

Package: maEndToEnd (via r-universe)

October 7, 2026

Title An end to end workflow for differential gene expression using Affymetrix microarrays

Version 2.32.0

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Description In this article, we walk through an end-to-end Affymetrix microarray differential expression workflow using Bioconductor packages. This workflow is directly applicable to current ``Gene" type arrays, e.g. the HuGene or MoGene arrays, but can easily be adapted to similar platforms. The data analyzed here is a typical clinical microarray data set that compares inflamed and non-inflamed colon tissue in two disease subtypes. For each disease, the differential gene expression between inflamed- and non-inflamed colon tissue was analyzed. We will start from the raw data CEL files, show how to import them into a Bioconductor ExpressionSet, perform quality control and normalization and finally differential gene expression (DE) analysis, followed by some enrichment analysis.

Depends R (>= 3.5.0), Biobase, oligoClasses, ArrayExpress, pd.hugene.1.0.st.v1, hugene10sttranscriptcluster.db, oligo, arrayQualityMetrics, limma, topGO, ReactomePA, clusterProfiler, gplots, ggplot2, geneplotter, pheatmap, RColorBrewer, dplyr, tidyr, stringr, matrixStats, genefilter, openxlsx, Rgraphviz, enrichplot

Suggests BiocStyle, knitr, devtools, rmarkdown

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Encoding UTF-8

VignetteBuilder knitr

biocViews GeneExpressionWorkflow

NeedsCompilation no

URL <https://www.bioconductor.org/help/workflows/>

Workflow True

Config/pak/sysreqs libcairo2-dev cmake libfontconfig1-dev libfreetype6-dev libfribidi-dev libglpk-dev make libharfbuzz-dev libicu-dev libjpeg-dev libpng-dev libuv1-dev libxml2-dev libssl-dev zlib1g-dev

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