Resource Summary Report

Generated by dkNET on Apr 23, 2025

cortex var

RRID:SCR_005081
Type: Tool

Proper Citation

cortex var (RRID:SCR_005081)

Resource Information

URL: http://cortexassembler.sourceforge.net/index_cortex_var.html

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Description: A tool for genome assembly and variation analysis from sequence data. You can use it to discover and genotype variants on single or multiple haploid or diploid samples. If you have multiple samples, you can use Cortex to look specifically for variants that distinguish one set of samples (eg phenotype=X, cases, parents, tumour) from another set of samples (eg phenotype=Y, controls, child, normal). cortex_var features * Variant discovery by de novo assembly - no reference genome required * Supports multicoloured de Bruijn graphs - have multiple samples loaded into the same graph in different colours, and find variants that distinguish them. * Capable of calling SNPs, indels, inversions, complex variants, small haplotypes * Extremely accurate variant calling - see our paper for base-pair-resolution validation of entire alleles (rather than just breakpoints) of SNPs, indels and complex variants by comparison with fully sequenced (and finished) fosmids - a level of validation beyond that demanded of any other variant caller we are aware of - currently cortex_var is the most accurate variant caller for indels and complex variants. * Capable of aligning a reference genome to a graph and using that to call variants * Support for comparing cases/controls or phenotyped strains * Typical memory use: 1 high coverage human in under 80Gb of RAM, 1000 yeasts in under 64Gb RAM, 10 humans in under 256 Gb RAM

Abbreviations: cortex_var

Synonyms: cortex_var - for variant and population assembly

Resource Type: software resource

Defining Citation: PMID:22231483

Keywords: genome assembly, variation analysis, sequence, variation, genotype variant, haploid, diploid, snp, indel, inversion, variant, haplotype, de novo assembly, genotyping, variant-calling, population analysis, population assembly

Funding:

Availability: GNU General Public License, v3, Acknowledgement requested

Resource Name: cortex var

Resource ID: SCR_005081

Alternate IDs: OMICS_00056

Record Creation Time: 20220129T080228+0000

Record Last Update: 20250420T014243+0000

Ratings and Alerts

No rating or validation information has been found for cortex var.

No alerts have been found for cortex var.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 3 mentions in open access literature.

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

O'Hare JK, et al. (2017) Striatal fast-spiking interneurons selectively modulate circuit output and are required for habitual behavior. eLife, 6.

Pfeiffer W, et al. (2017) Whole-genome analysis of mycobacteria from birds at the San Diego Zoo. PloS one, 12(3), e0173464.

den Bakker HC, et al. (2014) Rapid whole-genome sequencing for surveillance of Salmonella enterica serovar enteritidis. Emerging infectious diseases, 20(8), 1306.