

Resource Summary Report

Generated by [FDI Lab - SciCrunch.org](https://fdi-lab.sci-crunch.org/) on Apr 18, 2025

LTSOFT

RRID:SCR_009266

Type: Tool

Proper Citation

LTSOFT (RRID:SCR_009266)

Resource Information

URL: <http://www.hsph.harvard.edu/faculty/alkes-price/software/>

Proper Citation: LTSOFT (RRID:SCR_009266)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on May 16,2023. A software suite designed to more powerfully leverage clinical-covariates such as age, bmi, smoking status, and gender when conducting case-control association studies. Including these covariates in standard regression models is not only suboptimal, but can in many instances reduce power. LTSOFT employs a liability threshold model approach that takes advantage of known epidemiological results to better model the covariates" relationship to the phenotype of interest (entry from Genetic Analysis Software)

Abbreviations: LTSOFT

Resource Type: software resource, software application

Keywords: gene, genetic, genomic

Funding:

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: LTSOFT

Resource ID: SCR_009266

Alternate IDs: nlx_154445

Record Creation Time: 20220129T080252+0000

Record Last Update: 20250416T063541+0000

Ratings and Alerts

No rating or validation information has been found for LTSOFT.

No alerts have been found for LTSOFT.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 3 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](#).

Pollack S, et al. (2019) Multiethnic Genome-Wide Association Study of Diabetic Retinopathy Using Liability Threshold Modeling of Duration of Diabetes and Glycemic Control. Diabetes, 68(2), 441.

Bhatia G, et al. (2013) Estimating and interpreting FST: the impact of rare variants. Genome research, 23(9), 1514.

Bhatia G, et al. (2011) Genome-wide comparison of African-ancestry populations from CARE and other cohorts reveals signals of natural selection. American journal of human genetics, 89(3), 368.