

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

Availability: Free, Available for download, Freely available

Resource Name: TCC

Resource ID: SCR_001779

Alternate IDs: OMICS_01952

License: GNU General Public License, v2

Record Creation Time: 20220129T080209+0000

Record Last Update: 20261017T202500+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 have not found any literature mentions for this resource.