Software tools at the Biostatnet-Granada node

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The Biostatnet node in Granada integrates researchers from six different institutions and universities. They are actively working to develop new statistical and machine-learning methods for analyzing biomedical data. An important aspect of their research lines is the deployment of software applications that make these methods available to the scientific community. Here we provide an overview of the main software applications available from this research group. These include dedicated databases, web-based applications, and R packages, covering a broad range of research needs.

Bioinformatics software tools

- ImaGEO: A web tool that implements a complete and comprehensive meta-analysis workflow to analyze gene expression datasets from GEO identifiers. [1]
- MetaGENyO: A web tool that implements a complete workflow for meta-analysis in Genetic Association Studies. [2]
- DExMA: R Package for Differential Expression Meta-Analysis. [3]
- mCSEA. R package that implements a GSEA-based approach to detect differentially methylated regions and gene expression-methylation data integration [4]

Agreement among raters

- Delta: a stand-alone application that implements the model *Delta* for evaluating the agreement between two raters on a nominal scale and the model *delta* for assessing the level of knowledge in a multiple-choice test [5]

Teaching Software

- BioestadísticaR: An R package for basic biostatistics teaching in medical sciences [6]

Keywords: Statistical Software, Web-based applications, R-packages.

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