

pyGMCA Lab, a python-based toolbox for blind source separation

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1 Sparse BSS with GMCA

The GMCA algorithm (Generalized Morphological Component Analysis) has first been published in [2] to tackle sparse blind source separation (BSS) problems of the form:

$$\min_{\mathbf{A}, \mathbf{S}} \sum_{i=1}^n \lambda_i \|s_i\|_{\ell_1} + \frac{1}{2} \|\mathbf{X} - \mathbf{AS}\|_F^2$$

One of the aspects of the GMCA algorithm is that the regularization parameters are automatically tuned based on the noise level. The latter is estimated straight from the data thanks to an empirical estimator coined the Median Absolute Deviation (MAD).

The current code assumes that the data are already expressed in the sparse domain. A first step then consist in applying your favorite sparsifying transform to the input data \mathbf{X} prior to perform the GMCA algorithm. For more details about the GMCA algorithm, we refer the interested reader to [2, 3].

One of the main limitations of most sparse BSS methods is that they rely on separation principles such as statistical independence for ICA-based methods or morphological component analysis for GMCA, which rarely holds in real-world applications. In many applications, the sources of interest generally exhibit some partial correlations that are not correctly accounted for by classical approaches. For that purpose, an extension of the GMCA algorithm has been introduced in [1], which allows accounting for partial correlations.

Both GMCA and AMCA can be applied using the same basic code, with the exception of a single change of option value.

The script `pyGMCA Lab/GMCA_scripts/script_example_1.py` shows how to use both GMCA and AMCA to tackle sparse BSS problems.

2 Sparse NMF with nGMCA

The nGMCA algorithm (non-negative Generalized Morphological Component Analysis) has been published in [4, 5] to tackle sparse non-negative matrix factorization problems (NMF) problems of the form:

$$\min_{\mathbf{A} \geq 0, \mathbf{S} \geq 0} \sum_{i=1}^n \lambda_i \|s_i \Phi^T\|_{\ell_1} + \frac{1}{2} \|\mathbf{X} - \mathbf{AS}\|_F^2$$

where Φ stands for the sparse representation. One novelty of the nGMCA algorithm is that it makes use of recent solvers for non-smooth convex optimization problems such as the (Generalized) Forward Backward splitting algorithm (FBS). The pyGMCA Lab toolbox provides implementations of the FBS to tackle the basic subproblems that compose the nGMCA algorithm.

The following scripts give examples of how to use the algorithms:

- `example_fb.py` for using the Forward-Backward algorithm. This example also shows how to take advantage of the Algorithm class, so as to display figures throughout the computation and save information for later display.

- `example_ngmca.py` for the nGMCA algorithms using sparsity in the direct domain, from article [4]
- `example_ngmca_wave.py` for the nGMCA algorithms using sparsity in transformed domain, on simulation of 1D NMR spectra, from article [5]
- `example_bench.py` for using the benchmark tools. The configuration files and some results are provided in the benchmarks folder.

3 Third-party codes

3.1 Undecimated wavelets with the pyredwave toolbox:

The algorithms using sparsity in a transformed domain need the pyredwave Toolbox: a specific toolbox computing 1D or 2D wavelet transform on any 1 or 2 dimensions of an up to 4 dimensional data. Execute "python setup.py build" in a terminal from the pyredwave folder so as to build it. The compilation requires Boost.Python (tested on Mac and Ubuntu, with Python 2.7). The toolbox uses OMP for CPU parallelization. To disable parallelization, remove the tag "`__PARALLELIZED__`" in `pygmca/pyredwave/pyredwave/cxx/redWaveTools.hpp`

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References

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- [3] J. BOBIN, J.-L. STARCK, Y. MOUDDEN, AND J. FADILI, *Blind Source Separation : the Sparsity Revolution*, Advances in Imaging and Electron Physics, 152 (2008), pp. 221–298.
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- [5] ———, *NMF with Sparse Regularizations in Transformed Domains*, SIAM Journal on Imaging Sciences (accepted), 7 (2014), pp. 2020–2047. SIAM J. Imaging Sci., 7(4), 2020–2047. (28 pages).