Resource Summary Report

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affylmGUI

RRID:SCR_001320
Type: Tool

Proper Citation

affylmGUI (RRID:SCR_001320)

Resource Information

URL: http://bioinf.wehi.edu.au/affylmGUI/

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Description: R software package providing a Graphical User Interface for analysis of Affymetrix microarray data, using the limma package (Linear Models for MicroArray data). While not as powerful as limma to the expert user, it offers a simple point-and-click interface to many of the commonly-used limma and affy functions. You need to have R 1.9.0 or later, Tcl/Tk 8.3 or later (ActiveTcl for Windows, Tcl/Tk Source for Linux/Unix, or X11 Tcl/Tk for MacOSX) and the limma, affylmGUI, and tkrplot R packages. It has been succesfully tested on Windows 2000, Windows XP, RedHat/Fedora Linux, and on Mac OSX with X11.

Abbreviations: affylmGUI

Synonyms: Affymetrix linear modeling Graphical User Interface

Resource Type: software resource

Defining Citation: PMID:16455752

Keywords: affymetrix, differential expression, r, data import, differential expression, gui, microarray, multiple comparison, one channel, preprocessing, quality control, bio.tools

Funding:

Availability: Acknowledgement requested, GNU Lesser General Public License

Resource Name: affylmGUI

Resource ID: SCR_001320

Alternate IDs: biotools:affylmgui, OMICS_02016

Alternate URLs: http://www.bioconductor.org/packages/release/bioc/html/affylmGUI.html, https://bio.tools/affylmgui

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Record Last Update: 20250420T014026+0000

Ratings and Alerts

No rating or validation information has been found for affylmGUI.

No alerts have been found for affylmGUI.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 31 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

Zanjirband M, et al. (2023) Evaluation of the p53 pathway in polycystic ovarian syndrome pathogenesis and apoptosis enhancement in human granulosa cells through transcriptome data analysis. Scientific reports, 13(1), 11648.

Saberi F, et al. (2023) Identification of Renal Transplantation Rejection Biomarkers in Blood Using the Systems Biology Approach. Iranian biomedical journal, 27(6), 375.

Bosteels C, et al. (2022) Loss of GM-CSF-dependent instruction of alveolar macrophages in COVID-19 provides a rationale for inhaled GM-CSF treatment. Cell reports. Medicine, 3(12), 100833.

Albertos P, et al. (2021) Redox feedback regulation of ANAC089 signaling alters seed germination and stress response. Cell reports, 35(11), 109263.

Moradpoor R, et al. (2021) Identification of CCNB2 as A Potential Non-Invasive Breast Cancer Biomarker in Peripheral Blood Mononuclear Cells Using The Systems Biology Approach. Cell journal, 23(4), 406.

Abbasi S, et al. (2021) Impact of human rhinoviruses on gene expression in pediatric

patients with severe acute respiratory infection. Virus research, 300, 198408.

Eren Gozel H, et al. (2021) A novel insight into differential expression profiles of sporadic cerebral cavernous malformation patients with different symptoms. Scientific reports, 11(1), 19351.

Ramamoorthy S, et al. (2020) EBF1 and Pax5 safeguard leukemic transformation by limiting IL-7 signaling, Myc expression, and folate metabolism. Genes & development, 34(21-22), 1503.

Shaabanpour Aghamaleki F, et al. (2019) Bioinformatics Analysis of Key Genes and Pathways for Medulloblastoma as a Therapeutic Target. Asian Pacific journal of cancer prevention : APJCP, 20(1), 221.

Gaillard H, et al. (2019) The Nup84 complex coordinates the DNA damage response to warrant genome integrity. Nucleic acids research, 47(8), 4054.

Cogburn LA, et al. (2018) Transcriptional profiling of liver during the critical embryo-to-hatchling transition period in the chicken (Gallus gallus). BMC genomics, 19(1), 695.

Seo S, et al. (2018) Mechanisms Underlying the Regulation of HP1? by the NGF-PKA Signaling Pathway. Scientific reports, 8(1), 15077.

Hosseinkhan N, et al. (2018) Comparison of gene co-expression networks in Pseudomonas aeruginosa and Staphylococcus aureus reveals conservation in some aspects of virulence. Gene, 639, 1.

Mucunguzi O, et al. (2017) Identification of the principal transcriptional regulators for low-fat and high-fat meal responsive genes in small intestine. Nutrition & metabolism, 14, 66.

Jauvin D, et al. (2017) Targeting DMPK with Antisense Oligonucleotide Improves Muscle Strength in Myotonic Dystrophy Type 1 Mice. Molecular therapy. Nucleic acids, 7, 465.

Pinho R, et al. (2016) Gene Expression Differences in Peripheral Blood of Parkinson's Disease Patients with Distinct Progression Profiles. PloS one, 11(6), e0157852.

Bencivenga S, et al. (2016) Control of Oriented Tissue Growth through Repression of Organ Boundary Genes Promotes Stem Morphogenesis. Developmental cell, 39(2), 198.

Goel R, et al. (2016) Genome-Wide Analysis of the Musa WRKY Gene Family: Evolution and Differential Expression during Development and Stress. Frontiers in plant science, 7, 299.

Adewoye AB, et al. (2015) Identification and functional analysis of early gene expression induced by circadian light-resetting in Drosophila. BMC genomics, 16(1), 570.

Ederli L, et al. (2015) Arabidopsis flower specific defense gene expression patterns affect resistance to pathogens. Frontiers in plant science, 6, 79.