Resource Summary Report

Generated by dkNET on Apr 29, 2025

Traph

RRID:SCR_005119
Type: Tool

Proper Citation

Traph (RRID:SCR_005119)

Resource Information

URL: http://www.cs.helsinki.fi/en/gsa/traph/

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Description: A software tool for transcript identification and quantification with RNA-Seq. The method has a two-fold advantage: on the one hand, it translates the problem as an established one in the field of network flows, which can be solved in polynomial time, with different existing solvers; on the other hand, it is general enough to encompass many of the previous proposals under the least sum of squares model.

Abbreviations: Traph

Synonyms: Transcripts in gRAPHs - Traph: A tool for transcript identification and quantification with RNA-Seq, Transcripts in gRAPHs

Resource Type: software resource

Defining Citation: PMID:23734627

Funding:

Availability: Acknowledgement requested

Resource Name: Traph

Resource ID: SCR_005119

Alternate IDs: OMICS_01295

Record Creation Time: 20220129T080228+0000

Record Last Update: 20250420T014244+0000

Ratings and Alerts

No rating or validation information has been found for Traph.

No alerts have been found for Traph.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 3 mentions in open access literature.

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

Tung LH, et al. (2019) Quantifying the benefit offered by transcript assembly with Scallop-LR on single-molecule long reads. Genome biology, 20(1), 287.

Gatter T, et al. (2019) Ry?t?: network-flow based transcriptome reconstruction. BMC bioinformatics, 20(1), 190.

Canzar S, et al. (2016) CIDANE: comprehensive isoform discovery and abundance estimation. Genome biology, 17, 16.