








SSALib: a Python Library for Time Series Decomposition using Singular Spectrum Analysis

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Summary

Singular Spectrum Analysis (SSA) is a method developed in the 1980s for analyzing and decomposing time series. Using time-delayed trajectories or covariance matrices, SSA takes advantage of temporal dependencies to identify structured components such as trends and cycles. Time series decomposition has various applications, including denoising, filtering, signal modeling, interpolation (or gap filling), and extrapolation (or forecasting). The Singular Spectrum Analysis Library (SSALib) is a Python package that simplifies SSA implementation and visualization for the decomposition of univariate time series, featuring component significance testing.

Statement of Needs

SSA is a non-parametric method that provides a low-assumption framework for exploring, discovering, and decomposing linear, nonlinear, or pseudo-periodic patterns in time series data, in contrast to methods that require strong *a priori* hypotheses about signal components ([Elsner & Tsonis, 1996](#); [Golyandina & Zhigljavsky, 2020](#)). The SSALib package includes Monte Carlo SSA to support statistical inference and reduce subjective user guidance. Its Python Application Programming Interface is designed to streamline the SSA workflow and facilitate time series exploration, including built-in plotting features.

SSALib is particularly relevant for researchers and practitioners working in domains where time series analysis is central, i.e., climate and environmental sciences, geophysics, neuroscience, econometrics, or epidemiology.

Mathematical Background

The mathematical background of Singular Spectrum Analysis (SSA) has been primarily developed during the 1980–2000 period ([Elsner & Tsonis, 1996](#); [Golyandina, 2020](#); [Golyandina & Zhigljavsky, 2020](#)). The basic Singular Spectrum Analysis (SSA) algorithm, as described by Broomhead & King (1986) (BK-SSA) or Vautard & Ghil (1989) (VG-SSA), applies to univariate time series. It consists of three major steps ([Golyandina & Zhigljavsky, 2020](#); [Hassani, 2007](#)). The first step is the time-delayed matrix construction. The second step consists in a Singular Value Decomposition of the trajectory matrix. The BK-SSA approach is based on a time-delayed trajectory matrix with dimensions depending on the window parameter and the number of unit lags. This matrix consists of lagged copies of time series segments of a specified

length, forming a Hankel matrix, i.e., a matrix with equal anti-diagonal values. In contrast, the VG-SSA approach captures time dependencies by constructing a special type of covariance matrix that has a Toeplitz structure, meaning that its diagonal values are identical. The eigenvalues of the SVD depend on the variance captured by each component, either composed of one eigenvector, for monotonic trends, or two eigenvectors, representing nonlinear trends, pseudo-periodic cycles or oscillations. In the third step, the eigenvectors are then grouped, for pseudo-periodic components, and their contributions to the time series are reconstructed via projection.

For testing the significance of the retrieved mode, Allen & Smith (1996) proposed a Monte Carlo approach, by comparison of the variance captured by the eigenvectors on the original time series with that captured in many random autoregressive (AR) surrogate time series (Schreiber & Schmitz, 2000). Many extensions have been proposed for the methods, paving the way for future developments, such as multivariate (or multichannel) SSA (M-SSA), SSA-based interpolation and extrapolation, and causality tests (Golyandina & Zhigljavsky, 2020).

Implementation Details

The Singular Spectrum Analysis Library (SSALib) Python package interfaces time series as `numpy.Array` (Harris et al., 2020) or `pandas.Series` (McKinney, 2010) objects. It uses decomposition algorithms from acknowledged Python scientific packages like `numpy` (Harris et al., 2020), `scipy` (Virtanen et al., 2020), and `sklearn` (Pedregosa et al., 2011). In particular, `sklearn` features a randomized SVD algorithm for efficient decomposition (Halko et al., 2010). Visualization features rely on `matplotlib`, drawing inspiration from the R `rSSA` package (Golyandina et al., 2018).

SSALib also incorporates the Monte Carlo SSA approach (Allen & Smith, 1996) for identifying significant components by comparison to randomly generated data (i.e., surrogate data), relying on `statsmodels` (Seabold & Perktold, 2010) for fitting AR processes and generate the surrogate data. In SSALib, an AR process of a specified maximum order is fitted relying on a state space modeling framework (Durbin & Koopman, 2012), which enables fitting AR processes from time series that contain masked or missing values.

Related Work

Golyandina & Zhigljavsky (2020) mention some existing software dedicated to SSA, such as the GUI-based SSA-MTM toolkit, Caterpillar-SSA software, and the `rSSA` R package. In Python, most SSA implementations are basic and part of large software packages, including `pyts` (Faouzi & Janati, 2020), `pyleoclim` (Khider et al., 2023), or `pyactigraphy` (Hammad et al., 2024), or are available primarily as unmaintained and untested projects. To address this gap, SSALib was developed as a fully dedicated and tested Python package for SSA that is suitable for both teaching and research purposes.

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