

Resource Summary Report

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PAGODA

RRID:SCR_017099

Type: Tool

Proper Citation

PAGODA (RRID:SCR_017099)

Resource Information

URL: <http://pklab.med.harvard.edu/scde/pagoda.links.html>

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Description: Software tool for analyzing transcriptional heterogeneity to detect statistically significant ways in which measured cells can be classified. Used to resolve multiple, potentially overlapping aspects of transcriptional heterogeneity by testing gene sets for coordinated variability among measured cells.

Synonyms: Pathway And Gene set OverDispersion Analysis, pagoda

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

Defining Citation: [PMID:26780092](#)

Keywords: heterogeneity, transcriptional, detect, statistically, cell, classified, overlapping, gene, set, coordinated, variability

Funding: Ellison Medical Foundation ;
NSF NSF-14-532;
NSF DGE1144152;
NIMH U01 MH098977;
NINDS R01 NS084398;
NIA T32 AG00216

Availability: Free, Available for download, Freely available

Resource Name: PAGODA

Resource ID: SCR_017099

Alternate URLs: <http://hms-dbmi.github.io/scde/index.html>

Record Creation Time: 20220129T080333+0000

Record Last Update: 20260801T190552+0000

Ratings and Alerts

No rating or validation information has been found for PAGODA.

No alerts have been found for PAGODA.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We have not found any literature mentions for this resource.