

Resource Summary Report

Generated by [kravitz2](#) on Jul 31, 2026

POPGEN

RRID:SCR_007315

Type: Tool

Proper Citation

POPGEN (RRID:SCR_007315)

Resource Information

URL: <http://www.stats.ox.ac.uk/%7Emarchini/software.html>

Proper Citation: POPGEN (RRID:SCR_007315)

Description: An R package that specifically focuses on statistical and population genetics methods. The motivation behind the package is to produce an easy to use interface to many of the commonly used methods and models used in statistical and population genetics and an alternative interface for some of the methodology produced by our group. (entry from Genetic Analysis Software)

Synonyms: R/POPGEN

Resource Type: software resource, software application

Keywords: gene, genetic, genomic, r

Resource Name: POPGEN

Resource ID: SCR_007315

Alternate IDs: nlx_154543, SCR_009374, nlx_154596

Old URLs: <http://mathgen.stats.ox.ac.uk/software.html>, <https://cran.r-project.org/web/packages/popgen/index.html>

Record Creation Time: 20220129T080241+0000

Record Last Update: 20260731T042736+0000

Ratings and Alerts

No rating or validation information has been found for POPGEN.

No alerts have been found for POPGEN.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 198 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Shen Z, et al. (2025) Assessment of Germplasm Improvement in Three Farmed Grass Carp Populations Based on Genetic Variability. *Biology*, 14(3).

Wolthuis DFGJ, et al. (2025) Model-informed repurposing of eliglustat for treatment and prophylaxis of Shiga toxin-producing *Escherichia coli* hemolytic-uremic syndrome (STEC-HUS) in children. *Pediatric nephrology (Berlin, Germany)*, 40(6), 2009.

Zhang Y, et al. (2025) Genetic Differentiation of Chinese Fir Populations From Mainland China and Taiwan as Revealed by Genotyping-By-Sequencing Analysis, With Implication for Taxonomic Position of the Species. *Ecology and evolution*, 15(4), e71270.

Kadibalban AS, et al. (2025) Metabolic modelling reveals increased autonomy and antagonism in type 2 diabetic gut microbiota. *Molecular systems biology*, 21(6), 720.

He Y, et al. (2025) Mendelian randomization study reveals causal association between skin microbiome and skin cancers. *Scientific reports*, 15(1), 21590.

Yin Y, et al. (2025) A Mendelian randomization analysis reveals the role of the skin microbiota in systemic lupus erythematosus. *Clinical rheumatology*, 44(8), 3191.

Yang L, et al. (2025) Whole genome resequencing reveals genetic markers for plumage colour in Jingyuan Chicken. *Poultry science*, 104(11), 105666.

Rao JH, et al. (2025) Plasma proteins mediate the effects of the gut microbiota on the development of head and neck cancer: a two-sample and mediated Mendelian randomized study. *Discover oncology*, 16(1), 202.

Huang Y, et al. (2025) Skin Microbiota and Pathological Scars: A Bidirectional Two-Sample Mendelian Randomization Study. *Journal of cosmetic dermatology*, 24(2), e16720.

Guo S, et al. (2025) Causal relationship between skin microbiota and Hidradenitis suppurativa: a two-sample Mendelian randomization study. *Archives of dermatological research*, 317(1), 238.

Chen H, et al. (2025) Bidirectional Mendelian Randomization Analysis to Study the Relationship Between Human Skin Microbiota and Radiation-Induced Skin Toxicity. *Microorganisms*, 13(1).

Op 't Hoog CJ, et al. (2025) Model-informed development of a cost-saving dosing regimen for enfortumab vedotin. *Cancer chemotherapy and pharmacology*, 95(1), 36.

Guo P, et al. (2025) Biology, Pathogenicity, and Genetic Diversity of the Rice Pathogen *Ustilaginoidea virens* in Heilongjiang Province, China. *Biology*, 14(1).

Zhang Z, et al. (2025) Unveiling the interplay among skin microbiota, cytokines, and T2DM: an insightful Mendelian randomization study. *Nutrition & metabolism*, 22(1), 29.

Fryer E, et al. (2025) Exploring the causal role of the human gut microbiome in endometrial cancer: a Mendelian randomization approach. *Scientific reports*, 15(1), 11953.

Zhang Y, et al. (2025) Inflammation biomarkers mediate causal inference of the effect of skin microbiota on the risk of allergic diseases. *AMB Express*, 15(1), 116.

Xing X, et al. (2025) Genetic Analysis and Fingerprint Construction for *Isatis indigotica* Fort. Using SSR Markers. *Current issues in molecular biology*, 47(3).

Sammour RH, et al. (2025) Evaluation of genetic diversity and elucidation of population structure of *Lathyrus* accessions using agro-morphological characters and ISSR technique. *Journal, genetic engineering & biotechnology*, 23(2), 100500.

Luo Z, et al. (2025) The Causal Relationship Between Gut and Skin Microbiota and Chronic Obstructive Pulmonary Disease: A Bidirectional Two-Sample Mendelian Randomization Analysis. *International journal of chronic obstructive pulmonary disease*, 20, 709.

Li Y, et al. (2025) Genetic Causal Association Between Skin Microbiota and Biological Aging: Evidence From a Mendelian Randomization Analysis. *Journal of cosmetic dermatology*, 24(1), e16762.