Resource Summary Report

Generated by dkNET on Apr 17, 2025

JLIN

RRID:SCR_009247
Type: Tool

Proper Citation

JLIN (RRID:SCR_009247)

Resource Information

URL: http://www.genepi.org.au/jlin

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Description: Software application designed for customizable, intuitive visualisation of LD analysis across all common computing platforms. Customisation allows the researcher to choose particular visualisation, statistical measures and measurement ranges. JLIN also allows the researcher to export images of the LD visualisation in several common document formats. As there appears to be no single best measure of LD under all possible circumstances, JLIN allows the researcher to visually compare and contrast the results of a range of statistical measures on the input data set(s). These measures include the commonly used D'' and R2 statistics and empirical p-values. New additions include calculation of HWE, a completely revamped interface, and a numer of minor bug fixes. We have added a display measure to show marker distances visually, embedded fonts to improve image clarity and additional LD measures including d,OR,Pexcess and Q. (entry from Genetic Analysis Software)

Abbreviations: JLIN

Synonyms: Java based LINkage disequilibrium plotter

Resource Type: software resource, software application

Keywords: gene, genetic, genomic, java, any with java 1.5 support

Funding:

Resource Name: JLIN

Resource ID: SCR_009247

Alternate IDs: nlx_154415

Record Creation Time: 20220129T080251+0000

Record Last Update: 20250416T063541+0000

Ratings and Alerts

No rating or validation information has been found for JLIN.

No alerts have been found for JLIN.

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.

Taylor PN, et al. (2015) Whole-genome sequence-based analysis of thyroid function. Nature communications, 6, 5681.

Pithukpakorn M, et al. (2014) Mycophenolic acid AUC in Thai kidney transplant recipients receiving low dose mycophenolate and its association with UGT2B7 polymorphisms. Pharmacogenomics and personalized medicine, 7, 379.

Setsirichok D, et al. (2013) An omnibus permutation test on ensembles of two-locus analyses can detect pure epistasis and genetic heterogeneity in genome-wide association studies. SpringerPlus, 2, 230.

Chang CY, et al. (2013) BMPR1B up-regulation via a miRNA binding site variation defines endometriosis susceptibility and CA125 levels. PloS one, 8(12), e80630.

Sartorius T, et al. (2012) Association of common genetic variants in the MAP4K4 locus with prediabetic traits in humans. PloS one, 7(10), e47647.

Böhm A, et al. (2012) Common genetic variation in the SERPINF1 locus determines overall adiposity, obesity-related insulin resistance, and circulating leptin levels. PloS one, 7(3), e34035.

Voisey J, et al. (2012) A DRD2 and ANKK1 haplotype is associated with nicotine

dependence. Psychiatry research, 196(2-3), 285.

Müssig K, et al. (2009) RARRES2, encoding the novel adipokine chemerin, is a genetic determinant of disproportionate regional body fat distribution: a comparative magnetic resonance imaging study. Metabolism: clinical and experimental, 58(4), 519.

Staiger H, et al. (2008) Genetic variation within the ANGPTL4 gene is not associated with metabolic traits in white subjects at an increased risk for type 2 diabetes mellitus. Metabolism: clinical and experimental, 57(5), 637.