Resource Summary Report

Generated by dkNET on Apr 16, 2025

PEDPACK

RRID:SCR_013125
Type: Tool

Proper Citation

PEDPACK (RRID:SCR_013125)

Resource Information

URL: http://www.stat.washington.edu/thompson/Genepi/Pedpack.shtml

Proper Citation: PEDPACK (RRID:SCR_013125)

Description: Software programs for pedigree analysis, including segregation analysis, gene extinction, and pedigree graphics. (entry from Genetic Analysis Software)

Synonyms: PANGAEA

Resource Type: software resource, software application

Keywords: gene, genetic, genomic, c, unix, (compaq-alpha/..)

Funding:

Resource Name: PEDPACK

Resource ID: SCR_013125

Alternate IDs: nlx_154523

Record Creation Time: 20220129T080314+0000

Record Last Update: 20250416T063637+0000

Ratings and Alerts

No rating or validation information has been found for PEDPACK.

No alerts have been found for PEDPACK.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 4 mentions in open access literature.

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

Badner JA, et al. (2012) Genome-wide linkage analysis of 972 bipolar pedigrees using single-nucleotide polymorphisms. Molecular psychiatry, 17(8), 818.

Sieh W, et al. (2005) Comparison of marker types and map assumptions using Markov chain Monte Carlo-based linkage analysis of COGA data. BMC genetics, 6 Suppl 1(Suppl 1), S11.

Daw EW, et al. (2003) Genetic Analysis Workshop 13: simulated longitudinal data on families for a system of oligogenic traits. BMC genetics, 4 Suppl 1(Suppl 1), S3.

George AW, et al. (2003) Approaches to mapping genetically correlated complex traits. BMC genetics, 4 Suppl 1(Suppl 1), S71.