Resource Summary Report

Generated by dkNET on Apr 17, 2025

ALTree

RRID:SCR_007562
Type: Tool

Proper Citation

ALTree (RRID:SCR_007562)

Resource Information

URL: http://claire.bardel.free.fr/software.html

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Description: Software package to perform phylogeny based association and localization analysis.Used for association detection and localization of susceptibility sites using haplotype phylogenetic trees. Performs these two phylogeny-based analysis: tests association between candidate gene and disease; pinpoints markers (SNPs) that are putative disease susceptibility loci.

Synonyms: ALTREE

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

Defining Citation: PMID:16595555, DOI:10.1093/bioinformatics/btl131

Keywords: phylogeny based association, association detection, susceptibility sites, haplotype phylogenetic trees, gene, genetic, genomic

Funding:

Availability: Free, Available for download, Freely available

Resource Name: ALTree

Resource ID: SCR_007562

Alternate IDs: OMICS_13032, nlx_154221

Alternate URLs: https://sources.debian.org/src/altree/, https://gitlab.inria.fr/NGS/ALTree,

License: GPL

Record Creation Time: 20220129T080242+0000

Record Last Update: 20250417T065321+0000

Ratings and Alerts

No rating or validation information has been found for ALTree.

No alerts have been found for ALTree.

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.

Zanardo LG, et al. (2021) Experimental evolution of cowpea mild mottle virus reveals recombination-driven reduction in virulence accompanied by increases in diversity and viral fitness. Virus research, 303, 198389.

Blein S, et al. (2015) An original phylogenetic approach identified mitochondrial haplogroup T1a1 as inversely associated with breast cancer risk in BRCA2 mutation carriers. Breast cancer research : BCR, 17(1), 61.

Dubertret C, et al. (2010) A genetic schizophrenia-susceptibility region located between the ANKK1 and DRD2 genes. Progress in neuro-psychopharmacology & biological psychiatry, 34(3), 492.