

Tutorial: rROMA, a tool for module activity calculation from omics data and networks

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In many analysis of high-throughput data in systems biology, the focus has shifted from single gene to the gene-set level. This important change has been motivated biologically, as many diseases are believed to be associated with modest regulation in a set of related genes rather than a strong increase in a single gene.

ROMA can be applied in many contexts, from estimating differential activities of transcriptional factors and for finding deregulated pathways in omics data from patients, single-cells and beyond.

The tutorial aims to explain and disseminate this method within the community of researchers involved in high-throughput genomic data analysis in health and disease.

In this tutorial, we present the ROMA (Representation and quantification Of Module Activities) software and the associated rROMA R interface, designed for fast and robust computation of the activity of gene sets (or modules) with coordinated expression. ROMA is a software package written in Java for the quantification and representation of biological module activity using expression data and calculation of the individual gene contribution to the module activity level. ROMA is using the first principal component of a PCA analysis to summarize the coexpression of a group of genes in the gene set.

ROMA is also accessible via ROMA Dashboard: complete R shiny interface providing a set of analysis and visualization tools for overdispersion, overcoordination, overexpression analysis of gene signatures and scoring sample-wise, using transcriptomics and quantitative proteomics data.

More information is available at:

<https://github.com/sysbio-curie/Roma>

<https://github.com/Albluca/rRoma>

<https://github.com/sysbio-curie/rRomaDash>

<https://doi.org/10.3389/fgene.2016.00018>