_A and mean values of Γ and N_s obtained from each algorithm.

Figures 1, 2 and 3 show simulation results for 3 SNR values (60 dB, 40 dB and 20 dB 379 respectively). The number of matrices to be jointly diagonalized was fixed to K = 64 whereas we 380 varied the matrix size N from 2 to 32. We first note that the estimation precision of the algorithms 381 logically increases with the ratio K/N and the SNR. Second, according to r_A criterion JUST 382 algorithm is consistently outperformed by other algorithms whatever the considered situation. 383 At 60 dB, figure 1(a) points out that the JDTM and JET algorithm outclass the sh-rt approach 384 concerning the estimation of eigenvectors matrix. According to this r_A criterion JET performs 385 slightly better than JDTM for matrix size lower or equal to 16 whereas for the largest size JDTM 386 clearly provides the best performances. The comparison of the average computational costs 387 displayed in figure 1(b) shows very closed results between all the algorithms. However JDTM 388 appears more clearly as the less costly algorithm for largest matrix sizes. This is explained by a 389 lower and remarkably stable number of sweeps (figure 1(c)). Previous conclusions hold at 40 dB. 390 However it is interesting to note that concerning the estimation of the eigenvectors matrix JDTM 391 is now significantly more accurate than JET for N = 16 and N = 32. Finally, the 20 dB case 392 highlights the efficiency of the JDTM algorithm which clearly improves JET and sh-rt results, for 393 matrix sizes larger than 8. However JET is now the faster algorithm. In conclusion JDTM appears 394 as a very versatile algorithm which provide very accurate results in all the considered situation 395 (in comparison to its competitors) for a lower number of sweeps. This number is remarkably 396 stable, being comprised between 3 and 10 in all the considered scenarios. Moreover JDTM 397 consistently provides the best estimate of the eigenvector matrix for the largest matrix size and 398 this gap increases with the SNR. To sum up, JDTM offers quite similar performances than its 399 best competitors (sh-rt or JET) in the easiest cases (regarding SNR and K/N ratio) whereas it 400 clearly becomes the better choice as the difficulty increases. 401

As part of this study, we also evaluate JDTM ability to deal with an ill-conditioned eigenvector matrix. For this purpose, we now compute the eigenvector matrix A with pairwise correlated columns as follows: odd columns, a_{2r-1} , are still randomly drawn as previously but even columns, a_{2r} , are built in the following way :

$$dr \in [1; N/2]_{\mathbb{N}}, \qquad \boldsymbol{a}_{2r} = \boldsymbol{\nu}\boldsymbol{a}_{2r-1} + (1-\boldsymbol{\nu})\boldsymbol{n}_r, \tag{60}$$

where n_r is a vector of \mathbb{R}^N whose components are randomly drawn according to a standard normal distribution. Thereby ν defines a collinearity factor which will vary from 0.1 to 0.9 so that matrices A can be very ill-conditioned. Figure 4 shows simulation results for a set of 10 matrices of size 10 (K = N = 10) at 80 dB. It can be seen that sh-rt, JDTM and JET perform well for $\nu < 0.9$. JDTM and JET provide the best results in terms of estimation precision but JDTM requires a minimal number of sweeps and computational cost.

412 4.2. Performance comparison of the DIAG algorithm

We now study performances of the DIAG algorithm for the decomposition of noisy tensors. Indeed, in most practical applications involving tensor analysis, a noisy tensor of rank R is mod-

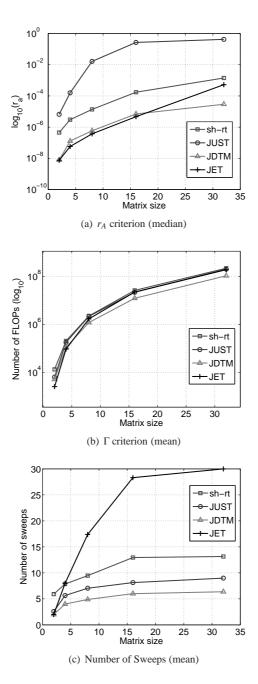


Figure 1: Evolution of the three comparison criteria as a function of the matrix size for a set of 64 matrices with an SNR value of 60 dB.

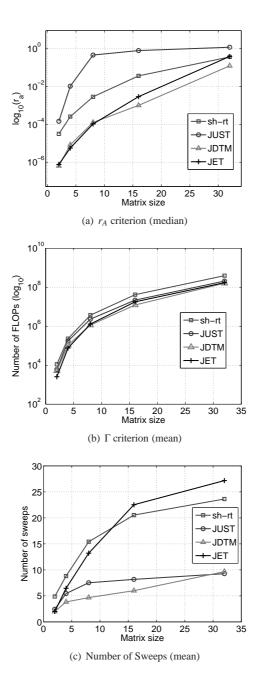


Figure 2: Evolution of the three comparison criteria as a function of the matrix size for a set of 64 matrices with an SNR value of 40 dB.

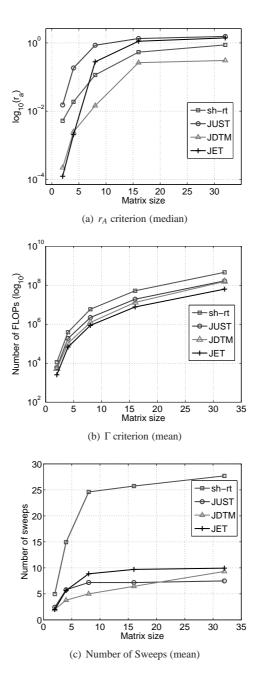


Figure 3: Evolution of the three comparison criteria as a function of the matrix size for a set of 64 matrices with an SNR value of 20 dB.

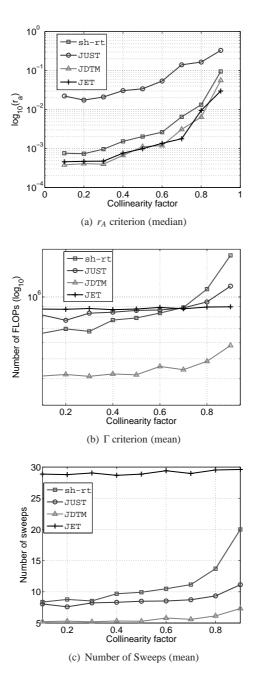


Figure 4: Evolution of the three comparison criteria as a function of the correlated factor between columns of matrix A for a set of 10 matrices of size 10 and an SNR value of 80 dB.

elized by "truncated" CPD of rank $R_m < R$ which is usually more relevant than the exact CPD:

$$\forall q \in [1; Q]_{\mathbb{N}}, \; \forall i_q \in [1; I_q]_{\mathbb{N}}, \; \mathcal{T}_{i_1, \cdots, i_Q} = \sum_{r=1}^{R_m} X^{(1)}_{i_1, r} X^{(2)}_{i_2, r} \cdots X^{(Q)}_{i_Q, r} + \mathcal{E}_{i_1, \cdots, i_Q}, \tag{61}$$

where \mathcal{E} is an error term. R_m is the model rank. The DIAG algorithm is compared with an ALS-ELS algorithm and with the CFS algorithm in various situations by means of Monte-Carlo experiments. For each new experiment, a noise free tensor is built from factor matrices of R_m columns whose entries are randomly drawn according to a standard normal distribution. We then add a Gaussian white noise whose the power is regulated according to the desired SNR value. The comparison criterion, r_X , is the Normalized Mean Squares Error (NMSE) computed between actual and estimated factor matrices. Hence for a tensor of order Q we have:

$$r_X = \frac{1}{Q} \sum_{q=1}^{Q} \operatorname{med}\left(\sqrt{\frac{\operatorname{vec}(X^{(q)} - \widehat{X^{(q)}})^{\mathsf{T}} \operatorname{vec}(X^{(q)} - \widehat{X^{(q)}})}{\operatorname{vec}(X^{(q)})^{\mathsf{T}} \operatorname{vec}(X^{(q)})}}\right),\tag{62}$$

where $X^{(q)}$ denotes the estimation of the factor matrix $X^{(q)}$, the vec(·) operator maps a matrix 423 to a column vector by stacking its columns one below the other and med(·) denotes the median 424 value computed from 100 MC experiments. Permutation and scaling ambiguities in the estimated 425 factor matrices are fixed in the same manner as in [21]. All algorithms were written in-house. The 426 ALS-ELS algorithm can be found in the tensor package web-page 1 . It is stopped as soon as the 427 relative deviation between two consecutive values of the CPD cost function becomes lower than 428 10^{-6} or the number of ALS iterations reaches 1000. ELS procedure is run every 5 iterations. For 429 the decomposition of order-3 tensors, we use the CFS algorithm described in [27] with the best 430 matching scheme proposed in section 4.2 of [27] whereas higher order tensors were decomposed 431 using the N-order version described in [28], using the sub-optimal matching rules proposed by 432 the authors. Implemented versions of DIAG and CFS resort to the JDTM algorithm to solve the 433 JEVD problem and are stopped as soon as the relative deviation between two consecutive values 434 of the JEVD cost function becomes lower than 10^{-6} or the number of JEVD iterations reaches 435 30. Unfolding matrix in the DIAG algorithm is generally chosen to be as squared as possible. 436

437 Since the number of test parameters is large, it would be impossible to perform here an exhaustive
438 comparison. As a consequence we have limited ourselves to some key situations which illustrate
439 the main features of the proposed approach : *i*. its ability to decompose high order tensors of
440 high rank, *ii*. tensors with almost collinear factors, *iii*. its insensitivity to over-factoring and *iv*.
441 its low computational complexity.

442 4.2.1. High order tensors

We first consider a set of 6-order tensors of rank 5 whose all the dimensions are equal to 5. DIAG parameter *P* is set to 3 and we vary the SNR from 10 dB to 80 dB. Results are plotted on figures 5(a). CFS only works for the highest SNR value, probably because this is a difficult situation for which we are very close to its intrinsic limitation. DIAG provides as accurate estimations as ALS-ELS for SNR values greater than 10 dB. ALS-ELS fails at 10 dB while DIAG still works. Notably it clearly outperforms ALS at 10 dB.

¹http://www.gipsa-lab.grenoble-inp.fr/~pierre.comon/TensorPackage/tensorPackage.html

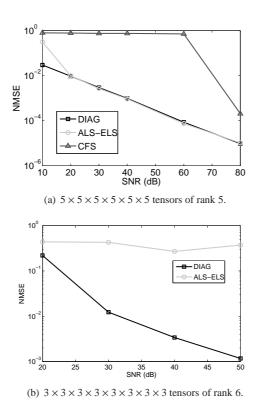


Figure 5: Median NMSE as a function of the SNR at the output of the ALS and DIAG algorithms applied to high order tensors.

We then consider 8-order tensors of rank 6 whose all the dimensions are equal to 3. For this
more difficult case, we vary SNR values from 20 dB to 50 dB. CFS is inapplicable because
of its restrictive necessary condition. Indeed tensor rank is larger than the two largest tensor
dimensions. *P* is set to 4. Figures 5(b) shows that in spite of ELS, ALS is usefulness here.
Conversely DIAG performs well for the three SNR values above 20 dB.

454 4.2.2. Influence of the collinearity factor

In the next two following examples we consider the CPD of rank 4 tensors whose columns of the random factor matrices are pairwise correlated in all the modes (swamp). For instance, correlated columns in mode q are built following the scheme of equation (60):

$$\forall r \in [1; R/2]_{\mathbb{N}} \mathbf{x}_{2r}^{(q)} = \nu \mathbf{x}_{2r-1}^{(q)} + (1-\nu)\mathbf{n}_{r}^{(q)}.$$
(63)

Note that it has been shown previously in [21] that in this kind of scenarios ALS performances 458 are significantly improved by using ELS. First simulation involves third order tensors of size 459 $4 \times 4 \times 4$. For the second simulation we consider fourth order tensors of size $4 \times 4 \times 4 \times 4$. Results 460 are plotted on figures 6(a) and 6(b) respectively. DIAG is the only algorithm which works well in 461 all the considered situations including the most difficult ones (high values of v) except for v = 0.9462 at order 3. ALS-ELS algorithm fails or is outperformed for largest values of ν ($\nu > 0.5$ at order 463 3 and $\nu > 0.7$ at order 4). At order 3 CFS results are slightly better than DIAG ones while at 464 order 4 we find an opposite situation when $\nu < 0.7$. When dealing with higher values only DIAG 465 works 466

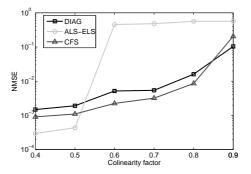
We then perform a third simulation with third order tensors of size $4 \times 4 \times 10 \times 4$. This time all the factors in each mode are mutually correlated:

$$\forall q \in [1; Q]_{\mathbb{N}}, \ \forall r \in [2; R]_{\mathbb{N}} \ \mathbf{x}_{r}^{(q)} = v \mathbf{x}_{1}^{(q)} + (1 - v) \mathbf{n}_{r}^{(q)}.$$
(64)

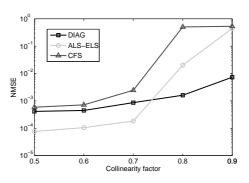
Then we vary tensors rank from 3 to 7 while ν is set to 0.8. This simulation again highlights the 469 main restriction of the CFS algorithm which cannot perform CPD of rank higher than 4. ALS-470 ELS results are slightly better than DIAG ones for ranks 3 and 4. On the opposite DIAG appears 471 as the best option for higher rank values. Notably it still provide satisfactory results for R = 7472 contrary to ALS-ELS. Finally we compare the complex version of our algorithm DIAG using 473 the complex JDTM method with the complex version of the ALS algorithm. Complex-valued 474 tensors are built as for the two first examples of this section but using complex-valued factor 475 matrices. We consider here third order tensors of size $5 \times 5 \times 5$ and rank 3. Results are displayed 476 in figure 6(d). Results obtained in the complex field are very similar to those obtained in the real 477 field for example 1. Indeed ALS starts to fail for $\nu > 0.4$ whereas DIAG still works at $\nu = 0.9$. 478

479 4.2.3. Over-factoring

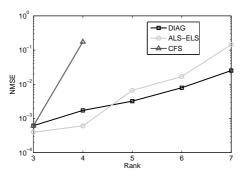
In many practical situations the actual model rank R_m of the data tensor to be decomposed 480 is unknown and it is usually not equal to the tensor rank. Few methods exist for estimating this 481 number. In addition, these sometimes provide ambiguous or contradictory results. This can lead 482 to overestimate the model rank. In other words the corresponding decomposition implies more 483 factors than it is necessary (over-factoring). Suppose that \widehat{R}_m is an overestimation of R_m and Q is 484 the tensor order. A classical problem with ALS is that the $Q(\widehat{R}_m - R_m)$ extra factors not only model 485 the additive noise but also the signal. Hence their estimation affects the estimation of the OR_m 486 actual factors. We study here the impact of over-factoring on DIAG results. For this purpose we 487 successively compute 5 CPD of 3-order noisy tensors of model rank 3 ($R_m = 3$, $I_1 = I_2 = I_3 = 7$, 488



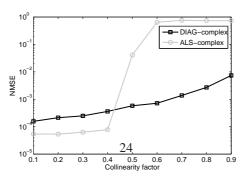
(a) Median NMSE versus collinearity factor for $4 \times 4 \times 4$ tensors of rank 4.



(b) Median NMSE versus collinearity factor for $4\times4\times4\times4$ tensors of rank 4.



(c) Median NMSE versus tensor rank for $4 \times 4 \times 10 \times 4$ tensors and v = 0.8.



(d) Median NMSE versus tensor rank for $5\times5\times5$ tensors of rank 3 in the complex field.

Figure 6: Influence of the collinearity factor on the CP decomposition

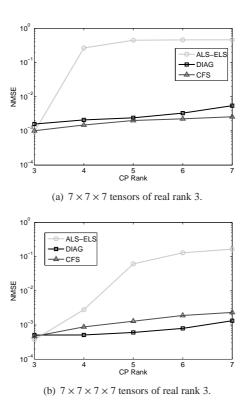


Figure 7: Median NMSE as a function of SNR at the output of the ALS-ELS, CFS and DIAG algorithms in the case of over-factoring.

Table 1: Median NMSE, averaged number of iterations and averaged number of flops for small tensors of order 3

Algorithm	Algorithm $R = 4, I =$			$\tilde{R} = 4, I = 5 \times 100 \times 5$			$R = 4, I = 5 \times 5 \times 100$		
	r_X	N_{it}	Г	r_X	N_{it}	Г	r_X	N_{it}	Г
ALS	2.3×10^{-3}	130	6×10 ⁶	2.5×10^{-3}	140	2×10^{7}	2.7×10^{-3}	192	2.8×10^{7}
ALS-ELS	2.3×10^{-3}	47	2×10^{6}	2.5×10^{-3}	46	7.5×10^{6}	2.7×10^{-3}	67	1.1×10^{7}
DIAG	5×10^{-3}	5	3×10^{5}	6.6×10^{-3}	5	1.7×10^{5}	2×10^{-2}	5	2.9×10^{7}
DIAG + ALS-ELS	2.2×10^{-3}	7	6×10^{5}	2.5×10^{-4}	8	1.4×10^{6}	2.7×10^{-3}	9	3×10^{7}

Table 2: Median NMSE, averaged number of iterations and averaged number of flops for large tensors of order 3

Algorithm	$R = 7, I = 50 \times 50 \times 50$			$R = 5, I = 100 \times 100 \times 100$			$R = 4, I = 50 \times 100 \times 50$		
	r_X	N_{it}	Г	r_X	N_{it}	Г	r_X	N_{it}	Г
ALS	5.6×10^{-4}	58		2.3×10^{-4}	23	4.6×10^{8}	3.4×10^{-4}	47	2.1×10^{8}
ALS-ELS	5.6×10^{-4}		1.8×10^{8}				3.3×10^{-4}		8.2×10^{7}
DIAG	2.1×10^{-3}	5	5.5×10^{7}	5.8×10^{-4}	5	2.8×10^{8}	5.7×10^{-4}	5	3.5×10^{7}
DIAG + ALS-ELS	5.4×10^{-4}	4	7.6×10^7	2.3×10^{-4}	3	3.3×10^{8}	3.3×10^{-4}	3	4.9×10^{7}

SNR=50 dB) truncated at rank 3 to 7 respectively. After each CPD and for each estimated factor 489 matrix we keep the three columns that best correspond to the actual 3 factors. Thereby at the end 490 of the process we can compute r_X for each CPD. DIAG results are compared with those of ALS-491 ELS and CFS on figure 7(a). It is worth mentioning that over-factoring has little impact on DIAG 492 and CFS results while ALS-ELS provides incorrect estimations of the actual factors as soon as 493 the model rank is overestimated. This is an important feature of direct approaches. A second 494 simulation is performed in the same way but with 4-order tensors of dimensions $7 \times 7 \times 7 \times 4$. 495 Model rank is still set to 3. Results are plotted on figure 7(b). Again over-factoring strongly 496 affects ALS-ELS estimates. Conversely DIAG and CFS results are consistent even in the case a 497 large number of extra factors is used. We can also note that at order 4 DIAG is less sensitive to 498 over-factoring than CFS. 499

- 500 4.2.4. A trade-off between speed and precision
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- 502
- 503

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We have shown some particular situations for which the DIAG algorithm provides the best estimation results. However one of the main advantages of the proposed approach with respect

Algorithm	$R = 5, I = 5 \times 10 \times 5 \times 10$			$R = 5, I = 5 \times 5 \times 10 \times 10$			$R = 8, I = 5 \times 5 \times 10 \times 5$		
	r_X						r_X		
	1.5×10^{-3}								
ALS-ELS	1.5×10^{-3}	29	9.4×10^{6}	1.4×10^{-3}	23	7.3×10^{6}	3.5×10^{-3}	54	2.4×10^{7}
DIAG							1.7×10^{-2}		
DIAG + ALS-ELS	1.5×10^{-3}	6	2.7×10^{6}	1.4×10^{-3}	6	2.5×10^{6}	3.5×10^{-3}	9	4.6×10^{6}
	•		•			•			

Table 3: Median NMSE, averaged number of iterations	and averaged number of flops for tensors of order 4
-----------------------------------------------------	-----------------------------------------------------

Algorithm	$I = 7 \times 7 \times 7 \times 7 \times 7 \times 7$			$I = 10 \times 10 \times 10 \times 10 \times 10$			$I = 10 \times 10 \times 10$		
	r_X	N_{it}	Г	r_X	N_{it}	Γ	r_X	N_{it}	Г
ALS	2.3×10^{-4}	21	2.6×10^{8}	2.5×10^{-4}	28	1.9×10^{8}	4.3×10^{-1}	831	4×10^{7}
ALS-ELS	2.6×10^{-4}	19	2.5×10^{8}				1.2×10^{-3}	444	2×10^{7}
DIAG	2.3×10^{-4}	4	5.4×10^{7}	2.8×10^{-4}	4	2×10^{7}	2.5×10^{-3}	5	3×10^{5}
DIAG + ALS-(ELS)	2.2×10^{-4}	2	8.3×10^{7}	2.5×10^{-4}	2	3.5×10^{7}	6.8×10^{-4}	10	7×10^{5}

Table 4: Median NMSE, averaged number of iterations and averaged number of flops for higher order tensor and tensors with correlated factors (all tensors are rank 4)

to iterative algorithms is its high convergence speed and its lower numerical complexity. Further-507 more we still have to evaluate DIAG performances in the case of big tensors. For this purpose, 508 we study here 12 representative examples by varying the tensor dimensions and the CPD rank. 509 Examples are classified into 4 groups of three examples: small tensors of order 3, large tensors 510 of order 3, tensors of order 4 and finally, higher order tensors and tensors with correlated CPD 511 factors. Median NMSE values, averaged numbers of iterations N_{it} and averaged numbers of flops 512 Γ are reported in tables 1, 2, 3 and 4 for each example of the four groups and for an SNR value 513 of 40 dB. DIAG is here compared to ALS and ALS-ELS . DIAG estimates can also be used as 514 initial guests of the ALS-ELS procedure. Hence in these tables, "DIAG + ALS-ELS" refers to 515 the ALS-ELS algorithm initialized with DIAG estimates. 516

Group of small third order tensors. In the two first examples we show that ALS and ALS-ELS 517 perform slightly better than DIAG in terms of estimation precision. However on average DIAG 518 only requires 5 JDTM iterations to converge against 46 and 140 for ALS-ELS and ALS, respec-519 tively. Hence Γ_{DIAG} is 10 to 100 times lower than Γ_{ALS} and $\Gamma_{\text{ALS}-\text{ELS}}$. Another interesting point 520 is that the DIAG + ALS-ELS procedure limits the number of ALS iterations to 7-8 (the averaged 521 number of iterations reported in the table for DIAG + ALS-ELS is the averaged number of ALS-522 ELS iterations used after an initialization with DIAG) and we can see from these results that this 523 is enough to obtain a precision similar or better than that of ALS-ELS. Consequently, the numer-524 ical complexity of this approach is 3 to 10 times lower than that those of Γ_{ALS} and $\Gamma_{ALS-ELS}$. 525 The last example is similar to the second one but tensor dimensions have been permuted so that 526 only the DIAG unfolding matrix is different. Here DIAG results are degraded both in terms of 527 precision and numerical complexity. We can conclude that if it is possible, it is better to not place 528 the larger dimension of the tensor at the end. 529

Group of large third order tensors. We consider now third order tensors whose all the dimensions are equal to 50 or 100. As a consequence, the CPD rank is far lower than the tensor dimensions and all algorithms perform better and need fewer iterations. This explain that the gap between the different algorithms is narrowing. However we can still draw the same general conclusion: DIAG remains the cheapest solution and DIAG + ALS-ELS provides the same precision than ALS and ALS-ELS for a lower numerical complexity.

Group of fourth order tensors. We obtain the same kind of results that with the first group so that DIAG + ALS-ELS still appears to give the best compromise between precision and cost. One should note however that in the last case DIAG is by far the cheapest whereas its results regarding the NMSE are not as good. This is explained by the fact than the rank is greater than three of the tensor dimensions and slightly lower than the remaining one.

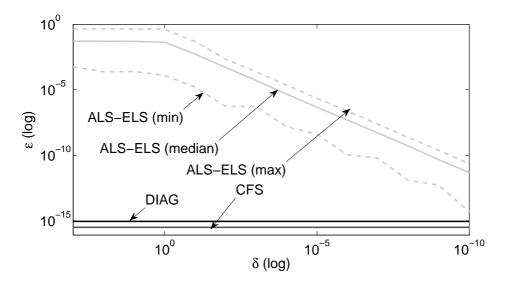


Figure 8: Decomposition of the Paatero tensor, evolution of the minimal median and maximal values of the ALS-ELS estimation error, according to a distance between the solution and the starting values and comparison with CFS and DIAG results.

Higher order tensors and tensors with correlated CPD factors. The first example of this group 541 deals with fifth order tensors (for which our version of ELS is not working). For the second 542 example we consider sixth order tensors. It is worth mentioning here that in both cases DIAG 543 provides as accurate estimates as ALS and ALS-ELS do while its numerical complexity remains 544 largely lower. Now looking at the last example with correlated factors, one can first note that 545 ALS doesn't work whereas ALS-ELS is more accurate than DIAG. The price to paid is a very 546 high number of iterations (444) and an increased computational cost (about 2×10^7 flops) against 547 5 iterations and about 3×10^5 flops for DIAG. In this case one should not that DIAG + ALS-ELS 548 is significantly better than ALS-ELS in terms of estimation precision for a limited numerical 549 complexity. 550

551

As a first conclusion DIAG appears as a good trade-off between estimation precision, speed and numerical complexity. Besides, the DIAG + ALS-ELS procedure provides a similar or better precision than that of ALS-ELS whereas its numerical complexity remains quite close to that of DIAG. Hence by combining both algorithms one can achieve the best precision, a good convergence speed and a reduced numerical complexity.

557 4.3. Results on the Paatero tensor

In [44], Paatero introduced a very simple 3-order tensor of size $2 \times 2 \times 2$ which has the following form:

$$\mathcal{T} = \begin{bmatrix} 0 & 1 & e & 0 \\ 1 & d & 0 & h \end{bmatrix}.$$
 (65)

560 Let's define its determinant Δ by:

$$\Delta = 4h + d^2 e. \tag{66}$$

Then, it can be shown that the equation $\Delta = 0$ partitions the space into two subspaces, which hence have a non zero volume: The inequality $\Delta > 0$ defines the subspace of rank-2 tensors, whereas $\Delta < 0$ defines the subspace of rank-3 tensors. Finally, the closed set of tensors of rank 1 lies on the hypersurface $\Delta = 0$. [21]

Some of these tensors have the particularity of misleading any iterative algorithm, although the chosen starting value is close to the solution. As an example, Paatero notably consider in [44] to decompose the tensor defined by (e, d, h) = (30, 0.26, 0.34) from the initial value (e, d, h) =(30, 0.3, 0.12). This tensor belongs to the rank 2 subspace but it is close to the variety $\Delta = 0$. Its decomposition is given by the three following factor matrices:

$$\boldsymbol{A} = \begin{bmatrix} 1/x & -1/x \\ y_1 & y_2 \end{bmatrix} \quad \boldsymbol{B} = \begin{bmatrix} 1/x & -1/x \\ y_1 & y_2 \end{bmatrix} \quad \boldsymbol{C} = \begin{bmatrix} 1/x & -1/x \\ y_3 & y_4 \end{bmatrix}, \tag{67}$$

with: $x = (4h/e + d^2)^{\frac{1}{6}}$, $y_2 = (x^3 - d)/(2x)$, $y_1 = x^2 - a_2$, $y_4 = h/(y_2(y_1 + y_2))$ and $y_3 = y_2y_4/y_1$. 570 Later in [21], authors confirmed that in this case, even the most efficient iterative algorithms 571 such as ALS-ELS and Levenberg-Marquardt get stuck in a local minimum of the cost function, 572 leading to a very bad estimation of the factor matrices. Actually, since the iterative algorithms 573 works by successive optimization of rank-2 tensors, they cannot take the shorter paths to the 574 solution which could cross the space of rank-3 tensors. Thereby, this is an other typical situation 575 where direct algorithms can help. In order to see this we have reproduced the experiment here not 576 only for the Paatero starting values but for different starting values around the solution. Hence 577 we define a parameter δ such that the initial factor matrices of the ALS-ELS, $A^{(0)}$, $B^{(0)}$ 578

$$A^{(0)} = A + \delta E_A; \ B^{(0)} = B + \delta E_B; \ C^{(0)} = C + \delta E_C, \tag{68}$$

where E_A , E_B and E_C are matrices of size 2 × 2 whose elements are randomly drawn according to a standard normal law. We now define ϵ as the mean estimation error upon the three estimated factor matrices, \widehat{A} , \widehat{B} and \widehat{C} :

$$\epsilon = \frac{1}{3} \left(\frac{\|\boldsymbol{A} - \widehat{\boldsymbol{A}}\|_F}{\|\boldsymbol{A}\|_F} + \frac{\|\boldsymbol{B} - \widehat{\boldsymbol{B}}\|_F}{\|\boldsymbol{B}\|_F} + \frac{\|\boldsymbol{C} - \widehat{\boldsymbol{C}}\|_F}{\|\boldsymbol{C}\|_F} \right).$$
(69)

The ALS-ELS algorithm is run 500 times on the tensor \mathcal{T} , with a new draw of the E_A, E_B and 582 E_C matrices at each time, and for different values of δ comprised between 1000 and 10⁻¹⁰. We 583 present on figure 8 the plots of the median, minimal and maximal values of $\epsilon_{ALS-ELS}$ according 584 to the δ value. For comparison, both ϵ_{DIAG} and ϵ_{CFS} values are also reported on the figure. It can 585 be seen that the iterative algorithm needs a very good initialisation in order to get an estimation 586 precision close to the machine precision. Recall that we are looking for an exact decomposition 587 since the considered tensors are noise free. Conversely, direct algorithms such as the closed-588 form solution or DIAG provide a perfect decomposition of \mathcal{T} and a thus an exact estimation of 589 the factor matrices. 590

591 5. Application to fluorescence spectroscopy

A good application example of the CPD is found in fluorescence spectroscopy since after some numerical corrections measured data can be modelled by a CPD with physical meaning. Standard spectrofluorimeters allow to measure the intensity of the fluorescence signal emitted

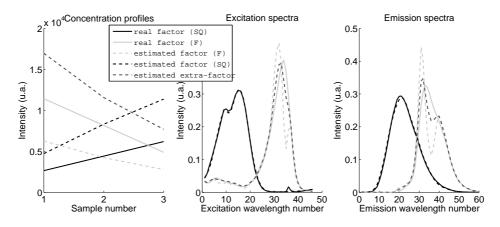


Figure 9: CPD factors of the fluorescence tensor using ALS.

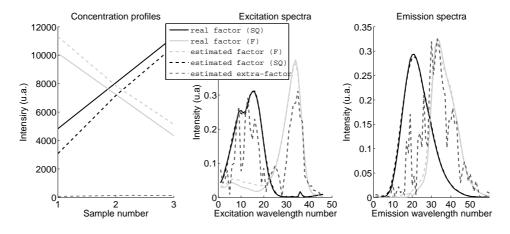


Figure 10: CPD factors of the fluorescence tensor using DIAG-JDTM.

by a diluted solution at wavelength λ_i by exciting the solution at wavelength λ_i . Hence, by 595 scanning the excitation-emission couples (λ_i, λ_i) one obtains an $I \times J$ matrix of fluorescence 596 which is called the Fluorescence Excitation-Emission Matrix (FEEM) of the solution. In many 597 applications one have to measure a FEEM set corresponding to a set of K solutions and thus 598 obtains a fluorescing data tensor X of order 3 and size $I \times J \times K$ which contains the K FEEM. 599 Solutions are often mixtures of a small number, R_m , of diluted fluorescing chemical species 600 (fluorophores). Fluorophore concentrations vary from a solution to an other. Hence fluorophore 601 r is characterized by its excitation spectrum, $e_r(\lambda_i)$, its fluorescence emission spectrum, $f_r(\lambda_i)$ 602 and the variation of its concentration through the solution set (concentration profile), $c_r(k)$. In 603 practice one wants to recover e_r , f_r and c_r $(r = 1 \cdots R_m)$ from the measured FEEMs. It can be 604 shown that after removing scattering effects and correcting (or preventing) inner filter effects, the 605 contribution of each fluorophore to the solution signal is linear in excitation, in emission and in 606 concentration. In other words we have: 607

$$\mathcal{X}_{i,j,k} = \sum_{r=1}^{R_m} E_{i,r} F_{j,r} C_{k,r},$$
(70)

where $E_{i,r} = e_r(\lambda_i)$, $F_{j,r} = f_r(\lambda_j)$ and $C_{k,r} = c_r(k)$, so that the CPD solves this inverse problem in a deterministic way. This is the reason why CPD has been largely applied to analyze FEEM sets since original works of Bro in this area [9, 10].

In most applications of fluorescence spectroscopy the number of fluorophores which defines the 611 model rank of the decomposition is unknown and has to be estimated. However few methods 612 exist and can give contradictory results and lead to over-factoring. A good example of this 613 situation can be found in [45]. This would be acceptable if in each estimated factor matrix 614 one obtain the R_m real factors aside with extra factors whose the contributions are almost null. 615 Actually this is not the case with ALS which is very commonly used for analyzing this kind of 616 data. Therefore this problem remains an important issue of FEEM analysis. In order to highlight 617 the reliability of DIAG in this context we consider here a fluorescence tensor which contains 618 the fluorescence intensity of 3 distinct mixtures of two fluorophores (fluorescein and quinine 619 sulphate) measured at 46×71 excitation-emission wavelength couples. Hence the tensor size is 620 $3 \times 46 \times 71$ and the model rank is 2. CPD of rank 3 were then used to decompose the tensor. 621 ALS and DIAG results are reported on figure 9 and 10 respectively and compared to the actual 622 factors after removing permutation and scaling indeterminacy. Excitation and Emission factors 623 are normalized so that factor contributions are condensed in the concentration mode. Actual 624 concentration profiles are perfectly known since these are laboratory mixtures and actual spectra 625 were measured aside from pure solutions of fluorescein and quinine sulphate. This is a simple 626 case for which both algorithms give perfect results when the good model rank $(R_m = 2)$ is 627 selected (data not shown). However ALS sensitivity to over-factoring effect in a concrete case 628 clearly appears here. Indeed actual factors are not well estimated (notably the fluorescein spectra 629 and the concentration profiles). Moreover contribution of the extra factor to the decomposition 630 is significant. Recall that this factor has no physical meaning. On the opposite DIAG results are 631 satisfying notably regarding the estimated spectra. One can verify that the contribution of the 632 extra factor is almost null. 633

634 6. Conclusion

We have described in this paper a CPD algorithm that takes advantage of the link between CPD and Joint EVD in an original way. A JEVD algorithm has been conjointly proposed. Com⁶³⁷ putational complexities and extension to the complex field have been given for both algorithms. ⁶³⁸ Numerical simulations point out the efficiency of the proposed JDTM algorithm to solve the ⁶³⁹ JEVD problem. This algorithm usually offers more accurate results than its competitors espe-⁶⁴⁰ cially in the most difficult cases involving big matrices and low SNR values. In terms of numer-⁶⁴¹ ical complexity, the JDTM algorithm also provides good performances thanks to a remarkably ⁶⁴² low and stable number of iterations.

⁶⁴³ Classical iterative CPD algorithms such as ALS are usually efficient but suffer from convergence ⁶⁴⁴ problem, notably in case of highly correlated factors, and are very sensitive to over-factoring. ⁶⁴⁵ In addition they require a large number of iterations to reach the convergence. ELS allows us ⁶⁴⁶ to reduce this number and deals with correlated factors in some situations but it remains useless ⁶⁴⁷ in case of over-factoring. In addition, we have seen that there are some simple cases for which ⁶⁴⁸ iterative approaches consistently fail for theoretical reasons.

In this context direct approaches such as the proposed DIAG algorithm have been designed 649 to prevent such issues. First the DIAG algorithm involves a limited iterative procedure which 650 requires very few iterations hence limiting global computational cost of the algorithm. Second it 651 is insensitive to over-factoring thanks to the initial SVD which is independent of the chosen rank. 652 These features have been verified in this paper by using many numerical simulations. Notably we 653 have shown that DIAG was able to deal with highly correlated factors in all the modes or a large 654 number of extra factor in case of over-factoring. Furthermore our results also demonstrates that 655 DIAG is very efficient to decompose high order tensors. Finally it is a very fast algorithm with a 656 lower computational complexity than ALS or ALS-ELS, notably in the case of small tensors or 657 correlated factors. 658

As a counterpart, DIAG implies more restricted necessary conditions on the CPD rank than 659 ALS. Therefore ALS-ELS is more accurate than DIAG when the rank is close to DIAG intrinsic 660 limit. This is usually not the case in fluorescence spectroscopy applications for which at least one 661 tensor dimension is largely greater than the model rank. In addition it has been shown that DIAG 662 results can be improved by adding very few ALS iterations with a limited impact on the overall 663 numerical complexity. Conversely, one should note that over-factoring is an important issue of 664 FEEM analysis. This makes DIAG an attractive alternative to the classical ALS procedure for 665 the CPD of fluorescence tensors, as it has been shown on a practical example. 666

Eventually, comparing to the CFS algorithm which is also a reference direct CPD approach, DIAG is a cheaper algorithm since it only involves one JEVD procedure and does not require to compare several estimates of the factor matrices. But its main advantage definitely comes from the necessary condition of CFS which is more restricted than DIAG's one. Hence there are many simple cases that CFS cannot handle. More generally CFS accuracy decreases as we get closer to its intrinsic limit. Otherwise CFS results are close to DIAG results.

673 Appendix A. Proof of proposition 1

Proof 2. $C_{CFS} \Rightarrow C_{DIAG}$ is trivial. Indeed if $\exists (q_1, q_2) \in [1; Q]_{\mathbb{N}}^2$, $q_1 \neq q_2$ such that $I(q_1) \geq R$ and $I(q_2) \geq R$ then taking any permutation f_I of the Q first natural number such that $f_I(1) = q_1$ and $f_I(2) = q_2$, P = 1 and $q_s = Q$ ensures C_{DIAG} . Let now suppose that C_{DIAG} is true and that C_{ALS} is false, i.e.:

$$\exists P \in [2; Q-1]_{\mathbb{N}}, \exists f_I, \exists q_s > P \text{ and } q \le Q \text{ such that:} \quad 1) \quad \prod_{i=1}^{P} I(f_I(i)) \ge R, \quad (A.1)$$

2)
$$\prod_{\substack{i=P+1\\i\neq q_s}}^{Q} I(f_I(i)) \ge R, \quad (A.2)$$

3)
$$\prod_{i=1}^{Q} I(i) < RI(q).$$
 (A.3)

678 Since we have $1 \le q \le Q$ thus $q \in \{f_I(1), \dots, f_I(P)\} \cup \{f_I(P+1), \dots, f_I(Q)\}.$

• We first assume that $q \in \{f_I(1), \dots, f_I(P)\}$. 2) and 3) give:

$$\frac{1}{I(f_I(q_s))} \prod_{i=P+1}^{Q} I(f_I(i)) > \frac{1}{I(q)} \prod_{i=1}^{Q} I(i),$$
(A.4)

$$\frac{1}{I(f_I(q_s))} \prod_{i=P+1}^{Q} I(f_I(i)) > \frac{1}{I(q)} \prod_{i=1}^{Q} I(f_I(i)),$$
(A.5)

$$I(q) > I(f_I(q_s)) \prod_{i=1}^{P} I(f_I(i)).$$
 (A.6)

680 Since $q \in \{f_I(1), \cdots, f_I(P)\},\$

$$\prod_{i=1}^{P} I(f_{I}(i)) = I(q) \prod_{\substack{i=1\\i \neq f_{I}^{-1}(q)}}^{P} I(f_{I}(i))$$
(A.7)

681 thereby,

$$1 > I(f_I(q_s)) \prod_{\substack{i=1\\i \neq f_I^{-1}(q)}}^P I(f_I(i))$$
(A.8)

682 which is absurd.

• Now we assume that $q \in \{f_I(P+1), \dots, f_I(Q)\}$. Thereby,

$$I(q) < \prod_{i=P+1}^{Q} I(f_I(i)),$$
 (A.9)

$$I(q) \prod_{i=1}^{P} I(f_{I}(i)) < \prod_{i=1}^{Q} I(f_{I}(i)),$$
(A.10)

⁶⁸⁴ *while* 1) *and* 3) *give:*

$$I(q) \prod_{i=1}^{P} I(f_{I}(i)) > \prod_{i=1}^{Q} I(i),$$
 (A.11)

$$I(q) \prod_{i=1}^{P} I(f_{I}(i)) > \prod_{i=1}^{Q} I(f_{I}(i)),$$
(A.12)
33

685 which is contradictory to (A.10).

⁶⁸⁶ Therefore if C_{DIAG} is verified then C_{ALS} is verified.

687 References

- [1] Carroll, J.D., Chang, J.J.: Analysis of Individual Differences in Multidimensional Scaling via N-Way Generalization
 of Eckart-Young Decomposition, Psychometrika, 35 (3) pp. 283-319 (1970)
- [2] Becker, A., Comon, P., Albera, L., Haardt, M., Merlet, I.: Multi-way Space-Time-Wave-Vector analysis for EEG
 source separation. Signal Processing, to appear in
- [3] Deburchgraeve W., Cherian P.J., De Vos M., Swarte R.M., Blok J.H., Visser G.H., Govaert P., Van Huffel S.: Neonatal seizure localization using PARAFAC decomposition, Clinical Neurophysiology, 120, pp. 1787-1796 (2009)
- [4] Vanderperren K., De Vos M., Mijovic B., Ramautar J.R., Novitskiy N., Vanrumste B., Stiers P., Van den Bergh
 B.R.H., Wagemans J., Lagae L., Sunaert S., Van Huffel S.: PARAFAC on ERP data from a visual detection task dur ing simultaneous fMRI acquisition, in Proc. of the International Biosignal Processing Conference., Berlin, Germany,
 Jul. 2010, 103, pp. 1-4 (2010)
- [5] Karfoul, A. , Albera, L., De Lathauwer, L.: Iterative methods for the canonical decomposition of multi-way arrays:
 Application to blind underdetermined mixture identification. Signal Processing, 91 (8), pp. 1789-1802 (2011)
- [6] Sidiropoulos, N.D., Giannakis, G.B., Bro, R.: Blind PARAFAC receivers for DS-CDMA systems, IEEE Transactions On Signal Processing, 48 (8), pp. 810-823 (2000)
- [7] Nion, D., Sidiropoulos, N.D., Tensor Algebra and Multi-dimensional Harmonic Retrieval in Signal Processing for
 MIMO Radar, IEEE Trans. on Signal Processing, 58 (11), pp. 5693-5705 (2010)
- [8] Bürgisser, P., Clausen, M., Shokrollahi, M.A.: Algebraic Complexity Theory, 315, Springer (1997)
- 705 [9] Bro, R.: PARAFAC, Tutorial and Applications, Chemom. Intel. Lab. Syst., 38, pp. 149-171 (1997)
- [10] Stedmon, C.A., Markager, S., Bro, R.: Tracing dissolved organic matter in aquatic environments using a new approach to fluorescence spectroscopy, Marine Chemistry, 82 (3-4), pp. 239-254 (2003)
- [11] Harshman, R.A.: Determination and proof of minimum uniqueness conditions for PARAFAC-1," UCLA Working
 Papers in Phonetics, 22, pp. 111-117 (1972)
- 710 [12] Kruskal, J.B.: Three-Way Arrays: Rank and Uniqueness of Trilinear Decompositions, Linear Algebra and Appli-711 cations, 18, pp. 95-138 (1977)
- [13] Ten Berge, J.M.F., Sidiropoulos, N.D.: On uniqueness in CANDECOMP/PARAFAC, Psychometrika, 67, pp. 399-409 (2002)
- [14] Jiang, T., Sidiropoulos, N.D.: Kruskal's permutation lemma and the identification of CANDECOMP/PARAFAC
 and bilinear models with constant modulus constraints, Trans. on Sig. Proc., 52 (9), pp. 2625-2636 (2004)
- [15] De Lathauwer, L.: A Link between Canonical Decomposition in Multilinear Algebra and Simultaneous Matrix
 Diagonalization, Journal on Matrix Analysis, 28 (3), pp. 642-666 (2006)
- [16] Stegeman, A., Sidiropoulos, N.D.: On Kruskal's uniqueness condition for the Candecomp/Parafac decomposition,
 Linear Algebra and its Applications, 420, pp. 540-552 (2007)
- [17] Hitchcock, F.L.: The expression of a tensor or a polyadic as a sum of products, J. Math. Phys, 6 (1), pp. 164-189
 (1927)
- [18] Harshman, R.A.: Foundations of the Parafac procedure: Models and conditions for an explanatory multimodal
 factor analysis, UCLA Working Papers in Phonetics, 16, pp. 1-84 (1970)
- [19] Tendeiro, J., Bennani Dosse, M., Ten Berge, J.M.F., First and second-order derivatives for CP and INDSCAL,
 Chemometrics and Intelligent Laboratory Systems, 102 (1), pp. 27-36 (2011)
- [20] Tomasi, G., Bro, R.: A comparison of algorithms for fitting the PARAFAC model, Comp. Stat. Data Anal., 50, pp. 1700-1734 (2006)
- [21] Comon, P., Luciani, X., De Almeida, A.L.F.: Tensor Decompositions, Alternating Least Squares and other Tales,
 Journal of Chemometrics, 23 (9), pp. 393-405 (2009)
- [22] Acar E., Dunlavy D.M., Kolda, T.G.: Scalable Tensor Factorizations with Missing Data, In SDM10: Proceedings
 of the 2010 SIAM International Conference on Data Mining, pp. 701-712 (2010)
- [23] Kindermann, S., Navasca, C.: New algorithms for tensor decomposition based on a reduced functional, Numer.
 Linear Algebra Appl. (2013)
- [24] Rajih, M., Comon, P., Harshman, R.: Enhanced Line Search : A Novel Method to Accelerate PARAFAC, SIAM Journal on Matrix Analysis Appl., 30 (3), pp. 1148-1171 (2008)
- [25] Faber, N.M., Buydens, L.M.C., Kateman, G.: Generalized rank annihilation method: II. Bias and variance in the
 estimated eigenvalues, J. Chemom., 8, pp.181-203 (1994)

- Faber N.M., Bro R., Hopke P.K: Recent developments in CANDECOMP/PARAFAC algorithms: a critical review,
 Chemom. Intel. Lab. Syst., 65 (1), pp. 119-137 (2003)
- [27] Roemer, F., Haardt, M.: A closed-form solution for Parallel Factor (PARAFAC) Analysis, In IEEE ICASSP'2008,
 pp. 2365-2368 (2008)
- [28] Roemer, F., Haardt, M.: A closed-form solution for multilinear PARAFAC decompositions, In IEEE SAM 2008,
 pp. 487-491 (2008)
- [29] De Lathauwer, L., De Moor, B., Vandewalle, J.: Computation of the Canonical Decomposition by Means of a
 Simultaneous Generalized Schur Decomposition, SIAM Journal on Matrix Analysis and Applications, 26, pp. 295 327 (2001)
- [30] Albera, L., Ferréol, A., Comon, P., Chevalier, P.: Blind Identification of Overcomplete MixturEs of sources
 (BIOME), Linear Algebra and its Applications, 391, pp. 3-11 (2004)
- [31] Luciani, X., Albera, A.: Joint Eigenvalue Decomposition using Polar Matrix Factorization, In LVA/ICA 2010, pp. 612-619 (2010)
- [32] Luciani, X., Albera, A.: Semi-algebraic canonical decomposition of multi-way arrays and joint eigenvalue decom position, In IEEE ICASSP'2011, pp. 4104-4107 (2011)
- [33] Karfoul, A., Albera, L., Birot, G.: Blind underdetermined mixture identification by joint canonical decomposition of HO cumulants, IEEE Trans. Signal Proc., 58 (2), pp. 638-649 (2010)
- [34] Ruhe, A.: On the quadratic convergence of a generalization of the Jacobi method to arbitrary matrices, BIT Numerical Mathematics, 8, pp. 210-231 (1968)
- 757 [35] Haardt, M., Nossek, J. A.: Simultaneous Schur decomposition of several nonsymmetric matrices to achieve auto-
- matic pairing in multidimensional harmonic retrieveal problems, IEEE Trans. Signal Proc., 46, pp. 161-169 (1998)
 [36] Strobach, P.: Bi-iteration multiple invariance subspace tracking and adaptive ESPRIT, IEEE Trans. Signal Proc.,
- 48, pp. 442-456 (2000)
- [37] Fu, T., Gao, X.: Simultaneous Diagonalization with Similarity Transformation for Non-defective Matrices. In IEEE
 ICASSP'2006, pp. 1137-1140 (2006)
- [38] Goldstine, H.H.: Horwitz, L.P.: A procedure for the diagonalization of normal matrices, J. ACM, 6 (2), pp. 176-195
 (1959)
- [39] Eberlein, P.J.: A Jacobi-like method for the automatic computation of eigenvalues and eigenvectors of an arbitrary
 matrix, Journal of the Society for Industrial and Applied Mathematics, 10 (1), pp. 74-88 (1962)
- [40] Souloumiac, A.: Nonorthogonal joint Diagonalization by Combining Givens and Hyperbolic Rotations, IEEE
 Trans. Signal Proc., 57 (6), pp. 2222-2231 (2009)
- [41] Iferroudjene, R., Abed Meraim, K., Belouchrani, A.: A New Jacobi-like Method for Joint Diagonalization of
 Arbitrary non-defective Matrices, Applied Mathematics and Computation 211, pp. 363-373 (2009)
- [42] Cardoso, J.-F., Souloumiac, A.: Jacobi Angles for Simultaneous Diagonalization, SIAM Journal on Matrix Analy sis and Applications, 17 (1), pp. 161-164 (1996)
- [43] De Lathauwer, L., De Moor, B., Vandewalle, J.: A multilinear singular value decomposition, SIAM Journal on Matrix Analysis and Applications, 21 (4), pp. 1253-1278, (2000)
- [44] Paatero, P.: Construction and analysis of degenerate Parafac models, Journal of Chemometrics, 14, pp. 285-299
 (2000)
- 177 [45] Luciani, X., Mounier, S., Paraquetti, H.H.M., Redon, R., Lucas, Y., Bois, A., Lacerda, L.D., Raynaud, M., Ripert,
- M.:Tracing of dissolved organic matter from the SEPETIBA Bay (Brazil) by PARAFAC analysis of total lumines cence matrices, Marine Environmental Research, 65 (2), pp. 148-157 (2008)