

Resource Summary Report

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snpStats: SnpMatrix and XSnpmatrix classes and methods

RRID:SCR_001249

Type: Tool

Proper Citation

snpStats: SnpMatrix and XSnpmatrix classes and methods (RRID:SCR_001249)

Resource Information

URL: <http://www.bioconductor.org/packages/release/bioc/html/snpStats.html>

Proper Citation: snpStats: SnpMatrix and XSnpmatrix classes and methods (RRID:SCR_001249)

Description: Software for classes and statistical methods for large single nucleotide polymorphism (SNP) association studies.

Abbreviations: snpStats

Resource Type: software resource

Defining Citation: [PMID:16720584](#)

Keywords: r, single nucleotide polymorphism, genetic variability, microarray

Availability: Free, Available for download, Freely available

Resource Name: snpStats: SnpMatrix and XSnpmatrix classes and methods

Resource ID: SCR_001249

Alternate IDs: OMICS_02091

License: GNU General Public License, v3

Record Creation Time: 20220129T080206+0000

Record Last Update: 20260808T185724+0000

Ratings and Alerts

No rating or validation information has been found for snpStats: SnpMatrix and XSnpmatrix classes and methods.

No alerts have been found for snpStats: SnpMatrix and XSnpmatrix classes and methods.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 79 mentions in open access literature.

Listed below are recent publications. The full list is available at [NIF](#) .

Ramirez-Gil JG, et al. (2026) GermVersity: A free and user-friendly interface to enhance the visualization and analysis of genebank data. PloS one, 21(1), e0340826.

Jaegle B, et al. (2025) k-mer-based GWAS in a wheat collection reveals novel and diverse sources of powdery mildew resistance. Genome biology, 26(1), 172.

Zatybekov A, et al. (2025) Uncovering the genetic landscape of soybean accessions from Kazakhstan in comparison with global germplasm using whole genome resequencing. BMC genomics, 26(1), 802.

Wozniak J, et al. (2025) Genetic and epigenetic markers in the METTL21C gene associated with umbilical hernia in pigs. BMC genomics, 26(1), 1096.

Ko H, et al. (2025) Exploring transcriptomic and genomic differences between susceptible and resistant fetal pigs to maternal PRRSV infection at late gestation. Veterinary research, 56(1), 208.

Bá?ová A, et al. (2025) Genomic Rewilding of Domestic Animals: The Role of Hybridization and Selection in Wolfdog Breeds. Genes, 16(1).

Singh D, et al. (2024) Genetic mapping of stripe rust resistance in a geographically diverse barley collection and selected biparental populations. Frontiers in plant science, 15, 1352402.

Kafyra M, et al. (2023) Robust Bioinformatics Approaches Result in the First Polygenic Risk Score for BMI in Greek Adults. Journal of personalized medicine, 13(2).

Yasukochi Y, et al. (2023) Cold-induced vasodilation response in a Japanese cohort: insights from cold-water immersion and genome-wide association studies. Journal of physiological anthropology, 42(1), 2.

Koganebuchi K, et al. (2023) Demographic history of Ryukyu islanders at the southern part of the Japanese Archipelago inferred from whole-genome resequencing data. Journal of human genetics, 68(11), 759.

Žítek J, et al. (2022) Genome-Wide Association Study for Body Conformation Traits and Fitness in Czech Holsteins. *Animals : an open access journal from MDPI*, 12(24).

Muller-Girard M, et al. (2022) A novel SNP assay reveals increased genetic variability and abundance following translocations to a remnant Allegheny woodrat population. *BMC ecology and evolution*, 22(1), 137.

Wooldridge TB, et al. (2022) An enhancer of Agouti contributes to parallel evolution of cryptically colored beach mice. *Proceedings of the National Academy of Sciences of the United States of America*, 119(27), e2202862119.

Al-Awadi AM, et al. (2022) ADIPOQ gene polymorphisms and haplotypes linked to altered susceptibility to PCOS: a case-control study. *Reproductive biomedicine online*, 45(5), 995.

Zhang S, et al. (2022) Genome-wide identification of the genetic basis of amyotrophic lateral sclerosis. *Neuron*, 110(6), 992.

Dreccer MF, et al. (2022) Multi-donor × elite-based populations reveal QTL for low-lodging wheat. *TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik*, 135(5), 1685.

Yang H, et al. (2022) The risk variant rs11836367 contributes to breast cancer onset and metastasis by attenuating Wnt signaling via regulating NTN4 expression. *Science advances*, 8(23), eabn3509.

Zhang S, et al. (2022) Multiomic analysis reveals cell-type-specific molecular determinants of COVID-19 severity. *Cell systems*, 13(8), 598.

Johnson TA, et al. (2021) Association of an IGHV3-66 gene variant with Kawasaki disease. *Journal of human genetics*, 66(5), 475.

Wittenburg D, et al. (2021) Grouping of genomic markers in populations with family structure. *BMC bioinformatics*, 22(1), 79.