Resource Summary Report

Generated by NIF on May 6, 2025

peddy

RRID:SCR_017287
Type: Tool

Proper Citation

peddy (RRID:SCR_017287)

Resource Information

URL: https://github.com/brentp/peddy

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Description: Software package that evaluates correspondence between stated sexes, relationships, and ancestries in pedigree file and those inferred from genotypes in VCF file resulting from human whole genome sequencing or whole exome sequencing studies. Facilitates both automated and interactive, visual detection of sample swaps, poor sequencing quality, and other indicators of sample problems.

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

Defining Citation: PMID:28190455

Keywords: sex, relation, ancestry, evaluate, pedigree, VCF file, genome, sequencing, exome, error, genotype

Funding: NHGRI R01 HG006693

Availability: Free, Available for download, Freely available

Resource Name: peddy

Resource ID: SCR_017287

Alternate URLs: http://quinlanlab.org/#portfolioModal8

License: MIT License

Record Creation Time: 20220129T080334+0000

Record Last Update: 20250506T061605+0000

Ratings and Alerts

No rating or validation information has been found for peddy.

No alerts have been found for peddy.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 8 mentions in open access literature.

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

Avery CN, et al. (2024) Shared genomic segments analysis identifies MHC class I and class III molecules as genetic risk factors for juvenile idiopathic arthritis. HGG advances, 5(2), 100277.

Sirvent S, et al. (2023) Impaired expression of metallothioneins contributes to allergen-induced inflammation in patients with atopic dermatitis. Nature communications, 14(1), 2880.

Sung W, et al. (2023) An analysis of variants in TARDBP in the Korean population with amyotrophic lateral sclerosis: comparison with previous data. Scientific reports, 13(1), 18805.

Ruiz-Arenas C, et al. (2022) Identification of autosomal cis expression quantitative trait methylation (cis eQTMs) in children's blood. eLife, 11.

Werling DM, et al. (2020) Whole-Genome and RNA Sequencing Reveal Variation and Transcriptomic Coordination in the Developing Human Prefrontal Cortex. Cell reports, 31(1), 107489.

Sasani TA, et al. (2019) Large, three-generation human families reveal post-zygotic mosaicism and variability in germline mutation accumulation. eLife, 8.

Igeta H, et al. (2019) Rare compound heterozygous missense SPATA7 variations and risk of schizophrenia; whole-exome sequencing in a consanguineous family with affected siblings, follow-up sequencing and a case-control study. Neuropsychiatric disease and treatment, 15, 2353.

Pedersen BS, et al. (2017) Who's Who? Detecting and Resolving Sample Anomalies in Human DNA Sequencing Studies with Peddy. American journal of human genetics, 100(3),

406.