# Resource Summary Report

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# 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/..)

**Funding:**

**Resource Name:** PEDPACK

**Resource ID:** SCR_013125

**Alternate IDs:** nlx_154523

**Record Creation Time:** 20220129T080314+0000

**Record Last Update:** 20250412T055712+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 FDI Lab - SciCrunch.org.

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.