Resource Summary Report

Generated by NIF on Sep 20, 2026

pyLMM

RRID:SCR_014525
Type: Tool

Proper Citation

pyLMM (RRID:SCR_014525)

Resource Information

URL: https://github.com/nickFurlotte/pylmm

Proper Citation: pyLMM (RRID:SCR_014525)

Description: A Python package for doing linear mixed model associations in genome wide association studies (GWAS). The software corrects for population structure using EMMA.

Resource Type: data analysis software, data processing software, software application, software resource, standalone software

Defining Citation: DOI:10.1534/genetics.107.080101

Keywords: python, data analysis software, linear mixed model, genome wide association studies, gwas, lmm, emma

Availability: Install using pip

Resource Name: pyLMM

Resource ID: SCR_014525

License: GNU Affero GPL

Record Creation Time: 20220129T080320+0000

Record Last Update: 20260919T195258+0000

Ratings and Alerts

No rating or validation information has been found for pyLMM.

No alerts have been found for pyLMM.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 12 mentions in open access literature.

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

Singh A, et al. (2024) Genome-wide DNA methylation and their transgenerational pattern differ in Arabidopsis thaliana populations originated along the elevation of West Himalaya. BMC plant biology, 24(1), 936.

Ball RL, et al. (2024) GenomeMUSter mouse genetic variation service enables multitrait, multipopulation data integration and analysis. Genome research, 34(1), 145.

Zhang X, et al. (2023) The genomic and epigenetic footprint of local adaptation to variable climates in kiwifruit. Horticulture research, 10(4), uhad031.

Nadiger N, et al. (2021) Protocol for a prospective, observational, deep phenotyping study on adipose epigenetic and lipidomic determinants of metabolic homoeostasis in South Asian Indians: the Indian Diabetes and Metabolic Health (InDiMeT) study. BMJ open, 11(5), e043644.

Rau CD, et al. (2020) Modeling epistasis in mice and yeast using the proportion of two or more distinct genetic backgrounds: Evidence for "polygenic epistasis". PLoS genetics, 16(10), e1009165.

Yao DW, et al. (2019) A linear mixed model approach to gene expression-tumor aneuploidy association studies. Scientific reports, 9(1), 11944.

Ashbrook DG, et al. (2018) Born to Cry: A Genetic Dissection of Infant Vocalization. Frontiers in behavioral neuroscience, 12, 250.

Thompson MJ, et al. (2018) A multi-tissue full lifespan epigenetic clock for mice. Aging, 10(10), 2832.

Kennedy EM, et al. (2018) An integrated -omics analysis of the epigenetic landscape of gene expression in human blood cells. BMC genomics, 19(1), 476.

Gai L, et al. (2018) Finding associated variants in genome-wide association studies on multiple traits. Bioinformatics (Oxford, England), 34(13), i467.

Ferland RJ, et al. (2017) Multidimensional Genetic Analysis of Repeated Seizures in the Hybrid Mouse Diversity Panel Reveals a Novel Epileptogenesis Susceptibility Locus. G3 (Bethesda, Md.), 7(8), 2545.

Orozco LD, et al. (2015) Epigenome-wide association of liver methylation patterns and complex metabolic traits in mice. Cell metabolism, 21(6), 905.