## **Resource Summary Report**

Generated by dkNET on Apr 30, 2025

## **MRFSEQ**

RRID:SCR\_002972 Type: Tool

**Proper Citation** 

MRFSEQ (RRID:SCR\_002972)

## **Resource Information**

URL: http://www.cs.ucr.edu/~yyang027/mrfseq.htm

Proper Citation: MRFSEQ (RRID:SCR\_002972)

**Description:** Algorithm based on a Markov random field (MRF) model that uses additional gene coexpression data to enhance differential gene expression prediction power. It is able to call differentially expressed (DE) genes but also assign confidence scores to each inferred DE gene.

Resource Type: algorithm resource, software resource

Defining Citation: PMID:23793751

Keywords: markov, algorithm, gene expression, prediction algorithm, bio.tools

Funding:

Availability: Available for download

**Resource Name: MRFSEQ** 

Resource ID: SCR\_002972

Alternate IDs: biotools:mrfseq, OMICS\_01309

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

Record Creation Time: 20220129T080216+0000

Record Last Update: 20250430T055159+0000

## **Ratings and Alerts**

No rating or validation information has been found for MRFSEQ.

No alerts have been found for MRFSEQ.

Data and Source Information

Source: <u>SciCrunch Registry</u>

**Usage and Citation Metrics** 

We have not found any literature mentions for this resource.