

NORMALIX: A SHINY-BASED APPLICATION TO INVESTIGATE PLANT TRANSCRIPTOME DATA

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Microarray and RNA-Seq technologies allow the study of gene expression data for several organisms under different conditions. Both are widely used to investigate plant transcript profiles; however, researchers without programming skills cannot easily approach and use the massive plant transcriptome data available online. NORMALIX is an application/open-source web tool implemented in R, using the Shiny framework, for the analysis of plant microarray and RNA-Seq data. It consists of 10 tabs allowing users to perform different operations, such as the normalization of *Affymetrix* microarray data for 11 plant species, the generation of several plots (heatmaps, PCA, dendrograms, scatterplots), Pearson correlation (between hybridizations and genes), and Differential Gene Expression analysis (for microarray and RNA-Seq data). Several datasets of normalized microarray will be freely downloadable and questionable. NORMALIX source code will be hosted at GitHub; therefore, users will be able to launch NORMALIX in any operating system with R and RStudio IDE installed. Additionally, NORMALIX will be also provided online as a shiny application in web browsers for users who are not familiar with R. NORMALIX is the first tool specifically designed for plant transcriptomics analysis, developed with a user-friendly web interface to help plant researchers in analyzing plant gene expression data. We aim to develop an application that makes plant transcriptomics approachable to everyone, and we hope to upgrade NORMALIX with other features. We thus encourage users to contribute to future developments of NORMALIX through comments and suggestions.