Resource Summary Report

Generated by PRECISE-TBI on Jul 31, 2026

Whap

RRID:SCR_007103
Type: Tool

Proper Citation

Whap (RRID:SCR_007103)

Resource Information

URL: http://pngu.mgh.harvard.edu/purcell/whap/

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Description: THIS RESOURCE IS NO LONGER IN SERVICE, documented on July 24, 2015. This package is no longer supported. The majority of the functionality for conditional haplotype tests in population-based samples has been implemented in PLINK, with a better interface and more robust, faster computation: please use that from now on. Software tool to perform haplotype-based association analysis, for quantitative and qualitative traits, in population and family samples, using single nucleotide polymorphism or multiallelic marker data. What whap can do: * Analyze quantitative and qualitative traits * Handle unrelated individuals and/or parent-offspring trio data * Perform a regression-based haplotype association test for SNP data * Perform a secondary test based on pairwise haplotype similarity * Phase genotype data using a standard E-M approach, and handle ambiguity in E-M inferred haplotypes * Include covariates and moderator variables * Flexibly constrain effects across haplotypes to tested nested models * Perform a robust within-family test when parental genotypes are present * Analyze multiallelic markers (new) * Use dominant or recessive (new) genetic models (new)

Abbreviations: Whap

Resource Type: software resource, software application

Defining Citation: PMID:17118959

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

Funding: MRC G9901258;
NEI EY-12562

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Whap

Resource ID: SCR_007103

Alternate IDs: nif-0000-31900

Record Creation Time: 20220129T080239+0000

Record Last Update: 20260731T042734+0000

Ratings and Alerts

No rating or validation information has been found for Whap.

No alerts have been found for Whap.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 9 mentions in open access literature.

Listed below are recent publications. The full list is available at PRECISE-TBI .

Pedrero-Chamizo R, et al. (2021) Influence of Physical Activity Levels and Functional Capacity on Brain ?-Amyloid Deposition in Older Women. Frontiers in aging neuroscience, 13, 697528.

Forgacs D, et al. (2016) Mitochondrial Genome Analysis Reveals Historical Lineages in Yellowstone Bison. PloS one, 11(11), e0166081.

Yang HY, et al. (2013) Role of the functional Toll-Like receptor-9 promoter polymorphism (-1237T/C) in increased risk of end-stage renal disease: a case-control study. PloS one, 8(3), e58444.

Su H, et al. (2010) Reduced expression of integrin alphavbeta8 is associated with brain arteriovenous malformation pathogenesis. The American journal of pathology, 176(2), 1018.

Barcellos LF, et al. (2009) High-density SNP screening of the major histocompatibility complex in systemic lupus erythematosus demonstrates strong evidence for independent susceptibility regions. PLoS genetics, 5(10), e1000696.

Sõber S, et al. (2009) Targeting 160 candidate genes for blood pressure regulation with a genome-wide genotyping array. PloS one, 4(6), e6034.

Nibali L, et al. (2009) Association between periodontitis and common variants in the promoter of the interleukin-6 gene. Cytokine, 45(1), 50.

Taylor KE, et al. (2008) Specificity of the STAT4 genetic association for severe disease manifestations of systemic lupus erythematosus. PLoS genetics, 4(5), e1000084.

Alarcón M, et al. (2008) Linkage, association, and gene-expression analyses identify CNTNAP2 as an autism-susceptibility gene. American journal of human genetics, 82(1), 150.