



Considerations for robust ICA: a discussion of the PICARD framework

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Abstract

This study explores the PICARD framework for Independent Component Analysis (ICA), focusing on robust implementation methods. We utilize the "Cocktail party" and handwritten digits datasets to discuss features of the framework's application and performance.

Keywords Robust Independent Component Analysis · Cocktail party problem · Bowl transform · Sweep Approach · Multivariate data · Outliers

1 Introduction

We congratulate the Authors on their valuable contribution to the Independent Component Analysis (ICA) literature within the robust framework. The proposed methodology, called Progressive Independent Component Analysis by Robust Dependence (PICARD), combines a robust approach to the “whitening” step in ICA using the Minimum Covariance Determinant estimators (Rousseeuw 1984, 1985; Rousseeuw and Van Driessen 1999) with a robust measure of dependence between vector variables, i.e., the distance correlation of Székely et al. (2007), based on the bowl transform. The latter is a newly proposed bounded, continuous, injective, and redescending transformation which offers an insightful solution to the estimation of components in the presence of outliers. The Authors prove the consistency of the

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separating matrix estimator both theoretically and through extensive simulations and real-data examples. We would like to raise a few points for discussion and learn the Authors' views on these issues.

2 Mild outlier contamination and sensitivity to the scaling constant in the bowl transform

The proposed transformation, called the bowl transform, relies on a scaling constant $q = \sqrt{\chi^2_{0.9975,p}}$, where $p \leq d$ denotes the dimension of the input vector at each sequential step. Even if effective in some applications, the default value for q can prove too conservative in certain scenarios. As shown in Table 1, on the cocktail party data from Brys et al. (2005), the Amari error remains essentially stable for thresholds ranging between the default value down to $q = \sqrt{\chi^2_{0.90,p}}$, while further reducing the scaling constant leads to substantial degradation. Indeed, excessive compression of tail observations induced by the bowl transform may adversely affect the dependence structure used by PICARD for source separation. Conversely, increasing the χ^2 quantile above the default causes the Amari error to increase, since fewer observations fall within the redescending region of the transform and the influence of outliers is therefore not adequately reduced.

The data from Brys et al. (2005) contain *gross* outliers: observations from 2001 to 2100 are contaminated with values of large magnitude. However, the sensitivity to the scaling constant q can also be assessed by reducing the magnitude of this contamination on the same observations, thereby obtaining *mild* outliers, as illustrated in Fig. 1. In this scenario, decreasing the scaling constant may improve the results (see Table 1). This improvement continues up to an optimal threshold, beyond which further tightening causes the Amari error to increase again, since “clean” observations in the non-Gaussian tails of the source distributions are also compressed, partially distorting the dependence structure exploited for source recovery.

In this example, outliers are concentrated in contiguous observations. However, it would be interesting that the Authors provide a sensitivity analysis to the scaling constant in different, and more complex, scenarios of contamination. Although the choice of the 99.75% quantile of a χ^2 distribution is consistent with the multivariate

Table 1 Amari error using different thresholds for the scaling constant $q = \sqrt{\chi^2_{1-\alpha,p}}$, under two contamination schemes (“gross outliers” correspond to the original contamination) in the cocktail party data (Brys et al. 2005). Minimum value in bold

	$\alpha\% (1 - \alpha)$										
	0.01%	0.05%	0.10%	0.25%	1.0%	2.5%	5%	10%	15%	20%	25%
	(0.9999)	(0.9995)	(0.9990)	(0.9975)	(0.99)	(0.975)	(0.95)	(0.90)	(0.85)	(0.80)	(0.75)
Gross out	0.030	0.026	0.023	0.017	0.017	0.017	0.017	0.017	0.023	0.067	0.109
Mild out	0.065	0.062	0.060	0.056	0.044	0.037	0.039	0.057	0.097	0.175	0.243

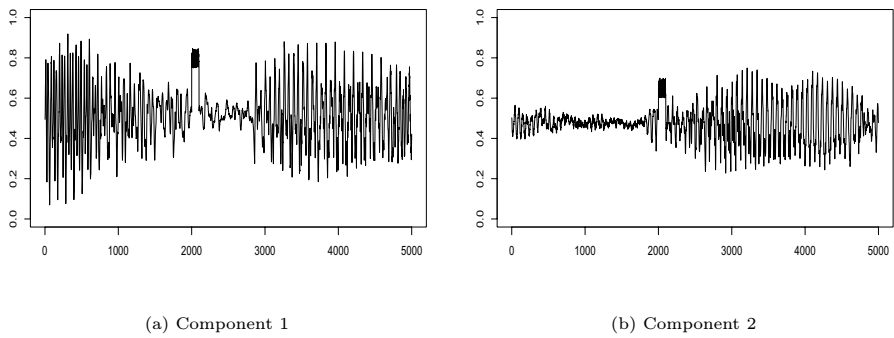


Fig. 1 Cocktail party example on Brys et al. (2005) data with mild contamination

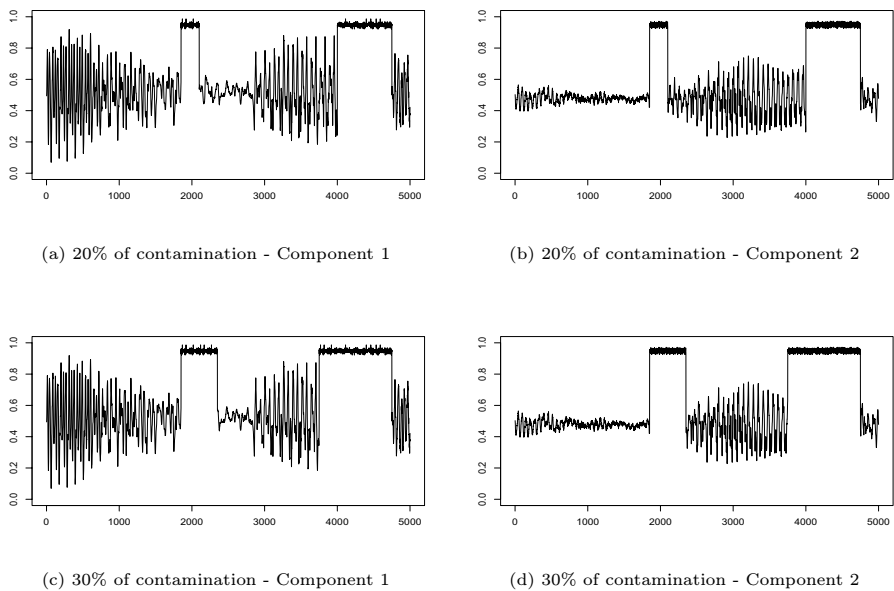


Fig. 2 Cocktail party example on Brys et al. (2005) data with higher level of contamination

generalization of the 3σ rule, readers could benefit from further clarification of this choice and possible guidelines for selecting the scaling constant.

3 Robustness under increasing contamination

The robustness of PICARD could be further assessed empirically by progressively increasing the contamination. Using the same data from Brys et al. (2005), we replicate the current contamination setup – which affects 2% of the observations – and increase contamination to 20% and 30% of the observations, as shown in Fig. 2. In the first case, the Amari error remains almost low (0.135), whereas under the higher contamination level, it reaches 0.228.

In Leyder et al. (2026), the Authors handle contamination levels of up to 20% in the simulation study. As shown in Figure 8 of Leyder et al. (2026), the Amari error increases with the number of outliers. However, under this contamination scheme, the value reached by PICARD remains below 0.20. To determine the point at which the Amari error begins to deteriorate beyond an acceptable value, higher percentages of contamination could be considered in designed scenarios.

4 Graphical tools

The use of the bowl transform may also provide useful exploratory graphical tools for assessing the presence of contamination. Generally speaking, the bowl transform shrinks observations with large norms toward the origin through a redescending radial transformation, while remaining continuous and injective.

Figure 3 illustrates this behavior under different contamination settings in the cocktail party example of Brys et al. (2005), after the whitening step. Observations satisfying $\|x\| \leq q$ are displayed in black, whereas the remaining observations are colored according to their value of $v_2(x)$, defined in display (5) of Leyder et al. (2026). Under gross contamination, the bowl transform clearly separates contaminated observations in the redescending region (blue points in panels a and c corresponding to contaminated observations in the original data and in the scenario displayed in Figs. 2c-d, respectively), while under mild contamination the separation becomes less pronounced (points corresponding to contaminated observations in the mild contamination scenario shown in Fig. 1 tend toward green). The quantity $v_2(x)$ may also be interpreted as reflecting the attenuation induced by the radial compression underlying the bowl transform.

Although we are aware that the bowl transform applied to the original data cannot be considered a formal outlier detection tool, graphical approaches along these lines could provide useful exploratory insight into the treatment of outlying observations. In the bivariate setting, a graphical interpretation can be linked directly to Eq. (10), where the bowl transform is applied to the two complementary components entering the robust distance correlation criterion. Since for $d = 2$ each component coincides

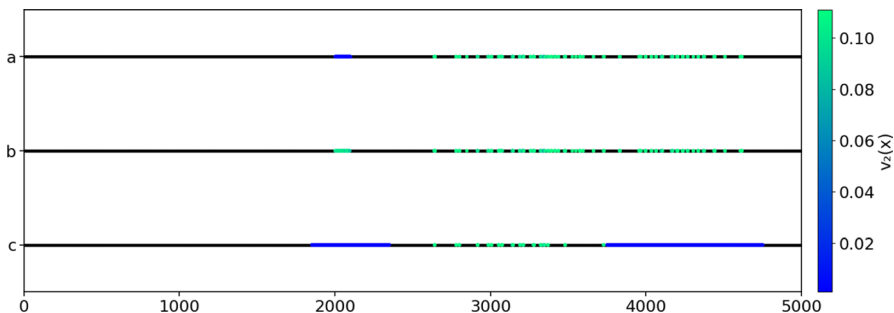


Fig. 3 Example of a graphical tool for outlier inspection based on the Cocktail party example on Brys et al. (2005) data after whitening. Black points correspond to observations with $\|x\| \leq q$. a. Original data; b. Data with mild contamination. c. Data with 30% of gross contamination

with the complement of the other (see also the discussion on “Sweep approach”), coloring the two signals according to $v_2(S_{n,1}(\mathbf{U}(\theta)))$ and $v_2(S_{n,2}(\mathbf{U}(\theta)))$ provides a visualization of the attenuation induced by the bowl transform within the robust dependence measure.

5 Sweep approach

PICARD proceeds sequentially by minimizing the robust dependence within successive orthogonal complements of the bowl-transformed sources, rather than solving a joint optimization problem. This approach is computationally efficient but order-dependent (Jin and Matteson 2018); thus, inspired by RADICAL (Learned-Miller and Fisher 2003), PICARD employs “sweeps”- iterative refinement steps based on component permutations. Sweeps can improve accuracy in higher dimensions ($d \geq 3$), since earlier sequential choices can influence later components. However, a single sweep consists of $d(d-1)/2$ Jacobi rotations, resulting in an $\mathcal{O}(d^2)$ computational cost per sweep. In the bivariate case, a single rotation fully characterizes the orthogonal transformation, and permutations impact neither the distance correlation nor the Amari error. Consequently, including both PICARD versions in $d = 2$ numerical comparisons may provide limited additional insight, while increasing computational cost. This contrasts with higher dimensions, where multiple rotation angles and component orderings allow sweeps to revisit earlier sequential choices.

6 PICARD limitations with long-tailed distributions

As highlighted by the Authors in their *Discussion* section, PICARD may be overly conservative when outlyingness reflects structural variability rather than contamination. An example is provided by the handwritten digits data used in Hastie et al. (2009). We consider four examples of “3” – three typical and one atypical, characterized by an elongated lower tail – mixed via a random matrix and arranged into a data set with pixels as observations and mixed signals as columns. As shown in Fig. 4, PICARD recovers the typical digits reasonably well but partially suppresses the atypical one, treating its distinctive features as outliers (Amari error of 0.502). In contrast, dCovICA, as well as FastICA (not reported in Fig. 4), recovers the atypical digit more faithfully (Amari errors of 0.211 and 0.291, respectively), as these methods do not incorporate the robust attenuation mechanism used by PICARD.

7 Final comments

Future developments for PICARD may extend the cellwise approach to contamination, which represents a new paradigm in the robust statistical literature (Raymaekers and Rousseeuw 2026; Hubert et al. 2026). We believe that PICARD’s treatment of atypical observations may provide a useful starting point for extensions to the cellwise framework. Additionally, allowing for non-i.i.d. observations, such as time

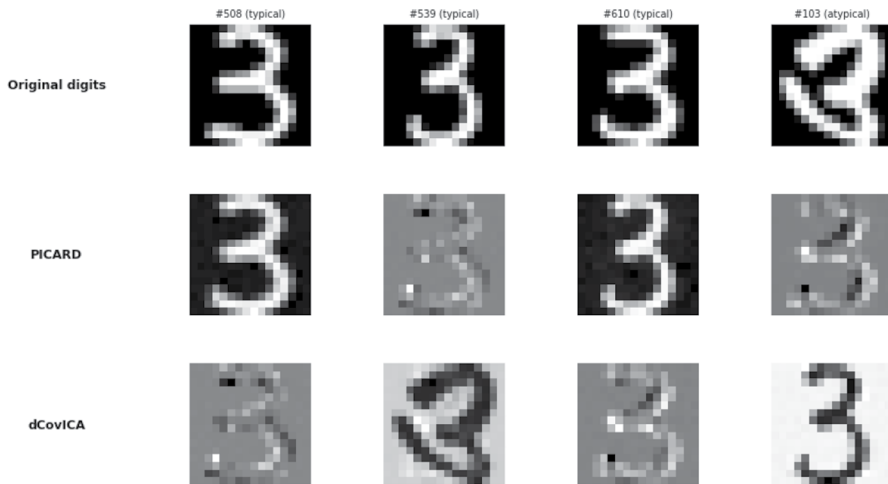


Fig. 4 Handwritten digits example

series data, would substantially broaden its applicability. Finally, inferential tools for the recovered components, including confidence intervals and hypothesis testing procedures, remain an open research direction.

Author contributions Both authors contributed to the study conception, design, and drafting of the manuscript. Data analysis was conducted by Giorgia Zaccaria. Both authors have read and approved the final manuscript.

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Data availability The datasets analyzed in this study are the “Cocktail party” benchmark from Brys et al. (2005) and the handwritten digits dataset utilized in Hastie et al. (2009).

Code availability The code employed in this study builds upon the publicly available source code provided by Leyder et al. (2026).

Declarations

Conflict of interest The authors have no conflict of interest to declare that are relevant to the content of this article.

Ethical approval Ethical approval was not required for this study as it did not involve the collection or analysis of personal identifying data.

Consent to participate Not applicable.

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