

Resource Summary Report

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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 application, software resource

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: 20260912T200236+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 [dkNET](#) .

Pedrero-Chamizo R, et al. (2021) Influence of Physical Activity Levels and Functional Capacity on Brain β -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 α v β 8 is associated with brain arteriovenous malformation pathogenesis. *The American journal of pathology*, 176(2), 1018.

Söber 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.

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.

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.

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