Resource Summary Report

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DistiLD - Diseases and Traits in LD

RRID:SCR_005943
Type: Tool

Proper Citation

DistiLD - Diseases and Traits in LD (RRID:SCR_005943)

Resource Information

URL: http://distild.jensenlab.org/

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Description: The DistiLD database aims to increase the usage of existing genome-wide association studies (GWAS) results by making it easy to query and visualize disease-associated SNPs and genes in their chromosomal context. The database performs three important tasks: # published GWAS are collected from several sources and linked to standardized, international disease codes ICD10 codes) # data from the International HapMap Project are analyzed to define linkage disequilibrium (LD) blocks onto which SNPs and genes are mapped # the web interface makes it easy to query and visualize disease-associated SNPs and genes within LD blocks. Users can query the database by diseases, SNPs or genes. No matter which of the three query modes was used, an intermediate page will be shown listing all the studies that matched the search with a link to the corresponding publication. The user can select either all studies related to a certain disease or one specific study for which to view the related LD blocks. The DistiLD resource integrates information on: * Associations between Single Nucleotide Polymorphisms (SNPs) and diseases from genome-wide association studies (GWAS) * Links between SNPs and genes based on linkage disequilibrium (LD) data from HapMap For convenience, we provide the complete datasets as two (zipped) tab-delimited files. The first file contains GWAS results mapped to LD blocks. The second file contains all SNPs and genes assigned to each LD block.

Abbreviations: DistiLD

Synonyms: DistiLD - Diseases & Traits in LD, Diseases and Traits In Linkage Disequilibrium blocks, Diseases and Traits In Linkage Disequilibrium, DistiLD Database, DistiLD - Diseases Traits in LD

Resource Type: analysis service resource, data analysis service, data or information resource, database, production service resource, service resource

Defining Citation: PMID:22058129

Keywords: disease, mutation, gene, linkage disequilibrium, trait, genome-wide association study, single nucleotide polymorphism, chromosomal region, chromosome, linkage disequilibrium block, bio.tools

Funding: Novo Nordisk Foundation Center for Protein Research

Resource Name: DistiLD - Diseases and Traits in LD

Resource ID: SCR_005943

Alternate IDs: biotools:distild, nlx_151291

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

Record Creation Time: 20220129T080233+0000

Record Last Update: 20260905T132544+0000

Ratings and Alerts

No rating or validation information has been found for DistiLD - Diseases and Traits in LD.

No alerts have been found for DistiLD - Diseases and Traits in LD.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 5 mentions in open access literature.

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

Sun J, et al. (2022) SMetABF: A rapid algorithm for Bayesian GWAS meta-analysis with a large number of studies included. PLoS computational biology, 18(3), e1009948.

Beck T, et al. (2020) GWAS Central: a comprehensive resource for the discovery and comparison of genotype and phenotype data from genome-wide association studies. Nucleic acids research, 48(D1), D933.

Patnala R, et al. (2013) Candidate gene association studies: a comprehensive guide to useful in silico tools. BMC genetics, 14, 39.

Bianco AM, et al. (2013) Database tools in genetic diseases research. Genomics, 101(2), 75.

Beck T, et al. (2012) Semantically enabling a genome-wide association study database. Journal of biomedical semantics, 3(1), 9.