Resource Summary Report

Generated by NIF on Apr 26, 2025

cn.mops

RRID:SCR_013036
Type: Tool

Proper Citation

cn.mops (RRID:SCR_013036)

Resource Information

URL: http://bioconductor.org/packages/2.12/bioc/html/cn.mops.html

Proper Citation: cn.mops (RRID:SCR_013036)

Description: A data processing pipeline for copy number variations and aberrations (CNVs and CNAs) from next generation sequencing (NGS) data.

Abbreviations: cn.mops

Synonyms: Copy Number estimation by a Mixture Of PoissonS

Resource Type: software resource

Keywords: bio.tools

Funding:

Resource Name: cn.mops

Resource ID: SCR_013036

Alternate IDs: biotools:cn.mops, OMICS_00335

Alternate URLs: https://bio.tools/cn.mops

Record Creation Time: 20220129T080313+0000

Record Last Update: 20250420T014630+0000

Ratings and Alerts

No rating or validation information has been found for cn.mops.

No alerts have been found for cn.mops.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 10 mentions in open access literature.

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

Louw N, et al. (2023) Incorporating CNV analysis improves the yield of exome sequencing for rare monogenic disorders-an important consideration for resource-constrained settings. Frontiers in genetics, 14, 1277784.

Bijarnia-Mahay S, et al. (2022) Growth and neurodevelopmental disorder with arthrogryposis, microcephaly and structural brain anomalies caused by Bi-allelic partial deletion of SMPD4 gene. Journal of human genetics, 67(3), 133.

Belyeu JR, et al. (2021) De novo structural mutation rates and gamete-of-origin biases revealed through genome sequencing of 2,396 families. American journal of human genetics, 108(4), 597.

Song L, et al. (2020) Integrated Analysis of Gene Expression, SNP, InDel, and CNV Identifies Candidate Avirulence Genes in Australian Isolates of the Wheat Leaf Rust Pathogen Puccinia triticina. Genes, 11(9).

Zhao L, et al. (2020) Comparative study of whole exome sequencing-based copy number variation detection tools. BMC bioinformatics, 21(1), 97.

Kommadath A, et al. (2019) A large interactive visual database of copy number variants discovered in taurine cattle. GigaScience, 8(6).

Raman L, et al. (2019) WisecondorX: improved copy number detection for routine shallow whole-genome sequencing. Nucleic acids research, 47(4), 1605.

Genova F, et al. (2018) First genome-wide CNV mapping in FELIS CATUS using next generation sequencing data. BMC genomics, 19(1), 895.

Krishnaprasad GN, et al. (2015) Variation in crossover frequencies perturb crossover assurance without affecting meiotic chromosome segregation in Saccharomyces cerevisiae. Genetics, 199(2), 399.

Petrovics G, et al. (2015) A novel genomic alteration of LSAMP associates with aggressive

prostate cancer in African American men. EBioMedicine, 2(12), 1957.