Resource Summary Report

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NOISeq

RRID:SCR_003002
Type: Tool

Proper Citation

NOISeq (RRID:SCR_003002)

Resource Information

URL: http://bioinfo.cipf.es/noiseq/doku.php?id=start

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Description: Software used for the identification of differentially expressed genes from count data or previously normalized count data. It empirically models the noise distribution of count changes by contrasting fold-change differences (M) and absolute expression differences (D) for all the features in samples within the same condition. This reference distribution is then used to assess whether the M-D values computed between two conditions for a given gene is likely to be part of the noise or represent a true differential expression.

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

Defining Citation: DOI:10.1101/gr.124321.111

Keywords: differentially expressed genes, gene identification

Funding:

Availability: Available for download, Acknowledgement requested

Resource Name: NOISeq

Resource ID: SCR_003002

Alternate IDs: OMICS_01311

Record Creation Time: 20220129T080216+0000

Record Last Update: 20250410T064935+0000

Ratings and Alerts

No rating or validation information has been found for NOISeq.

No alerts have been found for NOISeq.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 623 mentions in open access literature.

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

Suvanasuthi R, et al. (2025) Analysis of precancerous lesion-related microRNAs for early diagnosis of cervical cancer in the Thai population. Scientific reports, 15(1), 142.

Wu K, et al. (2025) Continuous cell lines derived from the Asian citrus psyllid, Diaphorina citri, harbor viruses and Wolbachia. Scientific reports, 15(1), 124.

Suppiah J, et al. (2025) Unraveling potential gene biomarkers for dengue infection through RNA sequencing. Virus genes, 61(1), 26.

Yu Y, et al. (2025) Combined transcriptome and whole genome sequencing analyses reveal candidate drug-resistance genes of Eimeria tenella. iScience, 28(1), 111592.

Ferreira LGA, et al. (2024) COUP-TFII regulates early bipotential gonad signaling and commitment to ovarian progenitors. Cell & bioscience, 14(1), 3.

Errichiello E, et al. (2024) Further evidence supporting the role of GTDC1 in glycine metabolism and neurodevelopmental disorders. European journal of human genetics : EJHG, 32(8), 920.

D'Alise AM, et al. (2024) Phase I Trial of Viral Vector-Based Personalized Vaccination Elicits Robust Neoantigen-Specific Antitumor T-Cell Responses. Clinical cancer research : an official journal of the American Association for Cancer Research, 30(11), 2412.

Wubshet NH, et al. (2024) Cellular mechanotransduction of human osteoblasts in microgravity. bioRxiv : the preprint server for biology.

Hazan JM, et al. (2024) Integration of transcription regulation and functional genomic data reveals lncRNA SNHG6's role in hematopoietic differentiation and leukemia. Journal of

biomedical science, 31(1), 27.

Li KX, et al. (2024) Identification of miR-20b-5p as an inhibitory regulator in cardiac differentiation via TET2 and DNA hydroxymethylation. Clinical epigenetics, 16(1), 42.

Han SY, et al. (2024) Elucidating the callus-to-shoot-forming mechanism in Capsicum annuum 'Dempsey' through comparative transcriptome analyses. BMC plant biology, 24(1), 367.

Jurado M, et al. (2024) Identification of consistent QTL and candidate genes associated with seed traits in common bean by combining GWAS and RNA-Seq. TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik, 137(6), 143.

Zhang X, et al. (2024) PbrWRKY62-PbrADC1 module involves in superficial scald development of Pyrus bretschneideri Rehd.fruit via regulating putrescine biosynthesis. Molecular horticulture, 4(1), 6.

Schwab J, et al. (2024) Features of chronic urticaria after COVID-19 mRNA vaccine over time. Communications medicine, 4(1), 254.

Ortiz-Vasco CC, et al. (2024) The stringent response regulates the poly-?-hydroxybutyrate (PHB) synthesis in Azotobacter vinelandii. PloS one, 19(4), e0299640.

Wubshet NH, et al. (2024) Cellular mechanotransduction of human osteoblasts in microgravity. NPJ microgravity, 10(1), 35.

Aurigemma I, et al. (2024) Endothelial gene regulatory elements associated with cardiopharyngeal lineage differentiation. Communications biology, 7(1), 351.

Zhang J, et al. (2024) The role of the transcriptional repressor CssR in Corynebacterium glutamicum in response to phenolic compounds. Heliyon, 10(6), e27929.

Desponds E, et al. (2024) Immuno-Transcriptomic Profiling of Blood and Tumor Tissue Identifies Gene Signatures Associated with Immunotherapy Response in Metastatic Bladder Cancer. Cancers, 16(2).

Contriciani RE, et al. (2024) Phenotypic divergence between broiler and layer chicken lines is regulated at the molecular level during development. BMC genomics, 25(1), 168.