

Resource Summary Report

Generated by [RRID](#) on Aug 13, 2026

NetShift

RRID:SCR_022733

Type: Tool

Proper Citation

NetShift (RRID:SCR_022733)

Resource Information

URL: <https://web.rniapps.net/netshift/>

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Description: Web tool for identification of driver nodes between case control association networks. Methodology for understanding driver microbes from healthy and disease microbiome datasets.

Synonyms: Netshif

Resource Type: software resource, data access protocol, web service

Defining Citation: [PMID:30287886](#)

Keywords: Driver microbes, identification of driver nodes, case control association networks, driver nodes between networks

Funding: CSIR-National Chemical Laboratory ;
Academy of Scientific and Innovative Research

Availability: Free, Freely available

Resource Name: NetShift

Resource ID: SCR_022733

Record Creation Time: 20220913T050150+0000

Record Last Update: 20260813T055256+0000

Ratings and Alerts

No rating or validation information has been found for NetShift.

No alerts have been found for NetShift.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 10 mentions in open access literature.

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

Hao H, et al. (2026) Phenolic acid biosynthesis is associated with deleterious microbiome changes during *Plasmodiophora brassicae*-induced clubroot in pakchoi. *Microbiome*, 14(1).

Ji X, et al. (2025) DnaK of *Parvimonas micra* extracellular vesicles interacts with the host fibroblasts BAG3-IKK- γ axis to accelerate TNF- α secretion in oral lichen planus. *Microbiome*, 13(1), 164.

Li Z, et al. (2025) Identification of stress-alleviating strains from the core drought-responsive microbiome of *Arabidopsis* ecotypes. *The ISME journal*, 19(1).

Yang X, et al. (2023) Ecological change of the gut microbiota during pregnancy and progression to dyslipidemia. *NPJ biofilms and microbiomes*, 9(1), 14.

Esquivel-Hernández DA, et al. (2023) A network perspective on the ecology of gut microbiota and progression of type 2 diabetes: Linkages to keystone taxa in a Mexican cohort. *Frontiers in endocrinology*, 14, 1128767.

Chen J, et al. (2023) Uncovering Predictive Factors and Interventions for Restoring Microecological Diversity after Antibiotic Disturbance. *Nutrients*, 15(18).

Bose T, et al. (2023) A cross-sectional study on the nasopharyngeal microbiota of individuals with SARS-CoV-2 infection across three COVID-19 waves in India. *Frontiers in microbiology*, 14, 1238829.

Wei ZY, et al. (2022) Characterization of Changes and Driver Microbes in Gut Microbiota During Healthy Aging Using A Captive Monkey Model. *Genomics, proteomics & bioinformatics*, 20(2), 350.

Li X, et al. (2022) Changes to bacterial communities and soil metabolites in an apple orchard as a legacy effect of different intercropping plants and soil management practices. *Frontiers in microbiology*, 13, 956840.

Galvez G, et al. (2021) Co-occurrence Interaction Networks of Extremophile Species Living in a Copper Mining Tailing. *Frontiers in microbiology*, 12, 791127.