

Resource Summary Report

Generated by [dkNET](#) on Aug 12, 2026

[scGBM](#)

RRID:SCR_025518

Type: Tool

Proper Citation

scGBM (RRID:SCR_025518)

Resource Information

URL: <https://github.com/phillipnicol/scGBM>

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Description: Software application for model-based dimensionality reduction of scRNA-seq data. Quantifies uncertainty in each cell's latent position and leverages these uncertainties to assess confidence associated with given cell clustering. On real and simulated single-cell data produces low-dimensional embeddings that better capture relevant biological information while removing unwanted variation. Used for model-based dimensionality reduction for single-cell RNA-seq with generalized bilinear models.

Resource Type: source code, software resource

Defining Citation: [PMID:37162914](#)

Keywords: Generalized bilinear models, model-based dimensionality reduction, scRNA-seq data, removing unwanted variation,

Funding: NCI T32CA009337;
NCI R01CA240299

Availability: Free, Available for download, Freely available,

Resource Name: scGBM

Resource ID: SCR_025518

Record Creation Time: 20240723T053255+0000

Record Last Update: 20260810T040845+0000

Ratings and Alerts

No rating or validation information has been found for scGBM.

No alerts have been found for scGBM.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 3 mentions in open access literature.

Listed below are recent publications. The full list is available at [dkNET](#) .

Simmons SK, et al. (2026) Experimental and computational methods for allelic imbalance analysis from single-nucleus RNA-seq data. Genome biology, 27(1).

Simmons SK, et al. (2024) Experimental and Computational Methods for Allelic Imbalance Analysis from Single-Nucleus RNA-seq Data. bioRxiv : the preprint server for biology.

Nicol PB, et al. (2024) Model-based dimensionality reduction for single-cell RNA-seq using generalized bilinear models. Biostatistics (Oxford, England), 26(1).