Resource Summary Report

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NarrowPeaks

RRID:SCR_012924
Type: Tool

Proper Citation

NarrowPeaks (RRID:SCR_012924)

Resource Information

URL: http://www.bioconductor.org/packages/release/bioc/html/NarrowPeaks.html

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Description: Software package for post-processing of peaks and differential binding in ChIP-seq based on standard wiggle visualization files. The double aim of the package is to apply a functional version of principal component analysis (FPCA) to: (1) Process data in wiggle track format (WIG) commonly produced by ChIP-seq peak finders by applying FPCA over a set of selected candidate enriched regions. This is done in order to shorten the genomic locations accounting for a given proportion of variation among the enrichment-score profiles. The function "narrowpeaks" allows the user to discriminate between binding regions in close proximity to each other and to narrow down the length of the putative transcription factor binding sites while preserving the information present in the variability of the dataset and capturing major sources of variation. (2) Analyze differential variation when multiple ChIP-seq samples need to compared. The function "narrowpeaksDiff" quantifies differences between the tag-enrichment, and uses non-parametric tests on the FPC scores for testing differences between conditions.

Abbreviations: NarrowPeaks

Synonyms: NarrowPeaks: Analysis of Variation in ChIP-seq using Functional PCA Statistics

Resource Type: software resource

Keywords: functional principal component analysis

Availability: Artistic License

Resource Name: NarrowPeaks

Resource ID: SCR_012924

Alternate IDs: OMICS_00449

Record Creation Time: 20220129T080313+0000

Record Last Update: 20260912T195755+0000

Ratings and Alerts

No rating or validation information has been found for NarrowPeaks.

No alerts have been found for NarrowPeaks.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 49 mentions in open access literature.

Listed below are recent publications. The full list is available at PRECISE-TBI .

Wang L, et al. (2026) Predictive prioritization of enhancers associated with pancreatic disease risk. Cell genomics, 6(1), 101040.

Reed KSM, et al. (2026) Genome reorganization and its functional impact during breast cancer progression. eLife, 14.

Aarts MT, et al. (2026) Mechanistic dissection of GRHL2 and PR transcriptional co-regulation in breast cells. PLoS genetics, 22(3), e1012088.

López-Fuentes E, et al. (2026) Epigenetic and Transcriptional Programs Define Osteosarcoma Subtypes and Establish Targetable Vulnerabilities. Cancer discovery, 16(2), 296.

Hendrickson CL, et al. (2025) Foxi2 and Sox3 are master transcription regulators that control ectoderm germ layer specification in Xenopus. PLoS biology, 23(11), e3003476.

Buonaiuto G, et al. (2025) LncRNA HSCHARME is altered in human cardiomyopathies and promotes stem cell-derived cardiomyogenesis via splicing regulation. Nature communications, 16(1), 7880.

Fernández JD, et al. (2025) Organ-level gene-regulatory networks inferred from transcriptomic data reveal context-specific regulation and highlight novel regulators of ripening and ABA-mediated responses in tomato. Plant communications, 6(11), 101499.

O'Dwyer MR, et al. (2025) Nucleosome fibre topology guides transcription factor binding to enhancers. Nature, 638(8049), 251.

Minaeva M, et al. (2025) Specifying cellular context of transcription factor regulons for exploring context-specific gene regulation programs. NAR genomics and bioinformatics, 7(1), lqae178.

Reed KSM, et al. (2025) Genome reorganization and its functional impact during breast cancer progression. bioRxiv : the preprint server for biology.

Karthikeyan SK, et al. (2025) MammOnc-DB, an integrative breast cancer data analysis platform for target discovery. NPJ breast cancer, 11(1), 35.

Ersoy-Fazlioglu B, et al. (2025) Distinct transcription factor interactions drive HOXB13 activity in different stages of prostate cancer. Proceedings of the National Academy of Sciences of the United States of America, 122(49), e2500327122.

Saelens W, et al. (2025) ChromatinHD connects single-cell DNA accessibility and conformation to gene expression through scale-adaptive machine learning. Nature communications, 16(1), 317.

Veerappa A, et al. (2025) scAED: a framework for mapping the enhancer state at single-cell resolution. Briefings in bioinformatics, 26(6).

Malkmus J, et al. (2025) WNT signaling coordinately controls mouse limb bud outgrowth and establishment of the digit-interdigit pattern. Development (Cambridge, England), 152(11).

Wang L, et al. (2024) Predictive Prioritization of Enhancers Associated with Pancreas Disease Risk. bioRxiv : the preprint server for biology.

Woo BJ, et al. (2024) Integrative identification of non-coding regulatory regions driving metastatic prostate cancer. Cell reports, 43(9), 114764.

Kabir A, et al. (2024) Advancing Transcription Factor Binding Site Prediction Using DNA Breathing Dynamics and Sequence Transformers via Cross Attention. bioRxiv : the preprint server for biology.

Bamgbose G, et al. (2024) Mono-methylated histones control PARP-1 in chromatin and transcription. eLife, 13.

Varambally S, et al. (2024) MammOnc-DB, an integrative breast cancer data analysis platform for target discovery. Research square.