Resource Summary Report

Generated by PRECISE-TBI on Jul 31, 2026

CNVassoc

RRID:SCR_002901
Type: Tool

Proper Citation

CNVassoc (RRID:SCR_002901)

Resource Information

URL: http://cran.r-project.org/web/packages/CNVassoc/

Proper Citation: CNVassoc (RRID:SCR_002901)

Description: Software package that carries out association analysis of common copy number variants in population-based studies. It includes functions for analysing association under a series of study designs (case-control, cohort, etc), using several dependent variables (class status, censored data, counts) as response, adjusting for covariates and considering various inheritance models. It also includes functions for inferring copy number (CNV genotype calling). Various classes and methods for generic functions (print, summary, plot, anova, ...) have been created to facilitate the analysis.

Synonyms: CNVassoc: Association analysis of CNV data

Resource Type: software resource

Defining Citation: PMID:21609482

Keywords: standalone software, mac os x, unix/linux, windows, r

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: CNVassoc

Resource ID: SCR_002901

Alternate IDs: OMICS_02609

License: GNU General Public License, v2, v3

Record Creation Time: 20220129T080216+0000

Record Last Update: 20260725T190534+0000

Ratings and Alerts

No rating or validation information has been found for CNVassoc.

No alerts have been found for CNVassoc.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 1 mentions in open access literature.

Listed below are recent publications. The full list is available at PRECISE-TBI .

Revilla M, et al. (2017) A global analysis of CNVs in swine using whole genome sequence data and association analysis with fatty acid composition and growth traits. PloS one, 12(5), e0177014.