mixOmics: an R package for the integration of biological data sets

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Abstract: It is generally admitted that single 'omics analysis does not provide enough information to give a deep understanding of a biological system, but we can obtain a more holistic view of a system by combining multiple 'omics analyses. In this context, this talk will present the mixOmics R package that proposes multivariate statistical methods to explore and integrate 'omics data sets with a specific focus on variable selection and visualisation.