Resource Summary Report

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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 application, software resource

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

Resource Name: MERLIN

Resource ID: SCR_009289

Alternate IDs: nlx_154475

Record Creation Time: 20220129T080252+0000

Record Last Update: 20260829T183109+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 931 mentions in open access literature.

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

Amin M, et al. (2026) Secondary analysis of GenRED data (Genetics of Recurrent Early-Onset major Depression) using MERLIN. European archives of psychiatry and clinical neuroscience, 276(2), 723.

Dorfsman D, et al. (2026) WDR12 and HIVEP3 are contributors to cognitive preservation in Amish SuperAgers. Alzheimer's & dementia : the journal of the Alzheimer's Association, 22(3), e71293.

Mbouamboua Y, et al. (2026) A single-cell and spatial atlas of early human olfactory development. Nature communications, 17(1).

Jiménez-Castaño R, et al. (2026) A hormetic transcriptional program coregulates invasion, proliferation and dormancy to define metastatic potential. Nature communications, 17(1).

Benteau T, et al. (2026) Heterozygous Nonsense Mutation in the Nuclear Transport Factor KPNA7, a Maternal Factor Active in Embryonic Tissues, Causes Autosomal Dominant Otosclerosis. International journal of molecular sciences, 27(11).

Eichhorn H, et al. (2026) Motion-robust T 2 ? $$ {\mathrm{T}}_2^{\ast } $$ quantification from low-resolution gradient echo brain MRI with physics-informed deep learning. Magnetic resonance in medicine, 95(1), 346.

Yakubovsky O, et al. (2026) A spatial atlas of the healthy human liver from live donors. Nature, 653(8116), 1148.

Oubninte S, et al. (2026) The reliability and accuracy of recombination inferred by Shapeit2 duoHMM on whole genome sequence. bioRxiv : the preprint server for biology.

Richmond GR, et al. (2026) Nutrient control enables metabolic reconstruction of L. rhamnosus GG and analysis of secretions. bioRxiv : the preprint server for biology.

Lodi MK, et al. (2026) Narrow Versus Broad Phenotype Definitions Affect Genetic Analysis of Language More than Other Broad Autism Phenotype Traits. Genes, 17(2).

Wayne CR, et al. (2026) Th17 effector cytokines induce shared and distinct microglial and endothelial cell responses in post-streptococcal encephalitis. bioRxiv : the preprint server

for biology.

Wachinger C, et al. (2026) Whole body CT attenuation and volume charts from routine clinical scans via LLM report filtering. NPJ digital medicine, 9(1).

Wagener N, et al. (2026) Risk factors for hip fractures: the role of femoral and acetabular morphology in predicting proximal femur fracture types. Hip international : the journal of clinical and experimental research on hip pathology and therapy, 36(1), 115.

Justice CM, et al. (2026) Combined family-based association and linkage analyses in families affected by attention-deficit hyperactivity disorder. Human genetics, 145(1).

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.

Ackermann J, et al. (2025) Influence of Sulcus-Deepening Trochleoplasty on Patellofemoral Cartilage Integrity in Patients With Severe Trochlear Dysplasia at Short-term to Midterm Follow-up: A Case-Control Study. Orthopaedic journal of sports medicine, 13(4), 23259671251326052.

Groh J, et al. (2025) Microglia activation orchestrates CXCL10-mediated CD8+ T cell recruitment to promote aging-related white matter degeneration. Nature neuroscience, 28(6), 1160.

Saunders RA, et al. (2025) Perturb-Multimodal: A platform for pooled genetic screens with imaging and sequencing in intact mammalian tissue. Cell, 188(17), 4790.

Li H, et al. (2025) Clonal dynamics shaped by diverse drug-tolerant persister states in melanoma resistance. bioRxiv : the preprint server for biology.

Shao L, et al. (2025) Synthetic efferocytic receptor microglia enhances anti-inflammatory clearance of amyloid-? for AD treatment in mice. Science advances, 11(28), eads6613.