Resource Summary Report

Generated by NIF on Apr 28, 2025

MANOR

RRID:SCR_001305

Type: Tool

Proper Citation

MANOR (RRID:SCR_001305)

Resource Information

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

Proper Citation: MANOR (RRID:SCR_001305)

Description: Software package for importation, normalization, visualization, and quality control functions to correct identified sources of variability in array-CGH (Comparative genomic hybridization) experiments.

Abbreviations: MANOR

Synonyms: CGH Micro-Array NORmalization

Resource Type: software resource

Keywords: copy number variation, data import, microarray, preprocessing, quality control,

two channel, comparative genomic hybridization

Funding:

Availability: GNU General Public License, v2

Resource Name: MANOR

Resource ID: SCR_001305

Alternate IDs: OMICS_02028

Record Creation Time: 20220129T080206+0000

Record Last Update: 20250420T014025+0000

Ratings and Alerts

No rating or validation information has been found for MANOR.

No alerts have been found for MANOR.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 15 mentions in open access literature.

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

Jung HS, et al. (2024) Coumarin derivatives ameliorate the intestinal inflammation and pathogenic gut microbiome changes in the model of infectious colitis through antibacterial activity. Frontiers in cellular and infection microbiology, 14, 1362773.

Chanda D, et al. (2024) Meta-analysis reveals obesity associated gut microbial alteration patterns and reproducible contributors of functional shift. Gut microbes, 16(1), 2304900.

Ye X, et al. (2024) Leveraging baseline transcriptional features and information from single-cell data to power the prediction of influenza vaccine response. Frontiers in cellular and infection microbiology, 14, 1243586.

Wang L, et al. (2024) Cyber warfare: a study of Zelenskyy's social media political performance strategies and effects. Frontiers in psychology, 15, 1478639.

Douglas GM, et al. (2022) Integrating phylogenetic and functional data in microbiome studies. Bioinformatics (Oxford, England), 38(22), 5055.

Xu D, et al. (2021) The bacterial community and metabolome dynamics and their interactions modulate fermentation process of whole crop corn silage prepared with or without inoculants. Microbial biotechnology, 14(2), 561.

Arslan Aydin Ü, et al. (2021) Speech Driven Gaze in a Face-to-Face Interaction. Frontiers in neurorobotics, 15, 598895.

Rapp JZ, et al. (2021) Divergent Genomic Adaptations in the Microbiomes of Arctic Subzero Sea-Ice and Cryopeg Brines. Frontiers in microbiology, 12, 701186.

Eidlin Levy H, et al. (2021) Numbers (but not words) make math anxious individuals sweat: Physiological evidence. Biological psychology, 165, 108187.

Liu J, et al. (2021) A high-risk retinoblastoma subtype with stemness features,

dedifferentiated cone states and neuronal/ganglion cell gene expression. Nature communications, 12(1), 5578.

Yuen NH, et al. (2021) Driving With Distraction: Measuring Brain Activity and Oculomotor Behavior Using fMRI and Eye-Tracking. Frontiers in human neuroscience, 15, 659040.

McGivern C, et al. (2021) Alcohol attention bias in 14-16 year old adolescents: an eye tracking study. Psychopharmacology, 238(3), 655.

Yin X, et al. (2020) A Comparative Evaluation of Tools to Predict Metabolite Profiles From Microbiome Sequencing Data. Frontiers in microbiology, 11, 595910.

Bolton KL, et al. (2010) Common variants at 19p13 are associated with susceptibility to ovarian cancer. Nature genetics, 42(10), 880.

van Hijum SA, et al. (2008) Supervised Lowess normalization of comparative genome hybridization data--application to lactococcal strain comparisons. BMC bioinformatics, 9, 93.