Resource Summary Report

Generated by NIF on Apr 29, 2025

SCAN.UPC

RRID:SCR_001334
Type: Tool

Proper Citation

SCAN.UPC (RRID:SCR_001334)

Resource Information

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

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Description: A microarray normalization software (SCAN) to facilitate personalized-medicine workflows with an extension (UPC) that estimates whether a given gene/transcript is active above background levels in a given sample. Rather than processing microarray samples as groups, which can introduce biases and present logistical challenges, SCAN normalizes each sample individually by modeling and removing probe- and array-specific background noise using only data from within each array. SCAN can be applied to one-channel (e.g., Affymetrix) or two-channel (e.g., Agilent) microarrays. The UPC method can be applied to one-channel or two-channel microarrays as well as to RNA-Seq read counts. Because UPC values are represented on the same scale and have an identical interpretation for each platform, they can be used for cross-platform data integration. A

Abbreviations: SCAN.UPC

Synonyms: Single-channel array normalization (SCAN) and Universal exPression Codes (UPC), Single-channel array normalization and Universal exPression Codes

Resource Type: software resource

Keywords: microarray, one channel, preprocessing, rna-seq, two channel

Funding:

Availability: MIT License

Resource Name: SCAN.UPC

Resource ID: SCR_001334

Alternate IDs: OMICS_02006

Record Creation Time: 20220129T080206+0000

Record Last Update: 20250420T014026+0000

Ratings and Alerts

No rating or validation information has been found for SCAN.UPC.

No alerts have been found for SCAN.UPC.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 11 mentions in open access literature.

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

Junet V, et al. (2021) CuBlock: a cross-platform normalization method for gene-expression microarrays. Bioinformatics (Oxford, England), 37(16), 2365.

Zogopoulos VL, et al. (2021) Arabidopsis Coexpression Tool: a tool for gene coexpression analysis in Arabidopsis thaliana. iScience, 24(8), 102848.

Lee J, et al. (2019) Blockade of integrin ?3 attenuates human pancreatic cancer via inhibition of EGFR signalling. Scientific reports, 9(1), 2793.

Taroni JN, et al. (2019) MultiPLIER: A Transfer Learning Framework for Transcriptomics Reveals Systemic Features of Rare Disease. Cell systems, 8(5), 380.

Lee J, et al. (2019) Scattered DUSP28 is a novel biomarker responsible for aggravating malignancy via the autocrine and paracrine signaling in metastatic pancreatic cancer. Cancer letters, 456, 1.

Tang J, et al. (2018) Genome-wide expression profiling of glioblastoma using a large combined cohort. Scientific reports, 8(1), 15104.

Kasendra M, et al. (2018) Development of a primary human Small Intestine-on-a-Chip using biopsy-derived organoids. Scientific reports, 8(1), 2871.

Boege Y, et al. (2017) A Dual Role of Caspase-8 in Triggering and Sensing Proliferation-Associated DNA Damage, a Key Determinant of Liver Cancer Development. Cancer cell, 32(3), 342.

Lee J, et al. (2017) Autocrine DUSP28 signaling mediates pancreatic cancer malignancy via regulation of PDGF-A. Scientific reports, 7(1), 12760.

Lee J, et al. (2015) Blockade of dual-specificity phosphatase 28 decreases chemo-resistance and migration in human pancreatic cancer cells. Scientific reports, 5, 12296.

Forreryd A, et al. (2015) Prediction of chemical respiratory sensitizers using GARD, a novel in vitro assay based on a genomic biomarker signature. PloS one, 10(3), e0118808.