

Resource Summary Report

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LAPSTRUCT

RRID:SCR_007550

Type: Tool

Proper Citation

LAPSTRUCT (RRID:SCR_007550)

Resource Information

URL: <http://galton.uchicago.edu/~junzhang/LAPSTRUCT.html>

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Description: Software application to describe population structure using biomarker data (typically SNPs, CNVs etc.) available in a population sample. The main features different from PCA are: (1) geometrically motivated and graphic model based; (2) robustness of outliers. (entry from Genetic Analysis Software)

Synonyms: R/LAPSTRUCT, LAPlacian eigenfunctions learn population STRUCTure

Resource Type: software application, software resource

Keywords: gene, genetic, genomic, r

Availability: Free

Resource Name: LAPSTRUCT

Resource ID: SCR_007550

Alternate IDs: nlx_154589, SCR_009367, nlx_154209

Record Creation Time: 20220129T080242+0000

Record Last Update: 20260727T040432+0000

Ratings and Alerts

No rating or validation information has been found for LAPSTRUCT.

No alerts have been found for LAPSTRUCT.

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 [nidm-terms](#) .

Wollstein A, et al. (2015) Detecting individual ancestry in the human genome. Investigative genetics, 6, 7.

Zhang J, et al. (2010) Ancestral informative marker selection and population structure visualization using sparse Laplacian eigenfunctions. PloS one, 5(11), e13734.

Zhang J, et al. (2009) Laplacian eigenfunctions learn population structure. PloS one, 4(12), e7928.