## **Resource Summary Report**

Generated by dkNET on Apr 28, 2025

# **Scoary**

RRID:SCR\_021087 Type: Tool

**Proper Citation** 

Scoary (RRID:SCR\_021087)

#### **Resource Information**

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

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**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 application, software resource, data analytics software

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

Record Last Update: 20250428T054219+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: <u>SciCrunch Registry</u>

### **Usage and Citation Metrics**

We found 15 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>dkNET</u>.

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.

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.

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.

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).

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

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.

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

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