Resource Summary Report

Generated by dkNET on Apr 17, 2025

MERLIN

RRID:SCR_009289
Type: Tool

Proper Citation

MERLIN (RRID:SCR_009289)

Resource Information

URL: http://www.sph.umich.edu/csg/abecasis/Merlin

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Description: Software application that carries out single-point and multipoint analyses of pedigree data, including IBD and kinship calculations, nonparametric and variance component linkage analyses, error detection and information content mapping. For multipoint analyses in dense maps, Merlin allows the user to impose constraints on the number of recombinants between consecutive markers. Merlin estimates haplotypes by finding the most likely path of gene flow or by sampling paths of gene flow at all markers jointly. It can also list all possible nonrecombinant haplotypes within short regions. Finally, Merlin provides swap-file support for handling very large numbers of markers as well as gene-dropping simulations for estimating empirical significance levels. (entry from Genetic Analysis Software)

Abbreviations: MERLIN

Synonyms: Multipoint Engine for Rapid Likelihood INference

Resource Type: software resource, software application

Keywords: gene, genetic, genomic, c++, unix. linux

Funding:

Resource Name: MERLIN

Resource ID: SCR_009289

Alternate IDs: nlx_154475

Record Creation Time: 20220129T080252+0000

Record Last Update: 20250416T063542+0000

Ratings and Alerts

No rating or validation information has been found for MERLIN.

No alerts have been found for MERLIN.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 877 mentions in open access literature.

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

Feuerriegel GC, et al. (2025) Longitudinal Assessment of Intersegmental Abnormalities in the Lumbar Spine of Adolescent Competitive Alpine Skiers Over 48 Months. The American journal of sports medicine, 53(1), 202.

Feuerriegel GC, et al. (2025) A visual marker for early atrophy of the supraspinatus muscle on conventional MRI: introduction of the blackbird sign. European radiology, 35(1), 313.

Zahid A, et al. (2025) Identifying genetic susceptibility loci associated with human coronary artery disease. PloS one, 20(1), e0315460.

Launay N, et al. (2025) Altered tubulin detyrosination due to SVBP malfunction induces cytokinesis failure and senescence, underlying a complex hereditary spastic paraplegia. Aging cell, 24(1), e14355.

Zibold J, et al. (2024) The new missense G376V-TDP-43 variant induces late-onset distal myopathy but not amyotrophic lateral sclerosis. Brain : a journal of neurology, 147(5), 1768.

Feuerriegel GC, et al. (2024) Superolateral Hoffa fat pad edema in adolescent competitive alpine skiers: temporal evolution over 4 years and risk factors. Insights into imaging, 15(1), 52.

Wang T, et al. (2024) A novel extracellular vesicles production system harnessing matrix homeostasis and macrophage reprogramming mitigates osteoarthritis. Journal of nanobiotechnology, 22(1), 79.

Zhu Y, et al. (2024) A mutation in CCDC91, Homo sapiens coiled-coil domain containing 91

protein, cause autosomal-dominant acrokeratoelastoidosis. European journal of human genetics : EJHG, 32(6), 647.

Gustavsson EK, et al. (2024) RAB32 Ser71Arg in autosomal dominant Parkinson's disease: linkage, association, and functional analyses. The Lancet. Neurology, 23(6), 603.

Feuerriegel GC, et al. (2024) Tumor-Like Distal Femoral Cortical Irregularities of the Knee in Adolescent Competitive Alpine Skiers: Longitudinal Assessment Over 48 Months. The American journal of sports medicine, 52(7), 1820.

Benton D, et al. (2024) Synergistic effect of PAK and Hippo pathway inhibitor combination in NF2-deficient Schwannoma. PloS one, 19(7), e0305121.

Vervelde L, et al. (2024) Invasion of Chicken Intestinal Cells Is Higher for Enterococcus cecorum Lesion Strains Compared to Cloacal Strains in an Organoid Model. Microorganisms, 13(1).

Aydin A, et al. (2024) ADAM19 cleaves the PTH receptor and associates with brachydactyly type E. Life science alliance, 7(4).

Li K, et al. (2024) Genetic diagnosis of facioscapulohumeral muscular dystrophy type 1 using rare-variant linkage analysis and long-read genome sequencing. Genetics in medicine open, 2, 101817.

Tillotson E, et al. (2024) Scanning Electron Microscopy Imaging of Twist Domains in Transition Metal Dichalcogenide Heterostructures. ACS nano, 18(50), 34023.

Saunders RA, et al. (2024) A platform for multimodal in vivo pooled genetic screens reveals regulators of liver function. bioRxiv : the preprint server for biology.

Mah CK, et al. (2024) Bento: a toolkit for subcellular analysis of spatial transcriptomics data. Genome biology, 25(1), 82.

Fischer F, et al. (2024) scTab: Scaling cross-tissue single-cell annotation models. Nature communications, 15(1), 6611.

Momenilandi M, et al. (2024) FLT3L governs the development of partially overlapping hematopoietic lineages in humans and mice. Cell, 187(11), 2817.

Kondratenko AA, et al. (2024) Decellularized Umbilical Cord as a Scaffold to Support Healing of Full-Thickness Wounds. Biomimetics (Basel, Switzerland), 9(7).