Resource Summary Report

Generated by NIF on Apr 28, 2025

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

Funding:

Availability: GNU General Public License, v3

Resource Name: snpStats: SnpMatrix and XSnpMatrix classes and methods

Resource ID: SCR_001249

Alternate IDs: OMICS_02091

Record Creation Time: 20220129T080206+0000

Record Last Update: 20250420T014024+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 74 mentions in open access literature.

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

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.

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.

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).

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.

?ítek 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.

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

Tang S, et al. (2021) Genome- and transcriptome-wide association studies provide insights into the genetic basis of natural variation of seed oil content in Brassica napus. Molecular plant, 14(3), 470.

Márquez Pete N, et al. (2021) Influence of the FCGR2A rs1801274 and FCGR3A rs396991 Polymorphisms on Response to Abatacept in Patients with Rheumatoid Arthritis. Journal of personalized medicine, 11(6).

van Deuren RC, et al. (2021) Impact of rare and common genetic variation in the interleukin-1 pathway on human cytokine responses. Genome medicine, 13(1), 94.

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

Zhang YJ, et al. (2021) Association of regular aerobic exercises and neuromuscular junction variants with incidence of frailty: an analysis of the Chinese Longitudinal Health and Longevity Survey. Journal of cachexia, sarcopenia and muscle, 12(2), 350.