Resource Summary Report

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INMEX

RRID:SCR_004173
Type: Tool

Proper Citation

INMEX (RRID:SCR_004173)

Resource Information

URL: http://www.inmex.ca./INMEX/

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Description: A web-based tool to support meta-analysis of multiple gene-expression data sets, as well as to enable integration of data sets from gene expression and metabolomics experiments. INMEX contains three functional modules. The data preparation module supports flexible data processing, annotation and visualization of individual data sets. The statistical analysis module allows researchers to combine multiple data sets based on P-values, effect sizes, rank orders and other features. The significant genes can be examined in functional analysis module for enriched Gene Ontology terms or Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways, or expression profile visualization. INMEX has built-in support for common gene/metabolite identifiers (IDs), as well as 45 popular microarray platforms for human, mouse and rat. Complex operations are performed through a user-friendly web interface in a step-by-step manner.

Abbreviations: INMEX

Synonyms: INtegrative Meta-analysis of EXpression data, INMEX - INtegrative Meta-analysis of EXpression data

Resource Type: production service resource, data analysis service, service resource, analysis service resource

Defining Citation: PMID:23766290

Keywords: gene expression, meta-analysis, metabolomics, pathway, gene, metabolite, visualization, bio.tools

Funding: Killam Trust ;

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Availability: Acknowledgement requested

Resource Name: INMEX

Resource ID: SCR_004173

Alternate IDs: biotools:inmex, OMICS_01546

Alternate URLs: https://bio.tools/inmex

Record Creation Time: 20220129T080223+0000

Record Last Update: 20250519T204648+0000

Ratings and Alerts

No rating or validation information has been found for INMEX.

No alerts have been found for INMEX.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 18 mentions in open access literature.

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

Zheng PF, et al. (2021) Weighted gene co-expression network analysis identifies specific modules and hub genes related to coronary artery disease. Scientific reports, 11(1), 6711.

Mishra A, et al. (2020) Host-Viral Interactions Revealed among Shared Transcriptomics Signatures of ARDS and Thrombosis: A Clue into COVID-19 Pathogenesis. TH open : companion journal to thrombosis and haemostasis, 4(4), e403.

Vorobyev A, et al. (2019) Gene-diet interactions associated with complex trait variation in an advanced intercross outbred mouse line. Nature communications, 10(1), 4097.

Zhang D, et al. (2019) Distinct gene expression characteristics in epithelial cell-Porphyromonas gingivalis interactions by integrating transcriptome analyses. International journal of medical sciences, 16(10), 1320.

Badr MT, et al. (2019) Gene expression profiling meta-analysis reveals novel gene

signatures and pathways shared between tuberculosis and rheumatoid arthritis. PloS one, 14(3), e0213470.

Akbari V, et al. (2019) Transcriptome and Network Dissection of Microsatellite Stable and Highly Instable Colorectal Cancer. Asian Pacific journal of cancer prevention : APJCP, 20(8), 2445.

Wang Z, et al. (2018) Meta-analysis of human gene expression in response to Mycobacterium tuberculosis infection reveals potential therapeutic targets. BMC systems biology, 12(1), 3.

Zhao H, et al. (2018) Network-based meta-analysis in the identification of biomarkers for papillary thyroid cancer. Gene, 661, 160.

Xu M, et al. (2018) Re-exploring the core genes and modules in the human frontal cortex during chronological aging: insights from network-based analysis of transcriptomic studies. Aging, 10(10), 2816.

Sezin T, et al. (2017) Gene Expression Analysis Reveals Novel Shared Gene Signatures and Candidate Molecular Mechanisms between Pemphigus and Systemic Lupus Erythematosus in CD4+ T Cells. Frontiers in immunology, 8, 1992.

Jiang B, et al. (2017) Gastric Cancer Associated Genes Identified by an Integrative Analysis of Gene Expression Data. BioMed research international, 2017, 7259097.

Muthuramalingam P, et al. (2017) Global Transcriptome Analysis of Combined Abiotic Stress Signaling Genes Unravels Key Players in Oryza sativa L.: An In silico Approach. Frontiers in plant science, 8, 759.

Zhang LL, et al. (2017) Transcriptomic meta-analysis identifies gene expression characteristics in various samples of HIV-infected patients with nonprogressive disease. Journal of translational medicine, 15(1), 191.

Vaiman D, et al. (2016) An Integrative Analysis of Preeclampsia Based on the Construction of an Extended Composite Network Featuring Protein-Protein Physical Interactions and Transcriptional Relationships. PloS one, 11(11), e0165849.

Jha PK, et al. (2016) Comprehensive Gene expression meta-analysis and integrated bioinformatic approaches reveal shared signatures between thrombosis and myeloproliferative disorders. Scientific reports, 6, 37099.

Thangaraj SV, et al. (2016) Molecular Portrait of Oral Tongue Squamous Cell Carcinoma Shown by Integrative Meta-Analysis of Expression Profiles with Validations. PloS one, 11(6), e0156582.

Paraboschi EM, et al. (2015) Meta-Analysis of Multiple Sclerosis Microarray Data Reveals Dysregulation in RNA Splicing Regulatory Genes. International journal of molecular sciences, 16(10), 23463.

Hounkpe BW, et al. (2015) Role of innate immunity-triggered pathways in the pathogenesis of Sickle Cell Disease: a meta-analysis of gene expression studies. Scientific reports, 5, 17822.