Resource Summary Report

Generated by RRID on Apr 9, 2025

SWEEP

RRID:SCR_009418
Type: Tool

Proper Citation

SWEEP (RRID:SCR_009418)

Resource Information

URL: http://archive.broadinstitute.org/mpg/sweep/

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Description: Software application that allows large-scale analysis of haplotype structure in genomes for the primary purpose of detecting evidence of natural selection. Primarily, it uses the Long Range Haplotype test to look for alleles of high frequency with long-range linkage disequilibrium, which suggest the haplotype rapidly rose to high frequency before recombination could break down associations with nearby markers. SWEEP takes phased genotype data as input, detects all haplotype blocks in that data, and then determines the frequency and long-range LD for each allele in each block. (entry from Genetic Analysis Software)

Abbreviations: SWEEP

Resource Type: software resource, software application

Keywords: gene, genetic, genomic, bio.tools

Funding:

Resource Name: SWEEP

Resource ID: SCR_009418

Alternate IDs: biotools:sweep, nlx_154667

Alternate URLs: https://bio.tools/sweep

Record Creation Time: 20220129T080252+0000

Record Last Update: 20250404T060815+0000

Ratings and Alerts

No rating or validation information has been found for SWEEP.

No alerts have been found for SWEEP.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 32 mentions in open access literature.

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

Nichio BTL, et al. (2025) Exploring diazotrophic diversity: unveiling Nif core distribution and evolutionary patterns in nitrogen-fixing organisms. BMC genomics, 26(1), 81.

Perico CP, et al. (2022) Genomic landscape of the SARS-CoV-2 pandemic in Brazil suggests an external P.1 variant origin. Frontiers in microbiology, 13, 1037455.

Vieira AZ, et al. (2021) Origin and evolution of nonulosonic acid synthases and their relationship with bacterial pathogenicity revealed by a large-scale phylogenetic analysis. Microbial genomics, 7(4).

Goisis A, et al. (2021) Medically assisted reproduction and parent-child relationships during adolescence: evidence from the UK Millennium Cohort Study. Human reproduction (Oxford, England), 36(3), 702.

Raittz RT, et al. (2021) Comparative Genomics Provides Insights into the Taxonomy of Azoarcus and Reveals Separate Origins of Nif Genes in the Proposed Azoarcus and Aromatoleum Genera. Genes, 12(1).

Peng Z, et al. (2020) Comparison of SNP Calling Pipelines and NGS Platforms to Predict the Genomic Regions Harboring Candidate Genes for Nodulation in Cultivated Peanut. Frontiers in genetics, 11, 222.

Ma L, et al. (2019) Genome changes due to artificial selection in U.S. Holstein cattle. BMC genomics, 20(1), 128.

Montes DE, et al. (2019) Selection signatures in candidate genes and QTL for reproductive traits in Nellore heifers. Animal reproduction science, 207, 1.

Zehra R, et al. (2018) Homo sapiens-Specific Binding Site Variants within Brain Exclusive Enhancers Are Subject to Accelerated Divergence across Human Population. Genome biology and evolution, 10(3), 956.

Chen M, et al. (2016) Identification of selective sweeps reveals divergent selection between Chinese Holstein and Simmental cattle populations. Genetics, selection, evolution : GSE, 48(1), 76.

Suke SG, et al. (2015) Role of Pharmacovigilance in India: An overview. Online journal of public health informatics, 7(2), e223.

Li Y, et al. (2015) Effective Population Size and Signatures of Selection Using Bovine 50K SNP Chips in Korean Native Cattle (Hanwoo). Evolutionary bioinformatics online, 11, 143.

Weetman D, et al. (2015) Contemporary evolution of resistance at the major insecticide target site gene Ace-1 by mutation and copy number variation in the malaria mosquito Anopheles gambiae. Molecular ecology, 24(11), 2656.

Valverde G, et al. (2015) A novel candidate region for genetic adaptation to high altitude in Andean populations. PloS one, 10(5), e0125444.

Amorim CE, et al. (2015) Differing evolutionary histories of the ACTN3*R577X polymorphism among the major human geographic groups. PloS one, 10(2), e0115449.

Junwang G, et al. (2014) New developed cylindrical TM010 mode EPR cavity for X-band in vivo tooth dosimetry. PloS one, 9(9), e106587.

Yang L, et al. (2014) A functional MiR-124 binding-site polymorphism in IQGAP1 affects human cognitive performance. PloS one, 9(9), e107065.

Janha RE, et al. (2014) Inactive alleles of cytochrome P450 2C19 may be positively selected in human evolution. BMC evolutionary biology, 14, 71.

McRae KM, et al. (2014) Signatures of selection in sheep bred for resistance or susceptibility to gastrointestinal nematodes. BMC genomics, 15(1), 637.

Lv FH, et al. (2014) Adaptations to climate-mediated selective pressures in sheep. Molecular biology and evolution, 31(12), 3324.