Resource Summary Report

Generated by RRID on May 7, 2025

GATE

RRID:SCR_002756
Type: Tool

Proper Citation

GATE (RRID:SCR_002756)

Resource Information

URL: http://yu68.github.io/GATE/

Proper Citation: GATE (RRID:SCR_002756)

Description: Model-based, open source software analysis tool for chromatin states prediction based on time-course epigenetic marks data. It uses a combinatory Finite Mixture model nested with HMM to model the time course marks data in which each single hidden markov model describes the hidden states for a region set across different time points.

Synonyms: Genomic Annotation from Time-couse Epigenomic data, Genomic Annotation from Time-couse Epigenomic data (GATE)

Resource Type: data analysis resource

Defining Citation: PMID:23033340

Keywords: chromatin state prediction software, time course epigenetic data, bio.tools

Funding:

Availability: Open source

Resource Name: GATE

Resource ID: SCR_002756

Alternate IDs: OMICS_03065, biotools:gate

Alternate URLs: https://github.com/yu68/GATE, https://bio.tools/gate

Record Creation Time: 20220129T080215+0000

Record Last Update: 20250420T014121+0000

Ratings and Alerts

No rating or validation information has been found for GATE.

No alerts have been found for GATE.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 276 mentions in open access literature.

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

Zhou L, et al. (2025) Unveiling patterns in spatial transcriptomics data: a novel approach utilizing graph attention autoencoder and multiscale deep subspace clustering network. GigaScience, 14.

Elswick A, et al. (2025) An exploration of desired abstinent and non-abstinent recovery outcomes among people who use methamphetamine. Harm reduction journal, 22(1), 7.

Karimipourfard M, et al. (2024) Impact of deep learning-based multiorgan segmentation methods on patient-specific internal dosimetry in PET/CT imaging: A comparative study. Journal of applied clinical medical physics, 25(2), e14254.

Hattab Z, et al. (2024) Heterogeneity within the Oregon Health Insurance Experiment: An application of causal forests. PloS one, 19(1), e0297205.

Oser CB, et al. (2024) Rural and urban clinician views on COVID-19's impact on substance use treatment for individuals on community supervision in Kentucky. Health & justice, 12(1), 12.

Dadgar M, et al. (2024) Evaluation of lesion contrast in the walk-through long axial FOV PET scanner simulated with XCAT anthropomorphic phantoms. EJNMMI physics, 11(1), 44.

Shoop G, et al. (2024) Combining PET and Compton imaging with edge-on CZT detectors for enhanced diagnostic capabilities. Advances in radiotherapy & nuclear medicine, 2(2).

Alibhai AY, et al. (2024) Comparing the Thin Plate Spline and Gaussian Interpolation Methods in Generating Hill of Visions for X-Linked Retinitis Pigmentosa Patients.

Translational vision science & technology, 13(12), 26.

Merlet A, et al. (2024) Validation of a discovery MI 4-ring model according to the NEMA NU 2-2018 standards: from Monte Carlo simulations to clinical-like reconstructions. EJNMMI physics, 11(1), 13.

Maguire MG, et al. (2024) Endpoints and Design for Clinical Trials in USH2A-Related Retinal Degeneration: Results and Recommendations From the RUSH2A Natural History Study. Translational vision science & technology, 13(10), 15.

Maroufpour S, et al. (2024) Validation of dosimetry programs (Olinda & IDAC) for evaluation of absorbed dose in 177LuPSMA therapy of metastatic castration-resistant prostate cancer (mCRPC) using Monte Carlo simulation. EJNMMI physics, 11(1), 102.

Wen S, et al. (2024) A method for miRNA diffusion association prediction using machine learning decoding of multi-level heterogeneous graph Transformer encoded representations. Scientific reports, 14(1), 20490.

Miller C, et al. (2024) Impact of cell geometry, cellular uptake region, and tumour morphology on 225Ac and 177Lu dose distributions in prostate cancer. EJNMMI physics, 11(1), 97.

McIntosh L, et al. (2024) Quantitative calibration of Tb-161 SPECT/CT in view of personalised dosimetry assessment studies. EJNMMI physics, 11(1), 18.

Michalek DA, et al. (2024) A multi-ancestry genome-wide association study in type 1 diabetes. Human molecular genetics, 33(11), 958.

De Benetti F, et al. (2024) DosePatch: physics-inspired cropping layout for patch-based Monte Carlo simulations to provide fast and accurate internal dosimetry. EJNMMI physics, 11(1), 51.

Saaidi R, et al. (2024) Crystal scatter effects in a large-area dual-panel Positron Emission Mammography system. PloS one, 19(3), e0297829.

Tang G, et al. (2024) Sampling clustering based on multi-view attribute structural relations. PloS one, 19(5), e0297989.

Sadeghi-Alavijeh O, et al. (2024) Quantifying variant contributions in cystic kidney disease using national-scale whole-genome sequencing. The Journal of clinical investigation, 134(19).

Gonzalez-Montoro A, et al. (2024) Design and proof of concept of a double-panel TOF-PET system. EJNMMI physics, 11(1), 73.