Resource Summary Report

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GeneCluster 2: An Advanced Toolset for Bioarray Analysis

RRID:SCR_008446
Type: Tool

Proper Citation

GeneCluster 2: An Advanced Toolset for Bioarray Analysis (RRID:SCR_008446)

Resource Information

URL: http://www.broad.mit.edu/cancer/software/genecluster2/gc2.html

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Description: THIS RESOURCE IS NO LONGER IN SERVICE, documented on July 17, 2013. A software package for analyzing gene expression and other bioarray data, giving users a variety of methods to build and evaluate class predictors, visualize marker lists, cluster data and validate results. GeneCluster 2.0 greatly expands the data analysis capabilities of GeneCluster 1.0 by adding supervised classification, gene selection, class discovery and permutation test methods. It includes algorithms for building and testing supervised models using weighted voting (WV) and k-nearest neighbor (KNN) algorithms, a module for systematically finding and evaluating clustering via self-organizing maps, and modules for marker gene selection and heat map visualization that allow users to view and sort samples and genes by many criteria. It enhances the clustering capabilities of GeneCluster 1.0 by adding a module for batch SOM clustering, and also includes a marker gene finder based on a KNN analysis and a visualization module. GeneCluster 2.0 is a stand-alone Java application and runs on any platform that supports the Java Runtime Environment version 1.3.1 or greater.

Synonyms: GeneCluster 2

Resource Type: software application, data analysis software, software toolkit, software resource, data processing software

Keywords: gene, cluster, software, analysis, expression, bioarray, data, class, predictor, visualization, marker, classification, algorithm, module, java, environment

Funding:

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: GeneCluster 2: An Advanced Toolset for Bioarray Analysis

Resource ID: SCR_008446

Alternate IDs: nif-0000-30293

Record Creation Time: 20220129T080247+0000

Record Last Update: 20250409T060738+0000

Ratings and Alerts

No rating or validation information has been found for GeneCluster 2: An Advanced Toolset for Bioarray Analysis.

No alerts have been found for GeneCluster 2: An Advanced Toolset for Bioarray Analysis.

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 NIF.

Mhibik M, et al. (2023) Cytotoxicity of the CD3×CD20 bispecific antibody epcoritamab in CLL is increased by concurrent BTK or BCL-2 targeting. Blood advances, 7(15), 4089.

Tanabe K, et al. (2022) Generation of functional human oligodendrocytes from dermal fibroblasts by direct lineage conversion. Development (Cambridge, England), 149(20).

Homans C, et al. (2022) Therapeutic Effects of Myriocin in Experimental Alcohol-Related Neurobehavioral Dysfunction and Frontal Lobe White Matter Biochemical Pathology. Journal of behavioral and brain science, 12(2), 23.

Nguyen THY, et al. (2021) Re-Identification of Patient Subgroups in Uveal Melanoma. Frontiers in oncology, 11, 731548.

Mellid S, et al. (2020) Novel DNMT3A Germline Variant in a Patient with Multiple Paragangliomas and Papillary Thyroid Carcinoma. Cancers, 12(11).

Shrestha A, et al. (2020) Integrated Proteo-Transcriptomic Analyses Reveal Insights into Regulation of Pollen Development Stages and Dynamics of Cellular Response to Apple Fruit Crinkle Viroid (AFCVd)-Infection in Nicotiana tabacum. International journal of molecular sciences, 21(22).

Kusmider M, et al. (2020) Time-course of changes in key catecholaminergic receptors and trophic systems in rat brain after antidepressant administration. Neurochemistry international, 141, 104885.

de la Monte SM, et al. (2020) Critical Shifts in Cerebral White Matter Lipid Profiles After Ischemic-Reperfusion Brain Injury in Fetal Sheep as Demonstrated by the Positive Ion Mode MALDI-Mass Spectrometry. Cell medicine, 12, 2155179019897002.

Ellestad LE, et al. (2019) Transcriptional profiling and pathway analysis reveal differences in pituitary gland function, morphology, and vascularization in chickens genetically selected for high or low body weight. BMC genomics, 20(1), 316.

Remacha L, et al. (2019) Recurrent Germline DLST Mutations in Individuals with Multiple Pheochromocytomas and Paragangliomas. American journal of human genetics, 104(4), 651.

Zhang M, et al. (2019) Expression Analysis of mRNA Decay of Maternal Genes during Bombyx mori Maternal-to-Zygotic Transition. International journal of molecular sciences, 20(22).

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Xu P, et al. (2019) iTRAQ-Based Quantitative Proteomic Analysis of Digestive Juice across the First 48 Hours of the Fifth Instar in Silkworm Larvae. International journal of molecular sciences, 20(24).

Barske L, et al. (2018) Essential Role of Nr2f Nuclear Receptors in Patterning the Vertebrate Upper Jaw. Developmental cell, 44(3), 337.

Wang X, et al. (2018) Metabolic adaptation of wheat grain contributes to a stable filling rate under heat stress. Journal of experimental botany, 69(22), 5531.

Liang X, et al. (2018) Transcriptomic analysis reveals candidate genes regulating development and host interactions of Colletotrichum fructicola. BMC genomics, 19(1), 557.

Talbott H, et al. (2017) Early transcriptome responses of the bovine midcycle corpus luteum to prostaglandin F2? includes cytokine signaling. Molecular and cellular endocrinology, 452, 93.

Talbott H, et al. (2017) Transcriptomic and bioinformatics analysis of the early time-course of the response to prostaglandin F2 alpha in the bovine corpus luteum. Data in brief, 14, 695.

Kim SH, et al. (2016) Upregulated expression of BCL2, MCM7, and CCNE1 indicate cisplatin-resistance in the set of two human bladder cancer cell lines: T24 cisplatin sensitive and T24R2 cisplatin resistant bladder cancer cell lines. Investigative and clinical urology, 57(1), 63.

Zhang N, et al. (2016) SIRT1 promotes metastasis of human osteosarcoma cells. Oncotarget, 7(48), 79654.