

Resource Summary Report

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Solar Eclipse Imaging Genetics tools

RRID:SCR_009645

Type: Tool

Proper Citation

Solar Eclipse Imaging Genetics tools (RRID:SCR_009645)

Resource Information

URL: http://www.nitrc.org/projects/se_linux/

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Description: Software tools optimized for performing univariate and multivariate imaging genetics analyses while providing practical correction strategies for multiple testing. The goal of this project is to merge two important research directions in modern science, genetics and neuroimaging. This entails combining modern statistical genetic methods and quantitative phenotyping performed with high dimensional neuroimaging modalities. So far, however, standard imaging tools are unable to deal with large-scale genetics data, and standard genetics tools, in turn, are unable to accommodate large size and binary format of the image data. Their focus is to create imaging genetics tools for classical genetic and epigenetic epidemiological analyses such as heritability, pleiotropy, quantitative trait loci (QTL) and genome-wide association (GWAS), gene expression, and methylation analyses optimized for traits derived from structural and functional brain imaging data

Abbreviations: Solar Eclipse Imaging Genetics tools

Resource Type: software application, software resource

Keywords: c++, genetic association, genomic analysis, gifti, imaging genomics, linux, loni pipeline, macos, microsoft, nifti, posix/unix-like, snp, gene, windows, windows xp, genetics, neuroimaging, heritability, pleiotropy, quantitative trait loci, genome-wide association, gene expression, methylation, trait, structural neuroimaging, functionalneuroimaging, brain imaging

Availability: Free, Non-commercial, Open Software License, v3,
[Http://www.nitrc.org/include/glossary.php#552](http://www.nitrc.org/include/glossary.php#552)

Resource Name: Solar Eclipse Imaging Genetics tools

Resource ID: SCR_009645

Alternate IDs: nlx_155966

Record Creation Time: 20220129T080254+0000

Record Last Update: 20260727T040508+0000

Ratings and Alerts

No rating or validation information has been found for Solar Eclipse Imaging Genetics tools.

No alerts have been found for Solar Eclipse Imaging Genetics tools.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 14 mentions in open access literature.

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

Bianco MG, et al. (2023) Heritability of human "directed" functional connectome. Brain and behavior, 13(5), e2839.

Pizzagalli F, et al. (2020) The reliability and heritability of cortical folds and their genetic correlations across hemispheres. Communications biology, 3(1), 510.

Tromp DPM, et al. (2019) The Relationship Between the Uncinate Fasciculus and Anxious Temperament Is Evolutionarily Conserved and Sexually Dimorphic. Biological psychiatry, 86(12), 890.

Bruce HA, et al. (2019) Clinical and genetic validity of quantitative bipolarity. Translational psychiatry, 9(1), 228.

Babajani-Feremi A, et al. (2018) Predicting seizure outcome of vagus nerve stimulation using MEG-based network topology. Neurolmage. Clinical, 19, 990.

Kochunov P, et al. (2016) The common genetic influence over processing speed and white matter microstructure: Evidence from the Old Order Amish and Human Connectome Projects. Neurolmage, 125, 189.

Kochunov P, et al. (2016) Heritability of complex white matter diffusion traits assessed in a population isolate. Human brain mapping, 37(2), 525.

Whelan CD, et al. (2016) Heritability and reliability of automatically segmented human hippocampal formation subregions. Neurolmage, 128, 125.

Kochunov P, et al. (2016) Heterochronicity of white matter development and aging explains regional patient control differences in schizophrenia. *Human brain mapping*, 37(12), 4673.

Ganjgahi H, et al. (2015) Fast and powerful heritability inference for family-based neuroimaging studies. *NeuroImage*, 115, 256.

Kochunov P, et al. (2015) Heritability of fractional anisotropy in human white matter: a comparison of Human Connectome Project and ENIGMA-DTI data. *NeuroImage*, 111, 300.

Kochunov P, et al. (2014) Multi-site study of additive genetic effects on fractional anisotropy of cerebral white matter: Comparing meta and megaanalytical approaches for data pooling. *NeuroImage*, 95, 136.

Kochunov P, et al. (2013) Transcriptomics of cortical gray matter thickness decline during normal aging. *NeuroImage*, 82, 273.

Jahanshad N, et al. (2013) Multi-site genetic analysis of diffusion images and voxelwise heritability analysis: a pilot project of the ENIGMA-DTI working group. *NeuroImage*, 81, 455.