Resource Summary Report

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RMA Express

RRID:SCR_008549
Type: Tool

Proper Citation

RMA Express (RRID:SCR_008549)

Resource Information

URL: http://rmaexpress.bmbolstad.com

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Description: RMAExpress is a standalone GUI program for Windows (and Linux) to compute gene expression summary values for Affymetrix Genechip data using the Robust Multichip Average expression summary and to carry out quality assessment using probe-level metrics. It does not require R nor is it dependent on any component of the BioConductor project. If focuses on processing 3'' IVT expression arrays, exon and WT gene arrays. What is RMA? RMA is the Robust Multichip Average. It consists of three steps: a background adjustment, quantile normalization (see the Bolstad et al reference) and finally summarization. Some references (currently published) for the RMA methodology are: Bolstad, B.M., Irizarry R. A., Astrand, M., and Speed, T.P. (2003), A Comparison of Normalization Methods for High Density Oligonucleotide Array Data Based on Bias and Variance. Bioinformatics 19(2):185-193 Supplemental information Rafael. A. Irizarry, Benjamin M. Bolstad, Francois Collin, Leslie M. Cope, Bridget Hobbs and Terence P. Speed (2003), Summaries of Affymetrix GeneChip probe level data Nucleic Acids Research 31(4):e15 Irizarry, RA, Hobbs, B, Collin, F, Beazer-Barclay, YD, Antonellis, KJ, Scherf, U, Speed, TP (2002) Exploration, Normalization, and Summaries of High Density Oligonucleotide Array Probe Level Data. Accepted for publication in Biostatistics. [Abstract, PDF, PS, Complementary Color Figures-PDF, Software] What do I need? You will need the appropriate CDF and CEL files for your dataset. For Exon and WT Gene arrays, the PGF and CLF should be used instead of the CDF file to build a CDFRME file. The process for doing this is explained in the user manual. Some pre-built CDFRME files are also available. CDFRME files HuEx_CDFRME.zip (95.9MB) HuGene_CDFRME.zip (5.5MB) MoEx_CDFRME.zip (79.6MB) MoGene_CDFRME.zip (6.3MB) RaEx_CDFRME.zip (48.4MB) RaGene_CDFRME.zip (5.7MB) Can I use affy/BioConductor instead? Of course. Hypothetically you will get the same results from both places, provided you have consistent settings in affy/BioConductor and RMAExpress. Some people prefer the power and flexibility of R and others like the point and click simplicity of a GUI. RMAExpress caters to the second option. Since RMAExpress outputs the computed expression values to a text file, you may of course load the expression measures into R and use features of Bioconductor for the analysis of your gene expression values. You can of course open the results file in any other application that supports importing plain text files. Will I get the same results as I would using affy/Bioconductor? Yes. The results from RMAExpress should be consistent. What are the machine requirements? A good rule of thumb is the more RAM you have the better. I would recommend at least 1GB, though 512MB will work in most situations. At this point the program has been tested using Windows 2000, Windows XP, Windows Vista and Linux. Most recently I have had a report of over 10,000 arrays processed in a single session. Can I do any quality assessment? Yes, store the residuals when you compute the expression values. Then you may examine chip pseudo-images of the residuals. Note that high positive residuals are colored increasingly read and low negative residuals are colored increasingly blue. To better interpret these images and gain a better feel for what is typical you may visit the PLM Image Gallery where images for a number of different datasets are shown. Access to the NUSE and RLE quality assessment metrics is also provided. How do I download and install it? Click here for the current release Windows version. Use the installer to install the program. The current release version number is 1.0 (released June 29, 2008). A pre-built linux version is not currently available, but you may build it using the source code. You can download pre-release versions from the following table (the release versions will be more stable, the development versions may have features that are incomplete or will be removed or altered before the next release was supported by the PGA U01 HL66583.

Synonyms: RMAX

Resource Type: software resource

Funding:

Resource Name: RMA Express

Resource ID: SCR_008549

Alternate IDs: nif-0000-31409

Record Creation Time: 20220129T080248+0000

Record Last Update: 20250410T065724+0000

Ratings and Alerts

No rating or validation information has been found for RMA Express.

No alerts have been found for RMA Express.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 97 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Xu S, et al. (2022) Capsaicin restores sodium iodine symporter-mediated radioiodine uptake through bypassing canonical TSH?TSHR pathway in anaplastic thyroid carcinoma cells. Journal of molecular cell biology, 13(11), 791.

Chen J, et al. (2021) Long-term dynamic compression enhancement TGF-?3-induced chondrogenesis in bovine stem cells: a gene expression analysis. BMC genomic data, 22(1), 13.

Schmauder L, et al. (2021) hsp-90 and unc-45 depletion induce characteristic transcriptional signatures in coexpression cliques of C. elegans. Scientific reports, 11(1), 12852.

Vilas-Boas V, et al. (2021) Primary Human Hepatocyte Spheroids as Tools to Study the Hepatotoxic Potential of Non-Pharmaceutical Chemicals. International journal of molecular sciences, 22(20).

Gijbels E, et al. (2021) Dataset on transcriptomic profiling of cholestatic liver injury induced by food additives and a cosmetic ingredient. Data in brief, 38, 107373.

Zhong Q, et al. (2021) Patterns of Immune Infiltration in Endometriosis and Their Relationship to r-AFS Stages. Frontiers in genetics, 12, 631715.

Iscan E, et al. (2021) TAp73? Can Promote Hepatocellular Carcinoma Dedifferentiation. Cancers, 13(4).

Qin HL, et al. (2021) Notoginsenoside R1 attenuates breast cancer progression by targeting CCND2 and YBX3. Chinese medical journal, 134(5), 546.

Han M, et al. (2020) Exosome-transmitted miR-567 reverses trastuzumab resistance by inhibiting ATG5 in breast cancer. Cell death & disease, 11(1), 43.

Sharad S, et al. (2020) Age and Tumor Differentiation-Associated Gene Expression Based Analysis of Non-Familial Prostate Cancers. Frontiers in oncology, 10, 584280.

Weber DG, et al. (2020) Circulating long non-coding RNA GAS5 (growth arrest-specific transcript 5) as a complement marker for the detection of malignant mesothelioma using liquid biopsies. Biomarker research, 8, 15.

Zhang T, et al. (2020) Differential O- and Glycosphingolipid Glycosylation in Human Pancreatic Adenocarcinoma Cells With Opposite Morphology and Metastatic Behavior.

Frontiers in oncology, 10, 732.

Oc S, et al. (2020) Dynamic transcriptional response of Saccharomyces cerevisiae cells to copper. Scientific reports, 10(1), 18487.

Katta S, et al. (2019) Curcumin-Gene Expression Response in Hormone Dependent and Independent Metastatic Prostate Cancer Cells. International journal of molecular sciences, 20(19).

Yan J, et al. (2019) Genome-wide and evolutionary analysis of the class III peroxidase gene family in wheat and Aegilops tauschii reveals that some members are involved in stress responses. BMC genomics, 20(1), 666.

Alfituri OA, et al. (2019) Effects of host-derived chemokines on the motility and viability of Trypanosoma brucei. Parasite immunology, 41(2), e12609.

Paris J, et al. (2019) Targeting the RNA m6A Reader YTHDF2 Selectively Compromises Cancer Stem Cells in Acute Myeloid Leukemia. Cell stem cell, 25(1), 137.

Engel T, et al. (2018) Bi-directional genetic modulation of GSK-3? exacerbates hippocampal neuropathology in experimental status epilepticus. Cell death & disease, 9(10), 969.

Nechama M, et al. (2018) The IL-33-PIN1-IRAK-M axis is critical for type 2 immunity in IL-33-induced allergic airway inflammation. Nature communications, 9(1), 1603.

Yan J, et al. (2018) Genome-wide classification, evolutionary analysis and gene expression patterns of the kinome in Gossypium. PloS one, 13(5), e0197392.