

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

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 application, software resource

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

Resource Name: PEDPACK

Resource ID: SCR_013125

Alternate IDs: nlx_154523

Record Creation Time: 20220129T080314+0000

Record Last Update: 20260905T133254+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 [Kravitz](#) .

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.