THESIAS
RRID:SCR_013449
Type: Tool

Proper Citation

THESIAS (RRID:SCR_013449)

Resource Information

URL:
http://genecanvas.ecgene.net/#!index.md#THESIAS:_testing_haplotype_effects_in_association_studies

Description: Software program that performs haplotype-based association analysis in unrelated individuals. This program is based on a maximum likelihood model described in Tregouet et al. 2002 and is linked to the stochastic EM (SEM) algorithm. THESIAS allows the simultaneous estimation of haplotype frequencies and of their associated effects on the phenotype of interest. In its current version, both quantitative and qualitative phenotypes can be studied. Covariate-adjusted haplotype effects as well as haplotype x covariate interactions can be investigated. (entry from Genetic Analysis Software)

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Resource Type: Resource, software resource, software application

Keywords: gene, genetic, genomic, ms-windows, linux

Resource ID: SCR_013449

Website Status: Last checked down

Alternate IDs: nlx_154102

Old URLs: http://ecgene.net/genecanvas/downloads.php?cat_id=1

Abbreviations: THESIAS

Mentions Count: 35
Ratings and Alerts

No rating or validation information has been found for THESIAS.

No alerts have been found for THESIAS.

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 FDI Lab - SciCrunch Infrastructure.

Royo JL, et al. (2020) Monoamino oxidase alleles correlate with the presence of essential hypertension among hypogonadic patients. Molecular genetics & genomic medicine, 8(1), e1040.


Fava VM, et al. (2017) Age-Dependent Association of Variants and Leprosy Type 1 Reaction. Frontiers in immunology, 8, 155.

Reddy BM, et al. (2016) Association of type 2 diabetes mellitus genes in polycystic ovary syndrome aetiology among women from southern India. The Indian journal of medical research, 144(3), 400-408.
