Extensions of CCA and PLS to unravel relationships between two data sets

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In the context of systems biology and in post-genomic studies, it becomes usual to analyze simultaneously transcriptomics, proteomics and/or metabolomics data. Several approaches have been proposed to understand and to highlight the mutual interactions between two different data sets. The main challenge of the proposed methodologies relies on their ability to handle very large data sets, where the number of variables is much greater than the number of observations. Lê Cao et al. (2008) proposed a sparse PLS method in a canonical correlation framework which includes variables selection while integrating data. González et al. (2009) developed a regularized version of Canonical Correlation Analysis to deal with singular matrices occurring in the classical CCA.

On the basis of the CCA package (González et al., 2008), we developed the package CCAsPLS to implement these two approaches (Fig. 1).

The interpretation of the results is made easier with the use of various graphical display such as correlation loading plots as in factorial analysis (previously implemented in the CCA package). CCAsPLS also proposes heat maps and networks to better visualize the relationships between variables from the two data sets. These graphs are often used when dealing with high-throughput biological data.

References

