

## Feature selection for kernel methods in systems biology

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The substantial development of high-throughput bio-technologies has rendered large-scale multi-omics datasets increasingly available. New challenges have emerged to process and integrate this large volume of information, often obtained from widely heterogeneous sources. Kernel methods have proven successful to handle the analysis of different types of datasets obtained on the same individuals. However, they usually suffer from a lack of interpretability since the original description of the individuals is lost due to the kernel embedding. We propose novel feature selection methods that are adapted to the kernel framework and go beyond the well established work in supervised learning by addressing the more difficult tasks of unsupervised learning and kernel output learning. The method is expressed under the form of a non-convex optimization problem with a l1 penalty, which is solved with a proximal gradient descent approach. It is tested on several systems biology datasets and shows good performances in selecting relevant and less redundant features compared to existing alternatives. It also proved relevant for identifying important governmental measures best explaining the time series of Covid-19 reproducing number evolution during the first months of 2020.

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