Resource Summary Report

Generated by NIF on Apr 17, 2025

Tunable Biclustering Algorithm

RRID:SCR_017121
Type: Tool

Proper Citation

Tunable Biclustering Algorithm (RRID:SCR_017121)

Resource Information

URL: https://github.com/KhiabanianLab/TuBA

Proper Citation: Tunable Biclustering Algorithm (RRID:SCR_017121)

Description: Software tool as graph based unsupervised biclustering algorithm to identify alterations in tumors based on hypothesis that gene pairs relevant to clinical process share statistically significant number of samples with extreme expression.

Abbreviations: TuBA

Resource Type: data processing software, data analysis software, software resource, software application

Keywords: graph, unsupervised, algorithm, identify, alteration, tumor, gene, pair, significant, expression

Funding:

Availability: Free, Available for download, Freely available

Resource Name: Tunable Biclustering Algorithm

Resource ID: SCR_017121

Record Creation Time: 20220129T080333+0000

Record Last Update: 20250417T065609+0000

Ratings and Alerts

No rating or validation information has been found for Tunable Biclustering Algorithm.

No alerts have been found for Tunable Biclustering Algorithm.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Panda A, et al. (2020) Tissue- and development-stage-specific mRNA and heterogeneous CNV signatures of human ribosomal proteins in normal and cancer samples. Nucleic acids research, 48(13), 7079.

Singh A, et al. (2019) TuBA: Tunable biclustering algorithm reveals clinically relevant tumor transcriptional profiles in breast cancer. GigaScience, 8(6).