Resource Summary Report

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MetaQC

RRID:SCR_006000
Type: Tool

Proper Citation

MetaQC (RRID:SCR_006000)

Resource Information

URL: http://cran.r-project.org/web/packages/MetaQC/

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Description: Software for quality control and diagnosis for microarray meta-analysis. Quantitative quality control measures include: (1) internal homogeneity of co-expression structure among studies (internal quality control; IQC); (2) external consistency of co-expression structure correlating with pathway database (external quality control; EQC); (3) accuracy of differentially expressed gene detection (accuracy quality control; AQCg) or pathway identification (AQCp); (4) consistency of differential expression ranking in genes (consistency quality control; CQCg) or pathways (CQCp). For each quality control index, the p-values from statistical hypothesis testing are minus log transformed and PCA biplots were applied to assist visualization and decision. Results generate systematic suggestions to exclude problematic studies in microarray meta-analysis and potentially can be extended to GWAS or other types of genomic meta-analysis. The identified problematic studies can be scrutinized to identify technical and biological causes (e.g. sample size, platform, tissue collection, preprocessing etc) of their bad quality or irreproducibility for final inclusion / exclusion decision.

Synonyms: MetaQC: Objective Quality Control and Inclusion/Exclusion Criteria for Genomic Meta-Analysis, MetaQC: Objective Quality Control and Inclusion / Exclusion Criteria for Genomic Meta-Analysis

Resource Type: software resource

Defining Citation: PMID:22116060

Keywords: standalone software, mac os x, unix/linux, windows, r, FASEB list

Funding:

Availability: GNU General Public License, v2

Resource Name: MetaQC

Resource ID: SCR_006000

Alternate IDs: OMICS_04032

Alternate URLs: https://github.com/donkang34/MetaQC

Record Creation Time: 20220129T080233+0000

Record Last Update: 20250420T014309+0000

Ratings and Alerts

No rating or validation information has been found for MetaQC.

No alerts have been found for MetaQC.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 39 mentions in open access literature.

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

Farhangniya M, et al. (2023) Integrated Bioinformatic Analysis of Differentially Expressed Genes Associated with Wound Healing. Cell journal, 25(12), 874.

Chen Q, et al. (2022) Over-expression of IL1R2 in PBMCs of Patients with Coronary Artery Disease and Its Clinical Significance. Anatolian journal of cardiology, 26(9), 710.

Zhao S, et al. (2021) Identification of Diagnostic Markers for Major Depressive Disorder Using Machine Learning Methods. Frontiers in neuroscience, 15, 645998.

Yoon S, et al. (2021) Powerful p-value combination methods to detect incomplete association. Scientific reports, 11(1), 6980.

Luo D, et al. (2021) A predictive model for assessing prognostic risks in gastric cancer patients using gene expression and methylation data. BMC medical genomics, 14(1), 14.

Cao W, et al. (2021) Identification of novel prognostic genes of triple-negative breast cancer using meta-analysis and weighted gene co-expressed network analysis. Annals of translational medicine, 9(3), 205.

Lee T, et al. (2021) Identification of Disease-Related Genes That Are Common between Alzheimer's and Cardiovascular Disease Using Blood Genome-Wide Transcriptome Analysis. Biomedicines, 9(11).

Sun X, et al. (2021) Identification of key genes in osteoarthritis using bioinformatics, principal component analysis and meta-analysis. Experimental and therapeutic medicine, 21(1), 18.

Zhang Q, et al. (2021) The paeonol target gene autophagy-related 5 has a potential therapeutic value in psoriasis treatment. PeerJ, 9, e11278.

Han Y, et al. (2021) Screening of characteristic genes in ulcerative colitis by integrating gene expression profiles. BMC gastroenterology, 21(1), 415.

Ghazvini K, et al. (2020) Expression changes of cytotoxicity and apoptosis genes in HTLV-1-associated myelopathy/tropical spastic paraparesis patients from the perspective of system virology. Access microbiology, 2(3), acmi000088.

Ke H, et al. (2020) Creation of a Prognostic Risk Prediction Model for Lung Adenocarcinoma Based on Gene Expression, Methylation, and Clinical Characteristics. Medical science monitor : international medical journal of experimental and clinical research, 26, e925833.

Long G, et al. (2020) A six?gene support vector machine classifier contributes to the diagnosis of pediatric septic shock. Molecular medicine reports, 21(3), 1561.

Xie H, et al. (2019) A Six-Gene Signature Predicts Survival of Adenocarcinoma Type of Non-Small-Cell Lung Cancer Patients: A Comprehensive Study Based on Integrated Analysis and Weighted Gene Coexpression Network. BioMed research international, 2019, 4250613.

Wang S, et al. (2019) Integrated analysis of 34 microarray datasets reveals CBX3 as a diagnostic and prognostic biomarker in glioblastoma. Journal of translational medicine, 17(1), 179.

Li Y, et al. (2019) Identification of Candidate Genes and MicroRNAs for Acute Myocardial Infarction by Weighted Gene Coexpression Network Analysis. BioMed research international, 2019, 5742608.

Forés-Martos J, et al. (2019) Transcriptomic metaanalyses of autistic brains reveals shared gene expression and biological pathway abnormalities with cancer. Molecular autism, 10, 17.

Miraji MK, et al. (2019) Identification of primary genes in glomeruli compartment of immunoglobulin A nephropathy by bioinformatic analysis. PeerJ, 7, e7067.

Mozhgani SH, et al. (2019) An insight to HTLV-1-associated myelopathy/tropical spastic paraparesis (HAM/TSP) pathogenesis; evidence from high-throughput data integration and meta-analysis. Retrovirology, 16(1), 46.

Kim IW, et al. (2019) Screening of Drug Repositioning Candidates for Castration Resistant Prostate Cancer. Frontiers in oncology, 9, 661.