Resource Summary Report

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JOINMAP

RRID:SCR_009248
Type: Tool

Proper Citation

JOINMAP (RRID:SCR_009248)

Resource Information

URL: http://www.joinmap.nl/

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Description: Software application for construction of genetic linkage maps for several types of mapping populations: BC1, F2, RILs, (doubled) haploids, outbreeders full-sib family. Can combine ("join") data derived from several sources into an integrated map. Further: linkage group determination, automatic phase determination for outbreeders full-sib family, several diagnostics, and map charts. Everything available in an intuitive MS-Windows user interface. (entry from Genetic Analysis Software)

Abbreviations: JOINMAP

Synonyms: Software for the calculation of genetic linkage maps

Resource Type: software application, software resource

Keywords: gene, genetic, genomic, ansi c, delphi, ms-windows, (95/98/me/nt4.0/2000)

Funding:

Resource Name: JOINMAP

Resource ID: SCR_009248

Alternate IDs: nlx_154416

Record Creation Time: 20220129T080251+0000

Record Last Update: 20250412T055401+0000

Ratings and Alerts

No rating or validation information has been found for JOINMAP.

No alerts have been found for JOINMAP.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 1021 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Yang X, et al. (2025) Novel candidate genes and genetic basis analysis of kernel starch content in tropical maize. BMC plant biology, 25(1), 105.

Yamazaki H, et al. (2025) QTL-Based Evidence of Population Genetic Divergence in Male Territorial Aggressiveness of the Japanese Freshwater Threespine Stickleback. Ecology and evolution, 15(1), e70795.

Liu S, et al. (2025) Development and application of the GenoBaits WheatSNP16K array to accelerate wheat genetic research and breeding. Plant communications, 6(1), 101138.

Joshi P, et al. (2025) Identification and validation of two quantitative trait loci for dwarf bunt in the resistant cultivar 'UI Silver'. TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik, 138(1), 18.

Bi Y, et al. (2024) Identification of candidate gene associated with maize northern leaf blight resistance in a multi-parent population. Plant cell reports, 43(7), 189.

Ji Y, et al. (2024) GWAS combined with QTL mapping reveals the genetic loci of leaf morphological characters in Nicotiana tabacum. BMC plant biology, 24(1), 583.

Lei S, et al. (2024) Identification of a major QTL and candidate genes analysis for branch angle in rapeseed (Brassica napus L.) using QTL-seq and RNA-seq. Frontiers in plant science, 15, 1340892.

Mathiazhagan M, et al. (2024) A high-density linkage map construction in guava (Psidium guajava L.) using genotyping by sequencing and identification of QTLs for leaf, peel, and pulp color in an intervarietal mapping population. Frontiers in plant science, 15, 1335715.

Pan Y, et al. (2024) QTL mapping and genome-wide association analysis reveal genetic loci and candidate gene for resistance to gray leaf spot in tropical and subtropical maize germplasm. TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik, 137(12), 266.

Ryu JS, et al. (2024) Quantitative trait loci analysis for molecular markers linked to agricultural traits of Pleurotus ostreatus. PloS one, 19(8), e0308832.

Fan C, et al. (2024) Natural variations of HvSRN1 modulate the spike rachis node number in barley. Plant communications, 5(1), 100670.

Fan S, et al. (2024) Mapping QTLs for blight resistance and morpho-phenological traits in inter-species hybrid families of chestnut (Castanea spp.). Frontiers in plant science, 15, 1365951.

Zheng Z, et al. (2024) Chloroplast and whole-genome sequencing shed light on the evolutionary history and phenotypic diversification of peanuts. Nature genetics, 56(9), 1975.

Li Y, et al. (2024) Dissection of a rapidly evolving wheat resistance gene cluster by long-read genome sequencing accelerated the cloning of Pm69. Plant communications, 5(1), 100646.

Miao H, et al. (2024) Genomic evolution and insights into agronomic trait innovations of Sesamum species. Plant communications, 5(1), 100729.

Abbai R, et al. (2024) Grain yield trade-offs in spike-branching wheat can be mitigated by elite alleles affecting sink capacity and post-anthesis source activity. Journal of experimental botany, 75(1), 88.

Picarella ME, et al. (2024) Genetic and molecular mechanisms underlying the parthenocarpic fruit mutation in tomato. Frontiers in plant science, 15, 1329949.

Venkateshwarlu C, et al. (2024) Mapping genomic regions for reproductive stage drought tolerance in rice from exotic landrace-derived population. Frontiers in plant science, 15, 1495241.

Konuma J, et al. (2024) Odd-Paired is Involved in Morphological Divergence of Snail-Feeding Beetles. Molecular biology and evolution, 41(6).

Schafleitner R, et al. (2024) Molecular markers associated with resistance to squash leaf curl China virus and tomato leaf curl New Delhi virus in tropical pumpkin (Cucurbita moschata Duchesne ex Poir.) breeding line AVPU1426. Scientific reports, 14(1), 6793.