Resource Summary Report

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CNVpytor

RRID:SCR_021627
Type: Tool

Proper Citation

CNVpytor (RRID:SCR_021627)

Resource Information

URL: https://github.com/abyzovlab/CNVpytor

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Description: Software Python package and command line tool for CNV/CNA analysis from depth of coverage by mapped reads. Software tool for CNV/CNA detection and analysis from read depth and allele imbalance in whole genome sequencing.

Resource Type: software application, data analysis software, data processing software, sequence analysis software, software resource

Defining Citation: DOI:10.1101/2021.01.27.428472

Keywords: Copy number variations, copy number alternations, whole genome sequencing, Python

Funding: NCI U24 CA220242

Availability: Free, Available for download, Freely available

Resource Name: CNVpytor

Resource ID: SCR_021627

License: MIT License

Record Creation Time: 20220129T080356+0000

Record Last Update: 20250517T060450+0000

Ratings and Alerts

No rating or validation information has been found for CNVpytor.

No alerts have been found for CNVpytor.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 11 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Wang C, et al. (2024) High-depth whole-genome sequencing identifies structure variants, copy number variants and short tandem repeats associated with Parkinson's disease. NPJ Parkinson's disease, 10(1), 134.

Boehler NA, et al. (2024) A novel copy number variant in the murine Cdh23 gene gives rise to profound deafness and vestibular dysfunction. Human molecular genetics, 33(19), 1648.

Xie X, et al. (2024) Genome wide detection of CNV and their association with body size in Danzhou chickens. Poultry science, 103(12), 104266.

Liu YF, et al. (2024) Genetic architecture of long-distance migration and population genomics of the endangered Japanese eel. iScience, 27(8), 110563.

Panda A, et al. (2024) Genome-wide analysis and visualization of copy number with CNVpytor in igv.js. Bioinformatics (Oxford, England), 40(8).

Sun Z, et al. (2023) Performance comparisons of methylation and structural variants from low-input whole-genome methylation sequencing. Epigenomics, 15(1), 11.

Garrison MA, et al. (2023) Genomic data resources of the Brain Somatic Mosaicism Network for neuropsychiatric diseases. Scientific data, 10(1), 813.

Reis ALM, et al. (2023) The landscape of genomic structural variation in Indigenous Australians. Nature, 624(7992), 602.

Karetnikov DI, et al. (2023) Analysis of Genome Structure and Its Variations in Potato Cultivars Grown in Russia. International journal of molecular sciences, 24(6).

Davoudi P, et al. (2022) Genome-wide detection of copy number variation in American mink using whole-genome sequencing. BMC genomics, 23(1), 649.

Suvakov M, et al. (2021) CNVpytor: a tool for copy number variation detection and analysis

from read depth and allele imbalance in whole-genome sequencing. GigaScience, 10(11).