# **Resource Summary Report**

Generated by <u>dkNET</u> on May 18, 2025

# **FateID**

RRID:SCR\_017244 Type: Tool

**Proper Citation** 

FateID (RRID:SCR\_017244)

#### **Resource Information**

URL: https://github.com/dgrun/FateID

Proper Citation: FateID (RRID:SCR\_017244)

**Description:** Software R package for inference of cell fate bias from single cell RNA-seq data. Iterative supervised learning algorithm for probabilistic quantification of cell fate bias in progenitor populations.

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

Defining Citation: PMID:29630061

**Keywords:** inference, cell, fate, bias, single, RNAseq, data, iterative, supervised, learning, algorithm, probabilistic, quantification, progenitor, population, bio.tools

Funding:

Availability: Free, Available for download, Freely available

Resource Name: FateID

Resource ID: SCR\_017244

Alternate IDs: biotools:fateid

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

**Record Creation Time:** 20220129T080334+0000

### **Ratings and Alerts**

No rating or validation information has been found for FateID.

No alerts have been found for FateID.

## 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 <u>dkNET</u>.

Xie X, et al. (2024) Decoding human bone marrow hematopoietic stem and progenitor cells from fetal to birth. iScience, 27(8), 110445.

Takada H, et al. (2023) Single-cell transcriptomics uncovers EGFR signaling-mediated gastric progenitor cell differentiation in stomach homeostasis. Nature communications, 14(1), 3750.