Resource Summary Report

Generated by NIF on Apr 19, 2025

R/SPECTRAL-GEM

RRID:SCR_007414
Type: Tool

Proper Citation

R/SPECTRAL-GEM (RRID:SCR_007414)

Resource Information

URL: http://wpicr.wpic.pitt.edu/WPICCompGen/

Proper Citation: R/SPECTRAL-GEM (RRID:SCR_007414)

Description: Software application (entry from Genetic Analysis Software)

Synonyms: SPECTRAL graph approach for GEnetic Matching, SPECTRAL-GEM

Resource Type: software application, software resource

Keywords: gene, genetic, genomic, r

Funding:

Resource Name: R/SPECTRAL-GEM

Resource ID: SCR_007414

Alternate IDs: nlx_154600, nlx_154655, SCR_009408

Record Creation Time: 20220129T080241+0000

Record Last Update: 20250419T055115+0000

Ratings and Alerts

No rating or validation information has been found for R/SPECTRAL-GEM.

No alerts have been found for R/SPECTRAL-GEM.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 10 mentions in open access literature.

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

He X, et al. (2013) Integrated model of de novo and inherited genetic variants yields greater power to identify risk genes. PLoS genetics, 9(8), e1003671.

Ringquist S, et al. (2013) Clustering and alignment of polymorphic sequences for HLA-DRB1 genotyping. PloS one, 8(3), e59835.

Luca D, et al. (2008) On the use of general control samples for genome-wide association studies: genetic matching highlights causal variants. American journal of human genetics, 82(2), 453.

Yu CE, et al. (2007) Comprehensive analysis of APOE and selected proximate markers for late-onset Alzheimer's disease: patterns of linkage disequilibrium and disease/marker association. Genomics, 89(6), 655.

Kato H, et al. (2006) Association of single-nucleotide polymorphisms in the suppressor of cytokine signaling 2 (SOCS2) gene with type 2 diabetes in the Japanese. Genomics, 87(4), 446.

Roeder K, et al. (2006) Using linkage genome scans to improve power of association in genome scans. American journal of human genetics, 78(2), 243.

Zhao JH, et al. (2006) Integrated analysis of genetic data with R. Human genomics, 2(4), 258.

Reck BH, et al. (2005) Analysis of alcohol dependence phenotype in the COGA families using covariates to detect linkage. BMC genetics, 6 Suppl 1(Suppl 1), S143.

Bulik CM, et al. (2003) Significant linkage on chromosome 10p in families with bulimia nervosa. American journal of human genetics, 72(1), 200.

Seltman H, et al. (2001) Transmission/disequilibrium test meets measured haplotype analysis: family-based association analysis guided by evolution of haplotypes. American journal of human genetics, 68(5), 1250.