

Resource Summary Report

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Conditional AutoRegressive Deconvolution

RRID:SCR_026310

Type: Tool

Proper Citation

Conditional AutoRegressive Deconvolution (RRID:SCR_026310)

Resource Information

URL: <https://github.com/YingMa0107/CARD/>

Proper Citation: Conditional AutoRegressive Deconvolution (RRID:SCR_026310)

Description: Software R package for spatial transcriptomics. Deconvolution method that combines cell-type-specific expression information from single-cell RNA sequencing (scRNA-seq) with correlation in cell-type composition across tissue locations.

Abbreviations: CARD

Synonyms: , CARD: Conditional AutoRegressive Deconvolution, Conditional autoregressive-based deconvolution

Resource Type: software resource, software toolkit, source code

Defining Citation: [PMID:35501392](#)

Keywords: Deconvolution method, spatial transcriptomics, cell-type-specific expression, single-cell RNA sequencing, cell-type composition across tissue locations,

Funding: NHGRI R01HG011883;
NIGMS R01GM126553;
NIGMS R01GM144960

Availability: Free, Available for download, Freely available

Resource Name: Conditional AutoRegressive Deconvolution

Resource ID: SCR_026310

License: GNU GPL v3

Record Creation Time: 20250118T053338+0000

Record Last Update: 20260905T133518+0000

Ratings and Alerts

No rating or validation information has been found for Conditional AutoRegressive Deconvolution.

No alerts have been found for Conditional AutoRegressive Deconvolution.

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](#) .

Emery BA, et al. (2025) MEA-seqX: High-Resolution Profiling of Large-Scale Electrophysiological and Transcriptional Network Dynamics. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 12(20), e2412373.

Yang X, et al. (2025) Spatialsmooth: a spatially-aware convolutional autoencoder framework for enhanced deconvolution of spatial transcriptomics data. BMC genomics, 26(1), 791.

Kuo C, et al. (2025) Spatial Profiling Identifies Tumor-Associated Stroma Enrichment and MIF as Potential Immunotherapy Targets in Primary Ewing Sarcomas. Clinical cancer research : an official journal of the American Association for Cancer Research, 31(23), 5051.