Resource Summary Report

Generated by RRID on Apr 11, 2025

proMODMatcher

RRID:SCR_017219
Type: Tool

Proper Citation

proMODMatcher (RRID:SCR_017219)

Resource Information

URL: http://research.mssm.edu/integrative-network-biology/Software.html

Proper Citation: proMODMatcher (RRID:SCR_017219)

Description: Software tool as probabilistic multi omics data matching procedure to curate data, identify and correct data annotation and errors in large databases. Used to check potential labeling errors in profiles where number of cis relationships is small, such as miRNA and RPPA profiles.

Synonyms: probabilisticMulti Omics DataMatcher

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

Keywords: probabilistic, matching, curate, omic, data, identify, correct, error, large, database, analysis, sample, label, bio.tools

Funding: NHGRI U01 HG008451;
NIA R01 AG046170;
NIAID U19 AI118610

Resource Name: proMODMatcher

Resource ID: SCR_017219

Alternate IDs: biotools:modmatcher

Alternate URLs: https://bio.tools/modmatcher

Record Creation Time: 20220129T080334+0000

Record Last Update: 20250411T055934+0000

Ratings and Alerts

No rating or validation information has been found for proMODMatcher.

No alerts have been found for proMODMatcher.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Lee E, et al. (2019) A probabilistic multi-omics data matching method for detecting sample errors in integrative analysis. GigaScience, 8(7).