Resource Summary Report

Generated by NIF on Apr 28, 2025

betr

RRID:SCR_001332
Type: Tool

Proper Citation

betr (RRID:SCR_001332)

Resource Information

URL: http://www.bioconductor.org/packages/release/bioc/html/betr.html

Proper Citation: betr (RRID:SCR_001332)

Description: Software package that implements the Bayesian Estimation of Temporal Regulation algorithm to identify differentially expressed genes in microarray time-course data.

Abbreviations: betr

Synonyms: Bayesian Estimation of Temporal Regulation

Resource Type: software resource

Defining Citation: PMID:20003283

Keywords: differentially expression, gene, microarray, time-course

Funding:

Availability: GNU Lesser General Public License

Resource Name: betr

Resource ID: SCR_001332

Alternate IDs: OMICS_01997

Record Creation Time: 20220129T080206+0000

Record Last Update: 20250420T014026+0000

Ratings and Alerts

No rating or validation information has been found for betr.

No alerts have been found for betr.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 16 mentions in open access literature.

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

Zahroh RI, et al. (2024) Rising caesarean section rates and factors affecting women's decision-making about mode of birth in Indonesia: a longitudinal qualitative study. BMJ global health, 9(6).

Rienecke RD, et al. (2022) Treatment Outcome for Adults in a Residential Program for Binge Eating Spectrum Disorders: Protocol for a Prospective Pragmatic Single-Arm Trial. JMIR research protocols, 11(5), e32270.

Shen LL, et al. (2022) A hierarchical Bayesian entry time realignment method to study the long-term natural history of diseases. Scientific reports, 12(1), 4869.

Välikangas T, et al. (2022) Benchmarking tools for detecting longitudinal differential expression in proteomics data allows establishing a robust reproducibility optimization regression approach. Nature communications, 13(1), 7877.

van der Lem T, et al. (2021) [Wilhelm His, Sr., and the development of paraffin embedding. German version]. Der Pathologe, 42(4), 424.

Resaz R, et al. (2021) Exosomal MicroRNAs as Potential Biomarkers of Hepatic Injury and Kidney Disease in Glycogen Storage Disease Type Ia Patients. International journal of molecular sciences, 23(1).

Larriba E, et al. (2021) Tissue-Specific Metabolic Reprogramming during Wound-Induced Organ Formation in Tomato Hypocotyl Explants. International journal of molecular sciences, 22(18).

Resaz R, et al. (2020) Circulating exosomal microRNAs as potential biomarkers of hepatic injury and inflammation in a murine model of glycogen storage disease type 1a. Disease models & mechanisms, 13(9).

Ori APS, et al. (2019) A Longitudinal Model of Human Neuronal Differentiation for Functional

Investigation of Schizophrenia Polygenic Risk. Biological psychiatry, 85(7), 544.

Layeghifard M, et al. (2019) Microbiome networks and change-point analysis reveal key community changes associated with cystic fibrosis pulmonary exacerbations. NPJ biofilms and microbiomes, 5(1), 4.

Lombardo SD, et al. (2019) Transcriptomic Analysis Reveals Involvement of the Macrophage Migration Inhibitory Factor Gene Network in Duchenne Muscular Dystrophy. Genes, 10(11).

Michna A, et al. (2016) Natural Cubic Spline Regression Modeling Followed by Dynamic Network Reconstruction for the Identification of Radiation-Sensitivity Gene Association Networks from Time-Course Transcriptome Data. PloS one, 11(8), e0160791.

Yang Y, et al. (2016) Identification of Potential Key lncRNAs and Genes Associated with Aging Based on Microarray Data of Adipocytes from Mice. BioMed research international, 2016, 9181702.

Salazar G, et al. (2016) Time-course gene expression data on the transcriptional effects of Aminaphtone on ECV304 endothelial cells. Data in brief, 8, 836.

Clarke K, et al. (2015) Inference of Low and High-Grade Glioma Gene Regulatory Networks Delineates the Role of Rnd3 in Establishing Multiple Hallmarks of Cancer. PLoS genetics, 11(7), e1005325.

Spies D, et al. (2015) Dynamics in Transcriptomics: Advancements in RNA-seq Time Course and Downstream Analysis. Computational and structural biotechnology journal, 13, 469.