Resource Summary Report

Generated by NIF on Apr 9, 2025

ZINBA

RRID:SCR_010868
Type: Tool

Proper Citation

ZINBA (RRID:SCR_010868)

Resource Information

URL: http://code.google.com/p/zinba/

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Description: Software to identify genomic regions enriched in a variety of ChIP-seq and related next-generation sequencing experiments (DNA-seq), calling both broad and narrow modes of enrichment across a range of signal-to-noise ratios. ZINBA models and accounts for factors that co-vary with background or experimental signal, such as G/C content, and identifies enrichment in genomes with complex local copy number variations. ZINBA provides a single unified framework for analyzing DNA-seq experiments in challenging genomic contexts.

Abbreviations: ZINBA

Synonyms: zinba - Zero Inflated Negative Binomial Algorithm, Zero Inflated Negative Binomial Algorithm

Resource Type: software resource

Defining Citation: PMID:21787385

Keywords: bio.tools

Funding:

Availability: GNU General Public License, v3

Resource Name: ZINBA

Resource ID: SCR_010868

Alternate IDs: biotools:zinba, OMICS_00465

Alternate URLs: https://bio.tools/zinba

Record Creation Time: 20220129T080301+0000

Record Last Update: 20250214T183147+0000

Ratings and Alerts

No rating or validation information has been found for ZINBA.

No alerts have been found for ZINBA.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 13 mentions in open access literature.

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

Miyaji M, et al. (2020) Topoisomerase II? targets DNA crossovers formed between distant homologous sites to induce chromatin opening. Scientific reports, 10(1), 18550.

Fiziev P, et al. (2018) ChromTime: modeling spatio-temporal dynamics of chromatin marks. Genome biology, 19(1), 109.

Li T, et al. (2018) OCEAN-C: mapping hubs of open chromatin interactions across the genome reveals gene regulatory networks. Genome biology, 19(1), 54.

Arda HE, et al. (2018) A Chromatin Basis for Cell Lineage and Disease Risk in the Human Pancreas. Cell systems, 7(3), 310.

Ge Y, et al. (2017) Stem Cell Lineage Infidelity Drives Wound Repair and Cancer. Cell, 169(4), 636.

Schmitt AM, et al. (2016) An inducible long noncoding RNA amplifies DNA damage signaling. Nature genetics, 48(11), 1370.

Seuter S, et al. (2016) Epigenome-wide effects of vitamin D and their impact on the transcriptome of human monocytes involve CTCF. Nucleic acids research, 44(9), 4090.

Powers NR, et al. (2016) The Meiotic Recombination Activator PRDM9 Trimethylates Both H3K36 and H3K4 at Recombination Hotspots In Vivo. PLoS genetics, 12(6), e1006146.

Han Y, et al. (2016) Integrating Epigenomics into the Understanding of Biomedical Insight. Bioinformatics and biology insights, 10, 267.

Viny AD, et al. (2015) Dose-dependent role of the cohesin complex in normal and malignant hematopoiesis. The Journal of experimental medicine, 212(11), 1819.

Heinig M, et al. (2015) histoneHMM: Differential analysis of histone modifications with broad genomic footprints. BMC bioinformatics, 16, 60.

Tran NT, et al. (2014) A survey of motif finding Web tools for detecting binding site motifs in ChIP-Seq data. Biology direct, 9, 4.

Landt SG, et al. (2012) ChIP-seq guidelines and practices of the ENCODE and modENCODE consortia. Genome research, 22(9), 1813.