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

Funding:

Availability: Artistic License

Resource Name: NarrowPeaks

Resource ID: SCR_012924

Alternate IDs: OMICS_00449

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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 36 mentions in open access literature.

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

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.

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.

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.

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

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.

Bubb KL, et al. (2024) The regulatory potential of transposable elements in maize. bioRxiv : the preprint server for biology.

Caldas P, et al. (2024) Transcription readthrough is prevalent in healthy human tissues and associated with inherent genomic features. Communications biology, 7(1), 100.

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

Mononen J, et al. (2024) Genetic variation is a key determinant of chromatin accessibility and drives differences in the regulatory landscape of C57BL/6J and 129S1/SvImJ mice. Nucleic acids research, 52(6), 2904.

Bamgbose G, et al. (2024) PARP-1 is a transcriptional rheostat of metabolic and bivalent genes during development. Life science alliance, 7(2).

Minaeva M, et al. (2024) Specifying cellular context of transcription factor regulons for exploring context-specific gene regulation programs. bioRxiv : the preprint server for biology.

Tsaytler P, et al. (2023) BMP4 triggers regulatory circuits specifying the cardiac mesoderm lineage. Development (Cambridge, England), 150(10).

Kannan S, et al. (2023) Trajectory reconstruction identifies dysregulation of perinatal maturation programs in pluripotent stem cell-derived cardiomyocytes. Cell reports, 42(4), 112330.

John L, et al. (2023) Resolving the spatial architecture of myeloma and its microenvironment at the single-cell level. Nature communications, 14(1), 5011.

Fischer V, et al. (2023) Sperm chromatin accessibility's involvement in the intergenerational effects of stress hormone receptor activation. Translational psychiatry, 13(1), 378.

Kolterud Å, et al. (2023) Molecular subclass of uterine fibroids predicts tumor shrinkage in response to ulipristal acetate. Human molecular genetics, 32(7), 1063.

Lickwar CR, et al. (2022) Transcriptional Integration of Distinct Microbial and Nutritional Signals by the Small Intestinal Epithelium. Cellular and molecular gastroenterology and hepatology, 14(2), 465.

Bedi YS, et al. (2022) Chromatin alterations during the epididymal maturation of mouse sperm refine the paternally inherited epigenome. Epigenetics & chromatin, 15(1), 2.

Ka-Yue Chow L, et al. (2022) Epigenomic landscape study reveals molecular subtypes and EBV-associated regulatory epigenome reprogramming in nasopharyngeal carcinoma. EBioMedicine, 86, 104357.