ID de Contribution: **34**   Type: **Non spécifié**

IIDEA : Interactive Inference for Differential Expression Analyses

Differential gene expression studies aim to identify genes whose mean expression level differs significantly between two known populations. The state-of-the-art approach to this problem consists of performing one test per gene, followed by a multiple testing correction in order to control the False Discovery Rate (FDR), which is the expected proportion of errors among selected genes. The obtained gene list is then typically refined by further selecting genes with a large effect size (as in volcano plots).

Recent statistical developments in post hoc inference make it possible to obtain valid statistical guarantees for such gene lists. We have developed IIDEA, an interactive R/Shiny application that implements permutation-based post hoc inference methods for differential expression studies. IIDEA allows users to interactively select genes of interest and obtain valid statistical guarantees regarding the number of true/false positives among these genes.

Orateur: ENJALBERT COURRECH, Nicolas (Institut de Mathématiques de Toulouse)

Classification de Session: Session Poster

Classification de thématique: Session poster