Resource Summary Report

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MDR

RRID:SCR_013427
Type: Tool

Proper Citation

MDR (RRID:SCR_013427)

Resource Information

URL: http://www.multifactordimensionalityreduction.org/

Proper Citation: MDR (RRID:SCR_013427)

Description: Software application that is a data mining strategy for detecting and characterizing nonlinear interactions among discrete attributes (e.g. SNPs, smoking, gender, etc.) that are predictive of a discrete outcome (e.g. case-control status). The MDR software combines attribute selection, attribute construction and classification with cross-validation to provide a powerful approach to modeling interactions. (entry from Genetic Analysis Software)

Abbreviations: MDR

Synonyms: Multifactor Dimensionality Reduction

Resource Type: software resource, software application

Keywords: gene, genetic, genomic

Resource Name: MDR

Resource ID: SCR_013427

Alternate IDs: nlx_154096

Alternate URLs: http://www.nitrc.org/projects/mdr

Record Creation Time: 20220129T080316+0000

Record Last Update: 20260801T191054+0000

Ratings and Alerts

No rating or validation information has been found for MDR.

No alerts have been found for MDR.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 38 mentions in open access literature.

Listed below are recent publications. The full list is available at PRECISE-TBI .

Mok JW, et al. (2021) Association with Corneal Remodeling Related Genes, ALDH3A1, LOX, and SPARC Genes Variations in Korean Keratoconus Patients. Korean journal of ophthalmology : KJO, 35(2), 120.

Lopes C, et al. (2021) Genetic Variations in Prostaglandin E2 Pathway Identified as Susceptibility Biomarkers for Gastric Cancer in an Intermediate Risk European Country. International journal of molecular sciences, 22(2).

He D, et al. (2021) Vitamin D Receptor Is a Sepsis-Susceptibility Gene in Chinese Children. Medical science monitor : international medical journal of experimental and clinical research, 27, e932518.

Ponomarenko I, et al. (2020) Candidate Genes for Age at Menarche Are Associated With Uterine Leiomyoma. Frontiers in genetics, 11, 512940.

Ponomarenko I, et al. (2020) Candidate genes for age at menarche are associated with endometriosis. Reproductive biomedicine online, 41(5), 943.

Pereira da Silva A, et al. (2020) Impact on Longevity of Genetic Cardiovascular Risk and Lifestyle including Red Meat Consumption. Oxidative medicine and cellular longevity, 2020, 1305413.

P?óciennik ?A, et al. (2020) Detection of epistasis between ACTN3 and SNAP-25 with an insight towards gymnastic aptitude identification. PloS one, 15(8), e0237808.

Calabrò M, et al. (2019) Genes Involved in Neurodevelopment, Neuroplasticity and Major Depression: No Association for CACNA1C, CHRNA7 and MAPK1. Clinical psychopharmacology and neuroscience : the official scientific journal of the Korean College of Neuropsychopharmacology, 17(3), 364.

Chen Y, et al. (2019) Association of the gene polymorphisms of BMPR2, ACVRL1, SMAD9 and their interactions with the risk of essential hypertension in the Chinese Han population. Bioscience reports, 39(1).

Cui Z, et al. (2019) NR3C2 gene polymorphism is associated with risk of gestational hypertension in Han Chinese women. Medicine, 98(50), e18215.

Qiu P, et al. (2019) Associations between HMGB1 gene polymorphisms and susceptibility and clinical outcomes in Chinese Han sepsis patients. Gene, 687, 23.

Rhie A, et al. (2019) Genetic variations associated with response to dutasteride in the treatment of male subjects with androgenetic alopecia. PloS one, 14(9), e0222533.

Kalia N, et al. (2019) Impact of SNPs interplay across the locus of MBL2, between MBL and Dectin-1 gene, on women's risk of developing recurrent vulvovaginal infections. Cell & bioscience, 9, 35.

Zhang Z, et al. (2018) Susceptibility of multiple polymorphisms in ADIPOQ, ADIPOR1 and ADIPOR2 genes to myocardial infarction in Han Chinese. Gene, 658, 10.

Yue LL, et al. (2018) Association of ATM and BMI-1 genetic variation with breast cancer risk in Han Chinese. Journal of cellular and molecular medicine, 22(7), 3671.

Kobayashi M, et al. (2018) Association studies of WD repeat domain 3 and chitobiosyldiphosphodolichol beta-mannosyltransferase genes with schizophrenia in a Japanese population. PloS one, 13(1), e0190991.

Dato S, et al. (2018) The genetic component of human longevity: New insights from the analysis of pathway-based SNP-SNP interactions. Aging cell, 17(3), e12755.

Heffernan SM, et al. (2017) COL5A1 gene variants previously associated with reduced soft tissue injury risk are associated with elite athlete status in rugby. BMC genomics, 18(Suppl 8), 820.

Sandhu HS, et al. (2017) Associating genetic variation at Perilipin 1, Complement Factor D and Adiponectin loci to the bone health status in North Indian population. Gene, 610, 80.

Liu T, et al. (2017) Gene polymorphisms in the PI3K/AKT/mTOR signaling pathway contribute to prostate cancer susceptibility in Chinese men. Oncotarget, 8(37), 61305.