

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: 20260801T190144+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 78 mentions in open access literature.

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

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.

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

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.

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.

Žitek 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.

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.

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

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.

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.

Werme J, et al. (2021) Genome-wide gene-environment interactions in neuroticism: an exploratory study across 25 environments. *Translational psychiatry*, 11(1), 180.