SpaSM: A MATLAB Toolbox for Sparse Statistical Modeling

Applications in biotechnology such as gene expression analysis and image processing have led to a tremendous development of statistical methods with emphasis on reliable solutions to severely underdetermined systems. Furthermore, interpretations of such solutions are of importance, meaning that the surplus of inputs has been reduced to a concise model. At the core of this development are methods which augment the standard linear models for regression, classification and decomposition such that sparse solutions are obtained. This toolbox aims at making public available carefully implemented and well-tested variants of the most popular of such methods for the MATLAB programming environment. These methods consist of easy-to-read yet efficient implementations of various coefficient-path following algorithms and implementations of sparse principal component analysis and sparse discriminant analysis which are not available in MATLAB. The toolbox builds on code made public in 2005 and which has since been used in several studies.

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