RaJIVE: Robust Angle Based JIVE for Integrating Noisy Multi-Source Data

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Abstract

Motivation: With increasing availability of high dimensional, multi-source data, the identification of joint and data specific patterns of variability has become a subject of interest in many research areas. Several matrix decomposition methods have been formulated for this purpose, for example JIVE (Joint and Individual Variation Explained), and its angle based variation, aJIVE. Although the effect of data contamination on the estimated joint and individual components has not been considered in the literature, gross errors and outliers in the data can cause instability in such methods, and lead to incorrect estimation of joint and individual variance components.

Results: We focus on the aJIVE factorization method and provide a thorough analysis of the effect outliers on the resulting variation decomposition. After showing that such effect is not negligible when all data-sources are contaminated, we propose a robust extension of aJIVE (RaJIVE) that integrates a robust formulation of the singular value decomposition into the aJIVE approach. The proposed RaJIVE is shown to provide correct decompositions even in the presence of outliers and improves the performance of aJIVE. We use extensive simulation studies with different levels of data contamination to compare the two methods. Finally, we describe an application of RaJIVE to a multi-omics breast cancer dataset from The Cancer Genome Atlas.
1 Introduction

The analysis of high dimensional data has recently become a major statistical challenge in many different fields of scientific research, where advanced technologies and computing resources enable the collection of extremely large datasets. In several cases, data are collected from different measurement devices and techniques. For example, in genomic studies, multiple layers of omics data are collected on the same organisms or tissues, and measured on different platforms. Integration of these high-dimensional data, obtained from multiple sources, is required for their simultaneous analyses which has received growing interest in recent times (Tseng et al., 2015; Huang et al., 2017; Rappaport and Ron, 2018).

In such multi-source data, it is important to identify the variation patterns that are shared among the different data layers, arising from the underlying joint processes, and to separate them from the individual, source specific components of variation. Proper identification of both types of variation components can contribute to a more accurate interpretation of the underlying processes and yield better model predictions (Måge et al., 2019; Ponzi et al., 2020). Several methods have been proposed for this purpose of separating the common and the component-wise variations from multiple data sources (Lofsted et al., 2012; Lock et al., 2013; Schouteden et al., 2013; Feng et al., 2018; Tang and Allen, 2018; Fan et al., 2019); most of them are based on a common framework of matrix decomposition. Among these, JIVE (Joint and Individual Variation Explained) (Lock et al., 2013) has become widely popular, especially in medical applications (Hellton and Thoresen, 2016; Kuligowski et al., 2015; Kaplan and Lock, 2017). JIVE minimizes the squared residual components of the decomposition of the data matrix, using an iterative algorithm that alternatively estimates the joint and individual components using...
singular value decomposition (SVD). Subsequently, Feng et al. (2018) proposed an angle based variation of JIVE (aJIVE), which computes the matrix decomposition by using perturbations of the row spaces and is computationally more efficient than the original JIVE.

Although aJIVE improves JIVE by reducing its computational burden, it still relies on the SVD for factorization of the data matrices into joint, individual and residual components. Usual computation of SVD is, however, highly sensitive to the presence of any gross errors or outliers in the data (Zhang et al., 2013; Hawkins et al., 2001). As a consequence, both JIVE and aJIVE become extremely unstable in presence of noise in the data and often lead to incorrect inference on the resulting joint and individual variation components. But, modern large-scale datasets collected via different sources, e.g., multi-omics data, are prone to different kinds of noise and outlying observations, and hence, an appropriate robust algorithm is of utmost practical necessity to integrate such multi-source datasets for stable inferential conclusion.

Surprisingly, the existing literature on this important topic is very limited. A robust alternative to JIVE has recently been proposed (Sagonas et al., 2017) with successful applications in image recognition and facial analysis. However, since it does not utilize the idea of aJIVE to reduce the computational burden, it becomes even more computationally challenging than the original JIVE for large-scale datasets. Another alternative procedure for data integration, namely the Robust Correlated and Individual Components Analysis (Panagakis et al., 2016), provides a robust solution against outliers in the data; but it is limited to the analysis of two datasets only, and does not generalize for integration of more data-sources. Further, both methods have only been applied to image recognition problems but no biological application is found in the literature.

This present work focuses on robustly identifying the common and the distinct variation components from multi-source data in the presence of outliers in either (or some) of the data sources (≥ 2). We propose a novel robust extension of the aJIVE algorithm, which we will refer to as “RaJIVE”, by integrating a robust formulation of the SVD within the computationally efficient angle based approach of aJIVE. We assess the performance of the proposed RaJIVE method via extensive simulation studies, where we investigate the correct recovery of individual
and joint components in the presence of increasing proportions of outliers within appropriate synthetic datasets. Additionally, considering different outlier configurations, we also illustrate their effects on the standard aJIVE decomposition. To our knowledge, the effects of outliers on such decomposition of joint and individual variation components are not yet investigated in the literature; our thorough analyses of the consequences of different types of noises would be highly beneficial for a large class of multi-source studies. The proposed RaJIVE is shown to provide significantly improved results compared to the usual aJIVE under data contamination.

Finally, we describe a real-life application to multi-source omics data from The Cancer Genome Atlas (TCGA Research Network [https://www.cancer.gov/tcga]), where we apply RaJIVE to simultaneously analyze methylation, gene expression and miRNA data collected on breast cancer samples.

2 Methods

2.1 Angle Based JIVE (aJIVE)

In a data integration setup with $K$ data-sources and $n$ subjects, each data-block is denoted as $X_k$, $k = 1, \ldots, K$, which is a matrix with $n$ columns for $n$ subjects and $p_k$ rows corresponding to the variables in the $k$-th data-source. The overall dimensionality of the data is then $p = p_1 + \ldots + p_K$. Our aim is to identify the joint variation components among these $K$ data-matrices and separate them from the individual source-specific variation (and residual) components. Mathematically, we consider the decomposition of each data-matrix into the sum of three low-rank terms as follows.

\[
\begin{align*}
X_1 &= J_1 + I_1 + \epsilon_1 \\
\vdots \\
X_K &= J_K + I_K + \epsilon_K.
\end{align*}
\]
where $I_k$ is the individual component for the $k$-th data-block, $\epsilon_k$ is its residual (random error) component and

$$J = \begin{bmatrix} J_1 \\ \vdots \\ J_K \end{bmatrix}$$

(2)

is the joint structure matrix with each $J_k$ being the submatrix associated with $X_k$. We then need to identify (estimate) these submatrices $J_k$ and $I_k$, $k = 1, \ldots, K$, from the observed data-matrices $X_k$.

The aJIVE method (Feng et al., 2018) is a popular algorithm for this data-integration problem, which is structured in three phases: First it computes the low-rank approximation of each data block $X_k$, by using its SVD. In the second phase, called score space segmentation, it extracts the joint structure between the obtained low-rank approximations, by computing the SVD of the stacked row basis matrices, based on the principles of Principal Angle Analysis. Finally, each data block is projected onto the joint bases to obtain the joint components $J_k$; the individual components $I_k$ are then calculated by orthonormal basis subtraction. Ready-to-use implementation of aJIVE is available in both Matlab (Jiang, 2018) and R (Carmichael, 2019).

2.2 The Proposed Algorithm: RaJIVE

In order to correct the non-robust nature of aJIVE, we propose a new novel RaJIVE algorithm where we incorporate a robust SVD approach of Zhang et al. (2013) within the aJIVE framework of data integration. There are two existing approaches of robust SVD computation (Hawkins et al., 2001; Zhang et al., 2013); both use a robust loss for the minimization of the error between the data matrix and the SVD reconstruction after formulating the problem to an alternating (linear) regression procedure. Specifically, the robust $\ell_1$-loss is used in Hawkins et al. (2001) and Zhang et al. (2013) used the Huber loss associated with M-estimation of the regression coefficients (Huber and Ronchetti, 2011). This Huber loss is known to yield more efficient estimator of regression coefficients compared to the $\ell_1$-loss (Huber and Ronchetti, 2011) and also the corresponding robust SVD computation requires lower computation time. For these
reasons, after investigating both robust SVD approaches, we propose to use the one from Zhang et al. (2013) which additionally includes a suitable provision for allowing missing values in the datasets. This particular robust SVD algorithm, to be referred to as the robRSVD, is devised based on the idea of subsequently using iterative reweighted least-squares to compute the regression coefficients at each step. The weights are computed based on the Huber’s function (Zhang and Pan, 2013) to achieve robustness of the resulting singular values and the associated singular vectors. For the sake of completeness, a brief discussion about the computation of this robRSVD is presented in Appendix A.

Our proposed RaJIVE uses this robRSVD instead of the usual SVD in each step of iterations, but works in three phases as in aJIVE. In the first phase, it uses robRSVD to compute the low-rank approximations of each data-matrix $X_k$. Secondly, we stack the row basis matrices obtained from the robRSVD of each block, and extract the (robust estimate of) joint-structure by another application of robRSVD to the stacked matrix, following the same principle as in Algorithm 1

**Algorithm 1** Pseudo-code for RaJIVE

*Input*: Data $X_k$, $k = 1, ..., K$, initial individual ranks $r_1, ..., r_K$.

*Output*: Joint $J_k$, Individual $I_k$ and Noise $E_k$ Components

**Phase 1: Initial Signal Space Extraction**

1: for $k = 1, ..., K$ do
2: Compute the robust SVD of block $X_k$
3: Threshold based on initial rank specifications: $\tilde{U}_k \tilde{\Sigma}_k \tilde{V}_k^T$

**Phase 2: Score Space Segmentation**

4: $M \leftarrow \begin{bmatrix} \tilde{V}_1 \\ \vdots \\ \tilde{V}_K \end{bmatrix}$

Stacked singular vectors matrix

5: Compute the robust SVD of $M$ and identify principal angles

**Phase 3: Final decomposition**

6: for $k = 1, ..., K$ do
7: $P_j \leftarrow \tilde{V}_j \tilde{V}_j^T$ Projection matrix onto joint space
8: $J_k \leftarrow X_k P_j$ Projection of $X_k$ onto joint basis
9: $I_k \leftarrow X_k P_j^\perp$ Orthonormal basis subtraction
10: $I_k \leftarrow$ Threshold robust SVD of $I_k$
11: $E_k \leftarrow$ Remaining components of each SVD
aJIVE. Once the joint structure is obtained, each data block is projected onto the estimated robust joint-bases to compute the joint components $J_k$. Finally, the robust estimates of the individual $I_k$ are computed through orthonormal basis subtraction. Additionally, we have appropriately modified the implementation of RaJIVE (from that of aJIVE) to allow for parallel computation, which significantly reduces its computational time. The pseudo-code for the final RaJIVE algorithm is presented in Algorithm 1. We also provide an R package, RaJIVE, containing the ready-to-use implementation of our proposed algorithm.

3 Simulation studies

3.1 Simulation Scheme

Settings: $K = 3$ data sets were simulated, with $n$ columns each and different number of rows as $p_1, p_2, p_3$, respectively. The true joint rank was taken as $r$ and the true individual ranks as $r_1, r_2, r_3$, respectively. Outliers were generated by adding random errors from $\mathcal{N}(\mu_c, \sigma^2_c)$ to a given proportion of variables and observations, as per the following six configurations: (O1) outliers in $p_k/5$ variables across all three data-sources, (O2) outliers in $p_k/5$ variables in the data-source with highest initial rank, (O3) outliers in $p_k/5$ variables in the data-source with lowest initial rank, (O4) outliers in all $p_k$ variables across the three data sources, (O5) outliers in all $p_k$ variables in the data source with highest initial rank and (O6) outliers in all $p_k$ variables in the data source with lowest initial rank, where $p_k$ is the number of variables in the respective $k$-th data-matrix. Additionally, different proportions of observations were contaminated in each cases. The simulation study was repeated 100 times to see the variability in the results.

Performance measures: For each set of simulated data-matrices, the usual aJIVE and the proposed RaJIVE was performed with and without the outliers and results were compared in terms of the joint rank, the individual ranks and the proportions of variance explained. Additionally, the subspace recovery error was also considered, which measures the distance
between the true (simulated) and estimated joint subspaces as

\[ SRE = \frac{1}{r} \| \hat{\mathbf{U}}^T \hat{\mathbf{U}} - \mathbf{U}^T \mathbf{U} \|. \]

(3)

Here, \( \hat{\mathbf{U}} = [\hat{\mathbf{u}}_1, ..., \hat{\mathbf{u}}_r] \) and \( \mathbf{U} = [\mathbf{u}_1, ..., \mathbf{u}_r] \) are respectively the estimated and the true (simulated) joint eigenbasis of dimension \( r \). Finally, binary responses were simulated depending on the true joint scores, and a logistic model were fitted to classify this binary response based on the estimated joint scores; the resulting prediction AUCs were compared as another summary performance measure.

### 3.2 The effect of outliers on aJIVE

We first conducted simulation studies to investigate the effect of outliers on the aJIVE decomposition on synthetic datasets, which provided the motivation for developing a robust version of this data-integration algorithm. To this end, we have considered \( n = 100, (p_1, p_2, p_3) = (200, 180, 145), r = 2, \) and \( (r_1, r_2, r_3) = (20, 12, 12) \) and outliers were from \( \mathcal{N}(10, 4) \). For brevity, we report the results obtained by adding outliers to 10% of the total samples; the same pattern were observed for other outlier proportions as well.

Results show that only when outliers are added to all the three data sources (case O1 and case O4), the estimated aJIVE parameters are affected. This was observed both when \( p_k/5 \) (case O1) and \( p_k \) (case O4) variables were contaminated by outliers. In particular, the joint rank is higher when outliers are present (Table 1), suggesting that one or more joint components might actually be residual noise. The proportions of variance explained are also affected by outliers, specifically showing higher joint and lower individual proportions (Figure 1). The subspace recovery error is substantially higher when outliers are present (Figure 2a), while the AUC does not seem to be affected (Figure 2b).
Table 1: Median joint and individual ranks estimated by aJIVE in simulation studies without outliers and with six outlier configurations.

| Configuration | Joint | Ind Source 1 | Ind Source 2 | Ind Source 3 |
|---------------|-------|--------------|--------------|--------------|
| No outliers   | 2     | 18           | 10           | 10           |
| O1            | 3     | 17           | 9            | 9            |
| O2            | 2     | 18           | 10           | 10           |
| O3            | 2     | 18           | 10           | 10           |
| O4            | 3     | 17           | 9            | 9            |
| O5            | 2     | 18           | 10           | 10           |
| O6            | 2     | 18           | 10           | 10           |

3.3 Performance Evaluation of the RaJIVE

We evaluate the finite-sample performance of the proposed RaJIVE, in comparison with the usual aJIVE, via appropriate simulation studies similar to the one discussed in Section 3.1. Based on the results of Section 3.2 here, we consider outliers in all three datasets of size $n = 100$ each, by adding random normal errors to 5% and 10% of the variables in each dataset, and 10% observations for each of these variables. In particular, we consider two simulation scenarios – one (Set-A) similar to those in Section 3.2 and another one (Set B) resembling our real data situation.

**Set-A:** We take $(p_1, p_2, p_3) = (200, 180, 150)$, $r = 3$, and $(r_1, r_2, r_3) = (20, 12, 7)$. Outliers were generated from $\mathcal{N}(15, 1)$.

**Set-B:** We take $(p_1, p_2, p_3) = (100, 180, 150)$, $r = 3$, and $(r_1, r_2, r_3) = (10, 12, 7)$. Outliers were generated from a normal distribution with mean $\mu_c = 3m + 5s$ and standard-deviation $\sigma_c = 3s$, where $m$ and $s$ are mean and standard-deviation of the affected variable, respectively.

**Results:** Table 2 and Figures 3–5 illustrate the performance measures obtained by both aJIVE and RaJIVE in the simulation studies (Set A–B) with and without outliers. Note that, when outliers are generated in 5% of the variables as per either Set A or B, RaJIVE performs well and retrieved the correct joint ranks (Table 2a), as well as a correct estimation of the proportion of variance explained in most cases (Figures 3a, 4a). While the standard aJIVE has a very high subspace recovery error in the presence of outliers, that of RaJIVE stays significantly lower (Figures 5a, 5c). When affecting 10% of variables with outliers as per Set A, the RaJIVE
estimates still remains robust and better than the usual aJIVE under data contamination (Table 2b; Figures 3b, 5d). However, when outliers are added to 10% of variables in Set B, the quality of the RaJIVE estimates deteriorates (Table 2b; Figures 3b, 5d), due to the presence of significantly higher amount of contamination (more than what it can tolerate).

| Method                  | Outliers in 5% of p | Joint | Ind Source 1 | Ind Source 2 | Ind Source 3 |
|-------------------------|---------------------|-------|--------------|--------------|--------------|
| aJIVE                   |                     | 3     | 17           | 9            | 5            |
| RaJIVE                  |                     | 3     | 17           | 10           | 5            |
| aJIVE with outliers     |                     | 4     | 17           | 9            | 4            |
| RaJIVE with outliers    |                     | 3     | 18           | 10           | 5            |

| Method                  | Outliers in 10% of p | Joint | Ind Source 1 | Ind Source 2 | Ind Source 3 |
|-------------------------|----------------------|-------|--------------|--------------|--------------|
| aJIVE                   |                     | 3     | 17           | 9            | 5            |
| RaJIVE                  |                     | 3     | 17           | 10           | 5            |
| aJIVE with outliers     |                     | 4     | 17           | 9            | 4            |
| RaJIVE with outliers    |                     | 3     | 17           | 9            | 5            |

Table 2: Median joint and individual ranks estimated by aJIVE and RaJIVE in simulation studies with outliers in different proportions of variables.
4 Real-life application: TCGA breast cancer data

Finally we illustrate applicability of our proposed RaJIVE to a real-life dataset, from TCGA, on breast cancer samples. The data preprocessing is described in [Lock and Dunson (2013)] and used in [O’Connell and Lock (2016)]. It contains the records for 348 breast tumor samples relative to three sources of omics data, namely gene expression for 654 genes, DNA methylation for 574 CpG sites and miRNA expression for 423 miRNAs. To examine the robustness of our procedure, we further contaminate 5% of the variables and 10% of the data points, by adding normally distributed outliers with mean $\mu_c = 3m + 5s$ and standard deviation $\sigma_c = 3s$, where $m$ and $s$ are the mean and standard deviation of the affected variable (as in Set B of the simulation study). We compared the joint and individual ranks obtained by the standard aJIVE and the robust aJIVE, as well as the proportions of explained variation estimated by the two methods, both with and without data contamination.

Joint and individual ranks estimated by aJIVE and RaJIVE in the pure (with no outliers) and contaminated (with outliers) data are reported in Table 3. Although robust aJIVE is not able to recover the correct ranks, it is successful in estimating the correct proportion of variance explained (Figure 6). Also the heatmap decompositions show that, while the aJIVE decomposition is extremely sensitive to outliers, RaJIVE is able to estimate the correct decomposition in presence of outliers (Figure 7).

| Method | Data          | Joint | Ind Expression | Ind Methylation | Ind miRNA |
|--------|---------------|-------|----------------|-----------------|-----------|
| Standard aJIVE | pure        | 11    | 12             | 5               | 10        |
| Robust aJIVE    | pure        | 10    | 14             | 6               | 10        |
| Standard aJIVE | contaminated| 10    | 12             | 6               | 11        |
| Robust aJIVE    | contaminated| 10    | 13             | 7               | 11        |

Table 3: Joint and individual ranks obtained by aJIVE and RaJIVE.

5 Discussion

We propose a robust alternative to the aJIVE method for the estimation of joint and individual components in the presence of outliers in multi-source data. Our method (RaJIVE) uses a
robust formulation of the SVD within the standard aJIVE algorithm. The performance of this proposed RaJIVE is illustrated in a set of simulation studies and on real data from The Cancer Genome Atlas, specifically on multi-platform omics data collected on breast cancer samples.

We investigate, in detail, the effect of increasing proportions of outliers on the joint and individual components identified by aJIVE. Interestingly, our simulation study shows that the presence of outliers has an effect on the joint and individual components only when all the data sources are affected, and that the effect is negligible when only one source shows the presence of outliers, regardless of the proportion of affected variables. This appears very relevant when focusing our interest on the joint contributions of the data layers.

A major issue related to the aJIVE method is the selection of initial ranks, most commonly based on the visualization of screeplots, which is highly subjective and sensitive to noises in the data. Although an alternative based on the profile likelihood idea was suggested by Zhu and Ghodsi (2006), this addresses the problem only partially and still remains quite subjective. This issue is likely to affect the proposed RaJIVE as well, and the initial ranks need to be selected carefully before implementing both methods. We believe this to be a possible reason for the incorrect estimation of the ranks in the TCGA application.

Although we only consider normally distributed noise to generate outliers, the robust SVD formulation used in RaJIVE accounts for different types of noise in the data (Zhang et al., 2013). Therefore, we expect the proposed RaJIVE to be useful in situations with other types of error as well, and also in missing data situations. However, it has been observed through simulations that RaJIVE has a noise-tolerance limit (breakdown-point) and it may gets affected by the presence of contamination over this limit. It would be extremely important in future work to overcome this limitation of the proposed RaJIVE, possibly by using a more robust SVD computation procedure that would be able to produce stable results even under heavy contaminations.

**Data and software availability**

A R package with the implementation of RaJIVE is available at [https://github.com/ericaponzi/RaJIVE](https://github.com/ericaponzi/RaJIVE).
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A Computation of the robRSVD

The computation of the robRSVD is based on the alternating regression formulation of the SVD problem. It estimates one singular value and the corresponding singular vectors at a time. The original implementation of robRSVD in the R-package ‘RobRSVD’ Zhang et al. (2013) additionally considers the regularization of the singular vectors, which is not necessary in our context. An appropriately modified algorithm for computation of the robRSVD is used in our proposed RaJIVE to increase computational efficiency, which is described here.

Suppose that we wish to find the SVD of a matrix $X$ of order $m \times n$. In robRSVD, we first compute the rank-one approximation of the matrix as $X \approx ab^T$ for some vectors $a = (a_1, \ldots, a_m)^T$ and $b = (b_1, \ldots, b_n)^T$. To estimate $a$ and $b$, we re-express this problem of matrix decomposition as the linear regression problem given by

$$x_{ij} = a_ib_j + e_{ij}, \quad i = 1, \ldots, m; \quad j = 1, \ldots, n,$$

where $x_{ij}$ denotes the $(i, j)$-th element of matrix $X$ and $e_{ij}$ are residual (random error) components for all $i, j$. If we fix the values of $a_i$ and any one index $j$, we get a linear regression problem in (4) with coefficient $b_j$ and $m$ observations (by varying $i$) and any standard estimation method can be used to estimate the corresponding regression coefficients $b_j$. Varying over all $j$, we get estimates of $b = (b_1, \ldots, b_n)$ given $a$. Next, given these estimated values of $b_j$s, we treat them as covariates in (4) and estimate the $a_i$s as the unknown parameter in $m$ linear regressions for varying $i = 1, \ldots, m$ (with $n$ observations, varying $j$, for each $i$). These two
steps of regressions approach can be repeated alternatively, with the new estimated parameter values being used in each steps, until convergence to get the final estimates of $a$ and $b$.

In the usual SVD, in each step of the alternating regression as described above, the parameter estimation is done by the standard least-squares approach. In robRSVD, however, the regression coefficients are estimated by the robust M-estimation approach (Huber and Ronchetti, 2011) which is computed via an appropriate reweighted least-squares algorithm. More specifically, it converts the estimation of the parameters $a$ and $b$ in the above alternative regression approach to an optimization problem as

$$
(\hat{a}, \hat{b}) = \text{arg min}_{(a,b)} \rho \left( \frac{X - ab^T}{\sigma} \right),
$$

where $\sigma^2$ is the (assumed) common variance of $e_{ij}s$ and $\rho$ is the Huber’s loss function given by

$$
\rho(x) = \begin{cases} 
    x^2 & \text{if } |x| \leq c, \\
    2c|x| - c^2 & \text{if } |x| > c.
\end{cases}
$$

Here $c > 0$ is a robustness tuning parameter that controls the balance between efficiency and robustness of the resulting estimators; the suggested choice of $c$ is 1.345 which provides 95% efficiency under a linear regression model with normal errors (Huber and Ronchetti, 2011). Solving the optimization problem (5) numerically via iterative reweighted least-squares algorithm, we get the robust estimates $(\hat{a}, \hat{b})$ of $(a, b)$ in RobRSVD. Then, a singular value of $X$ is obtained as $\delta = ||\hat{a}|| ||\hat{b}||$, with $|| \cdot ||$ denoting the Euclidean norm, and the corresponding normalized left and right singular vectors as $u = \hat{a} / ||\hat{a}||$ and $v = \hat{b} / ||\hat{b}||$, respectively.

Once the first singular value and vectors for $X$ are obtained, in robRSVD, the second one needs to be obtained by applying the same procedure on the residual matrix $X_1 = X - \delta uv^T$. Repeating this procedure sequentially, we get all the singular values of $X$ and the corresponding (normalized) singular vectors.
Figure 1: Proportions of variance explained estimated by aJIVE in a standard setting (no outliers) vs in the six simulated outlier configurations O1–O6.

Figure 2: Subspace recovery error and classification AUC from aJIVE scores in a standard setting (no outliers) vs in the six simulated outlier configurations O1–O6.
Estimated proportions of variance explained

(a) Outliers in 5% of the variables

(b) Outliers in 10% of the variables.

Figure 3: Proportions of variance explained, estimated by aJIVE and RaJIVE, in simulation studies (Set A) with outliers in different proportion of variables and 10% samples.
Estimated proportions of variance explained

(a) Outliers in 5% of the variables

(b) Outliers in 10% of the variables.

Figure 4: Proportions of variance explained, estimated by aJIVE and RaJIVE, in simulation studies (Set B) with outliers in different proportion of variables and 10% samples.
Figure 5: Subspace recovery error of aJIVE and RaJIVE in simulation studies (Set A and Set B) with outliers in different proportion of variables and 10% samples.
Figure 6: Proportion of variance explained by the aJIVE and robust aJIVE (RaJIVE) components in the TCGA breast cancer data with and without data contamination.
Figure 7: Heatmaps of the standard aJIVE and proposed RaJIVE decompositions in the TCGA breast cancer data.

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