

Resource Summary Report

Generated by [NIF](#) on Aug 9, 2026

Scoary

RRID:SCR_021087

Type: Tool

Proper Citation

Scoary (RRID:SCR_021087)

Resource Information

URL: <https://github.com/AdmiralenOla/Scoary>

Proper Citation: Scoary (RRID:SCR_021087)

Description: Software tool that scores components of pan genome for associations to observed phenotypic traits while accounting for population stratification, with minimal assumptions about evolutionary processes. Designed to take gene presence absence.csv file from Roary as well as traits file created by user and calculate associations between all genes in accessory genome and traits. It reports list of genes sorted by strength of association per trait.

Resource Type: software resource, data analytics software, software application

Defining Citation: [PMID:27887642](#)

Keywords: Gene associations calculation, accessory genome, phenotypic traits, gene presence, gene absence, gene sort, association strenght

Funding: Norwegian Institute of Public Health ;
Norwegian Research Council

Availability: Free, Available for download, Freely available

Resource Name: Scoary

Resource ID: SCR_021087

Alternate IDs: OMICS_13120

Alternate URLs: <https://sources.debian.org/src/scoary/>

License: GPLv3

Record Creation Time: 20220129T080353+0000

Ratings and Alerts

No rating or validation information has been found for Scoary.

No alerts have been found for Scoary.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 20 mentions in open access literature.

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

Jia C, et al. (2026) Distinct genomic trajectory among invasive Salmonella Typhimurium ST313 infections. Nature communications, 17(1).

Yang Q, et al. (2025) Bacterial genome-wide association studies: exploring the genetic variation underlying bacterial phenotypes. Applied and environmental microbiology, 91(6), e0251224.

Kono T, et al. (2025) Protocol for characterizing craniopharyngioma subtypes and their microenvironments using single-cell RNA sequencing and immunohistochemistry. STAR protocols, 6(2), 103760.

Yang S, et al. (2024) Disease-Associated Streptococcus pneumoniae Genetic Variation. Emerging infectious diseases, 30(1), 39.

Yu D, et al. (2024) Emergence of potentially disinfection-resistant, naturalized Escherichia coli populations across food- and water-associated engineered environments. Scientific reports, 14(1), 13478.

Chen J, et al. (2024) Genome-based model for differentiating between infection and carriage Staphylococcus aureus. Microbiology spectrum, 12(10), e0049324.

Zhou H, et al. (2024) Simple and accurate genomic classification model for distinguishing between human and pig Staphylococcus aureus. Communications biology, 7(1), 1171.

Lin Y, et al. (2023) Comparative Genomic Analyses of Lactococcus garvieae Isolated from Bovine Mastitis in China. Microbiology spectrum, 11(3), e0299522.

Zhou Y, et al. (2023) Pan-genome wide association study of Glaesserella parasuis highlights genes associated with virulence and biofilm formation. Frontiers in microbiology, 14, 1160433.

Myintzaw P, et al. (2023) Association of Virulence, Biofilm, and Antimicrobial Resistance Genes with Specific Clonal Complex Types of *Listeria monocytogenes*. *Microorganisms*, 11(6).

Obolski U, et al. (2023) The metabolic, virulence and antimicrobial resistance profiles of colonising *Streptococcus pneumoniae* shift after PCV13 introduction in urban Malawi. *Nature communications*, 14(1), 7477.

Gonzalez-Diaz A, et al. (2022) Comparative pangenome analysis of capsulated *Haemophilus influenzae* serotype f highlights their high genomic stability. *Scientific reports*, 12(1), 3189.

Fang Y, et al. (2022) Lactic Acid Resistance and Population Structure of *Escherichia coli* from Meat Processing Environment. *Microbiology spectrum*, 10(5), e0135222.

Perrat A, et al. (2022) Wild Boars as Reservoir of Highly Virulent Clone of Hybrid Shiga Toxigenic and Enterotoxigenic *Escherichia coli* Responsible for Edema Disease, France. *Emerging infectious diseases*, 28(2), 382.

Mizzi R, et al. (2022) Global Phylogeny of *Mycobacterium avium* and Identification of Mutation Hotspots During Niche Adaptation. *Frontiers in microbiology*, 13, 892333.

Adedrian T, et al. (2022) Comparative Genomics Identifies Features Associated with Methicillin-Resistant *Staphylococcus aureus* (MRSA) Transmission in Hospital Settings. *mSphere*, 7(3), e0011622.

Myintzaw P, et al. (2022) Variability in Cold Tolerance of Food and Clinical *Listeria monocytogenes* Isolates. *Microorganisms*, 11(1).

Sodagari HR, et al. (2021) Whole-Genome Comparative Analysis Reveals Association Between *Salmonella* Genomic Variation and Egg Production Systems. *Frontiers in veterinary science*, 8, 666767.

Knight DR, et al. (2021) Major genetic discontinuity and novel toxigenic species in *Clostridioides difficile* taxonomy. *eLife*, 10.

Reis AC, et al. (2021) The open pan-genome architecture and virulence landscape of *Mycobacterium bovis*. *Microbial genomics*, 7(10).