

Resource Summary Report

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Vector Generalized Linear and Additive Models

RRID:SCR_022030

Type: Tool

Proper Citation

Vector Generalized Linear and Additive Models (RRID:SCR_022030)

Resource Information

URL: <https://cran.r-project.org/package=VGAM>

Proper Citation: Vector Generalized Linear and Additive Models (RRID:SCR_022030)

Description: Software R package implementating multiple major classes of statistical regression models.

Abbreviations: VGAM

Resource Type: software resource, software toolkit

Keywords: statistical regression models

Availability: Free, Available for download, Freely available

Resource Name: Vector Generalized Linear and Additive Models

Resource ID: SCR_022030

License: GPL v3

Record Creation Time: 20220421T050138+0000

Record Last Update: 20260725T191307+0000

Ratings and Alerts

No rating or validation information has been found for Vector Generalized Linear and Additive Models.

No alerts have been found for Vector Generalized Linear and Additive Models.

Data and Source Information

Usage and Citation Metrics

We found 6 mentions in open access literature.

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

Boelow H, et al. (2023) Epidemiological study on factors influencing the occurrence of helminth eggs in horses in Germany based on sent-in diagnostic samples. Parasitology research, 122(3), 749.

Saunders LM, et al. (2023) Embryo-scale reverse genetics at single-cell resolution. Nature, 623(7988), 782.

Coaston A, et al. (2023) Factors associated with mobile medical clinic use: a retrospective cohort study. International journal for equity in health, 22(1), 195.

Tresenrider A, et al. (2023) Single-cell sequencing of individual retinal organoids reveals determinants of cell-fate heterogeneity. Cell reports methods, 3(8), 100548.

Qian J, et al. (2020) A pan-cancer blueprint of the heterogeneous tumor microenvironment revealed by single-cell profiling. Cell research, 30(9), 745.

Liu R, et al. (2014) KRLMM: an adaptive genotype calling method for common and low frequency variants. BMC bioinformatics, 15, 158.