Resource Summary Report

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TCC

RRID:SCR_001779
Type: Tool

Proper Citation

TCC (RRID:SCR_001779)

Resource Information

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

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Description: An R package that provides a series of functions for differential expression analysis from RNA-seq count data using robust normalization strategy (called DEGES). The basic idea of DEGES is that potential differentially expressed genes or transcripts (DEGs) among compared samples should be removed before data normalization to obtain a well-ranked gene list where true DEGs are top-ranked and non-DEGs are bottom ranked. This can be done by performing a multi-step normalization strategy (called DEGES for DEG elimination strategy). A major characteristic of TCC is to provide the robust normalization methods for several kinds of count data (two-group with or without replicates, multi-group/multi-factor, and so on) by virtue of the use of combinations of functions in other sophisticated packages (especially edgeR, DESeq, and baySeq).

Abbreviations: TCC

Synonyms: Tag Count Comparison, TCC: Differential expression analysis for tag count data with robust normalization strategies

Resource Type: software resource

Defining Citation: PMID:23837715

Keywords: rna-seq, differential expression, high throughput sequencing

Funding:

Availability: GNU General Public License, v2

Resource Name: TCC

Resource ID: SCR_001779

Alternate IDs: OMICS_01952

Record Creation Time: 20220129T080209+0000

Record Last Update: 20250420T014039+0000

Ratings and Alerts

No rating or validation information has been found for TCC.

No alerts have been found for TCC.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 6 mentions in open access literature.

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

Chun D, et al. (2024) Flt3L enhances clonal diversification and selective expansion of intratumoral CD8+ T cells while differentiating into effector-like cells. Cell reports, 43(12), 115023.

Ota M, et al. (2021) Dynamic landscape of immune cell-specific gene regulation in immune-mediated diseases. Cell, 184(11), 3006.

Hisanaga T, et al. (2021) Deep evolutionary origin of gamete-directed zygote activation by KNOX/BELL transcription factors in green plants. eLife, 10.

Kitajima S, et al. (2018) Overcoming Resistance to Dual Innate Immune and MEK Inhibition Downstream of KRAS. Cancer cell, 34(3), 439.

Li Y, et al. (2017) Bioinformatics analysis of gene expression data for the identification of critical genes in breast invasive carcinoma. Molecular medicine reports, 16(6), 8657.

Li Y, et al. (2016) Identification of hub genes and regulatory factors of glioblastoma multiforme subgroups by RNA-seq data analysis. International journal of molecular medicine, 38(4), 1170.