Resource Summary Report

Generated by NIF on Apr 19, 2025

PEDSTATS

RRID:SCR_009323
Type: Tool

Proper Citation

PEDSTATS (RRID:SCR_009323)

Resource Information

URL: http://www.sph.umich.edu/csg/abecasis/Pedstats/

Proper Citation: PEDSTATS (RRID:SCR_009323)

Description: Software application for error checking and data summary of large or small data sets in QTDT, LINKAGE or MENDEL format. Checks for basic formatting errors, disconnected family groups, ancestor-descendant loops and can detect all Mendelian (including X-linked) inheritance errors in any pedigree without loops. Produces text and graphical (PDF) summaries of the family structure, trait and marker information of pedigree data and can break down summaries by sex, relative pair type or family. PEDSTATS also does Hardy-Weinberg testing using either a fast exact or asymptotic test and can summarize information in text or graphical PDF format. Additional features include a number of options for filtering data prior to summary and checks for inappropriate age or covariate values. Lastly, PEDSTATS can identify and trim uninformative individuals from a pedigree and rewrite the reorganized data to a new pedigree file. (entry from Genetic Analysis Software)

Abbreviations: PEDSTATS

Resource Type: software application, software resource

Keywords: gene, genetic, genomic, c, c++, linux, unix, ms-windows

Funding:

Resource Name: PEDSTATS

Resource ID: SCR_009323

Alternate IDs: nlx_154529

Record Creation Time: 20220129T080252+0000

Record Last Update: 20250419T055205+0000

Ratings and Alerts

No rating or validation information has been found for PEDSTATS.

No alerts have been found for PEDSTATS.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 30 mentions in open access literature.

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

Yang K, et al. (2023) Whole Genome Resequencing Revealed the Genetic Relationship and Selected Regions among Baicheng-You, Beijing-You, and European-Origin Broilers. Biology, 12(11).

Nudel R, et al. (2020) Language deficits in specific language impairment, attention deficit/hyperactivity disorder, and autism spectrum disorder: An analysis of polygenic risk. Autism research : official journal of the International Society for Autism Research, 13(3), 369.

Kirin M, et al. (2017) Determinants of retinal microvascular features and their relationships in two European populations. Journal of hypertension, 35(8), 1646.

Li Z, et al. (2017) Genome-wide genetic structure and differentially selected regions among Landrace, Erhualian, and Meishan pigs using specific-locus amplified fragment sequencing. Scientific reports, 7(1), 10063.

Avinun R, et al. (2017) Parental brain-derived neurotrophic factor genotype, child prosociality, and their interaction as predictors of parents' warmth. Brain and behavior, 7(5), e00685.

Sung YJ, et al. (2016) Genome-wide association studies suggest sex-specific loci associated with abdominal and visceral fat. International journal of obesity (2005), 40(4), 662.

Morales F, et al. (2016) A polymorphism in the MSH3 mismatch repair gene is associated with the levels of somatic instability of the expanded CTG repeat in the blood DNA of myotonic dystrophy type 1 patients. DNA repair, 40, 57.

Xu J, et al. (2016) Gender-Specific Association of ATP2B1 Variants with Susceptibility to Essential Hypertension in the Han Chinese Population. BioMed research international, 2016, 1910565.

Peter B, et al. (2016) Genetic Candidate Variants in Two Multigenerational Families with Childhood Apraxia of Speech. PloS one, 11(4), e0153864.

Ben-Israel S, et al. (2015) Dopamine D4 receptor polymorphism and sex interact to predict children's affective knowledge. Frontiers in psychology, 6, 846.

Si J, et al. (2015) Genetic associations and shared environmental effects on the skin microbiome of Korean twins. BMC genomics, 16, 992.

Kim S, et al. (2015) Non-coding genomic regions possessing enhancer and silencer potential are associated with healthy aging and exceptional survival. Oncotarget, 6(6), 3600.

Al-Sinani S, et al. (2014) Utility of large consanguineous family-based model for investigating the genetics of type 2 diabetes mellitus. Gene, 548(1), 22.

Garnai SJ, et al. (2014) Congenital cataracts: de novo gene conversion event in CRYBB2. Molecular vision, 20, 1579.

Gomez L, et al. (2014) Association of the KCNJ5 gene with Tourette Syndrome and Attention-Deficit/Hyperactivity Disorder. Genes, brain, and behavior, 13(6), 535.

Karayannis T, et al. (2014) Cntnap4 differentially contributes to GABAergic and dopaminergic synaptic transmission. Nature, 511(7508), 236.

Ryu S, et al. (2013) Genome-wide linkage scan of quantitative traits representing symptom dimensions in multiplex schizophrenia families. Psychiatry research, 210(3), 756.

Gonçalves VF, et al. (2012) DRD4 VNTR polymorphism and age at onset of severe mental illnesses. Neuroscience letters, 519(1), 9.

Giesecke K, et al. (2011) Evaluation of ACE, SP17, and FSHB as candidates for stallion fertility in Hanoverian warmblood horses. Animal reproduction science, 126(3-4), 200.

Avinun R, et al. (2011) AVPR1A variant associated with preschoolers' lower altruistic behavior. PloS one, 6(9), e25274.