Resource Summary Report

Generated by dkNET on Apr 17, 2025

RELPAIR

RRID:SCR_009358
Type: Tool

Proper Citation

RELPAIR (RRID:SCR_009358)

Resource Information

URL: http://csg.sph.umich.edu/boehnke/relpair.php

Proper Citation: RELPAIR (RRID:SCR_009358)

Description: Software program that infers the relationships of pairs of individuals based on genetic marker data, either within families or across an entire sample. (entry from Genetic Analysis Software)

Abbreviations: RELPAIR

Resource Type: software resource, software application

Keywords: gene, genetic, genomic, fortran77, ms-windows, (95), unix

Funding:

Resource Name: RELPAIR

Resource ID: SCR_009358

Alternate IDs: nlx_154573

Record Creation Time: 20220129T080252+0000

Record Last Update: 20250416T063545+0000

Ratings and Alerts

No rating or validation information has been found for RELPAIR.

No alerts have been found for RELPAIR.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 14 mentions in open access literature.

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

Fortes-Lima CA, et al. (2021) Complex genetic admixture histories reconstructed with Approximate Bayesian Computation. Molecular ecology resources, 21(4), 1098.

Masi S, et al. (2021) No evidence for female kin association, indications for extragroup paternity, and sex-biased dispersal patterns in wild western gorillas. Ecology and evolution, 11(12), 7634.

Hossain S, et al. (2019) The Interplay of Diet Quality and Alzheimer's Disease Genetic Risk Score in Relation to Cognitive Performance Among Urban African Americans. Nutrients, 11(9).

Sethuraman A, et al. (2018) Estimating Genetic Relatedness in Admixed Populations. G3 (Bethesda, Md.), 8(10), 3203.

Glusman G, et al. (2017) Ultrafast Comparison of Personal Genomes via Precomputed Genome Fingerprints. Frontiers in genetics, 8, 136.

Chou WC, et al. (2016) A combined reference panel from the 1000?Genomes and UK10K projects improved rare variant imputation in European and Chinese samples. Scientific reports, 6, 39313.

Chen H, et al. (2016) Exome Sequencing and Gene Prioritization Correct Misdiagnosis in a Chinese Kindred with Familial Amyloid Polyneuropathy. Scientific reports, 6, 26362.

Messina F, et al. (2016) Spatially Explicit Models to Investigate Geographic Patterns in the Distribution of Forensic STRs: Application to the North-Eastern Mediterranean. PloS one, 11(11), e0167065.

Palomba G, et al. (2015) Genome-wide association study of susceptibility loci for breast cancer in Sardinian population. BMC cancer, 15, 383.

Gazal S, et al. (2015) High level of inbreeding in final phase of 1000 Genomes Project. Scientific reports, 5, 17453.

Pemberton TJ, et al. (2010) Inference of unexpected genetic relatedness among individuals

in HapMap Phase III. American journal of human genetics, 87(4), 457.

Casselbrant ML, et al. (2009) Otitis media: a genome-wide linkage scan with evidence of susceptibility loci within the 17q12 and 10q22.3 regions. BMC medical genetics, 10, 85.

Murphy A, et al. (2009) PRKCA: a positional candidate gene for body mass index and asthma. American journal of human genetics, 85(1), 87.

Cox LA, et al. (2006) A second-generation genetic linkage map of the baboon (Papio hamadryas) genome. Genomics, 88(3), 274.