

Resource Summary Report

Generated by [RRID](#) on Sep 10, 2026

Bayesian Generalized Linear Regression

RRID:SCR_022522

Type: Tool

Proper Citation

Bayesian Generalized Linear Regression (RRID:SCR_022522)

Resource Information

URL: <https://cran.r-project.org/web/packages/BGLR/>

Proper Citation: Bayesian Generalized Linear Regression (RRID:SCR_022522)

Description: Software R package implements large collection of Bayesian regression models, including parametric variable selection and shrinkage methods and semiparametric procedures.

Abbreviations: BGLR

Resource Type: software resource, software toolkit

Defining Citation: [PMID:25009151](#)

Keywords: Bayesian regression models, parametric variable selection and shrinkage methods, semiparametric procedures

Funding: NIGMS R01GM099992;
NIGMS R01GM101219

Availability: Free, Available for download, Freely available

Resource Name: Bayesian Generalized Linear Regression

Resource ID: SCR_022522

Alternate URLs: <https://github.com/gdgc/BGLR-R>

License: GPL v3

Record Creation Time: 20220628T050153+0000

Record Last Update: 20260905T133310+0000

Ratings and Alerts

No rating or validation information has been found for Bayesian Generalized Linear Regression.

No alerts have been found for Bayesian Generalized Linear Regression.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 6 mentions in open access literature.

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

Fan Y, et al. (2026) Proximal regularization of deep residual neural networks applied to high-dimensional genomic data. Briefings in bioinformatics, 27(3).

Fan Y, et al. (2025) Multi-task genomic prediction using gated residual variable selection neural networks. BMC bioinformatics, 26(1), 167.

Ghafouri-Kesbi F, et al. (2025) Consequences of ignoring dominance genetic effects from genomic selection model for discrete threshold traits. Scientific reports, 15(1), 29693.

Farooq M, et al. (2022) Genomic prediction in plants: opportunities for ensemble machine learning based approaches. F1000Research, 11, 802.

Zhu S, et al. (2021) Evaluation of Bayesian alphabet and GBLUP based on different marker density for genomic prediction in Alpine Merino sheep. G3 (Bethesda, Md.), 11(11).

Beaulieu J, et al. (2020) Genomic selection for resistance to spruce budworm in white spruce and relationships with growth and wood quality traits. Evolutionary applications, 13(10), 2704.