

Resource Summary Report

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PIANO:Probabilistic Inference Autoencoder Networks for multi-Omics

RRID:SCR_027864

Type: Tool

Proper Citation

PIANO:Probabilistic Inference Autoencoder Networks for multi-Omics
(RRID:SCR_027864)

Resource Information

URL: <https://pypi.org/project/piano-integration/>

Proper Citation: PIANO:Probabilistic Inference Autoencoder Networks for multi-Omics
(RRID:SCR_027864)

Description: Software novel variational autoencoder framework for inferring integrated latent space representations for single cell transcriptomics data that uses a negative binomial generalized linear model for stronger batch correction, and code compilation for ten times faster training than existing tools. Enables superior analyses of multiple atlases, solving challenging integration tasks across sequencing platforms, development, and species, while simultaneously preserving desired biological signals.

Abbreviations: PIANO

Synonyms: piano

Resource Type: software application, software resource, source code

Defining Citation: [DOI:10.1101/2025.11.16.686778v2.full#sec-17](https://doi.org/10.1101/2025.11.16.686778v2.full#sec-17)

Keywords: Probabilistic Inference Autoencoder Networks, multi-Omics, variational autoencoder framework, inferring integrated latent space representations, single cell transcriptomics data,

Funding: NIMH 5T32MH065214;
NIMH DP2MH140136;
NIMH UM1MH130981

Availability: Free, Available for download, Freely available

Resource Name: PIANO:Probabilistic Inference Autoencoder Networks for multi-Omics

Resource ID: SCR_027864

Alternate URLs: <https://github.com/NingWang1729/piano>

License: GNU GPL v3

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Record Last Update: 20260905T133600+0000

Ratings and Alerts

No rating or validation information has been found for PIANO:Probabilistic Inference Autoencoder Networks for multi-Omics.

No alerts have been found for PIANO:Probabilistic Inference Autoencoder Networks for multi-Omics.

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 [PRECISE-TBI](#) .

Lin Z, et al. (2026) RMPore: a comprehensive database of single-molecule RNA modifications detected by Nanopore direct RNA sequencing. Nucleic acids research, 54(D1), D291.

Wang N, et al. (2025) Fast Optimization of Robust Transcriptomics Embeddings using Probabilistic Inference Autoencoder Networks for multi-Omics. bioRxiv : the preprint server for biology.