

Resource Summary Report

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Sparse Inverse Covariance Estimation for Ecological Association Inference

RRID:SCR_022646

Type: Tool

Proper Citation

Sparse Inverse Covariance Estimation for Ecological Association Inference
(RRID:SCR_022646)

Resource Information

URL: <https://psbweb05.psb.ugent.be/conet/microbialnetworks/spieceasi.php>

Proper Citation: Sparse Inverse Covariance Estimation for Ecological Association Inference (RRID:SCR_022646)

Description: Software R package estimates inverse covariance matrix from sequencing data. Statistical method for inference of microbial ecological networks from amplicon sequencing datasets.

Abbreviations: SPIEC-EASI

Synonyms: SParse Inverse Covariance Estimation for Ecological Association Inference

Resource Type: software toolkit, software resource

Defining Citation: [PMID:25950956](#)

Keywords: inverse covariance matrix estimation, sequencing data, microbial ecological networks inference, amplicon sequencing datasets microbial ecological networks,

Funding: NIAID T32AI007180;
NIDDK R01 DK103358;
NIGMS RO1 GM63270;
Simons Foundation

Availability: Free, Available for download, Freely available

Resource Name: Sparse Inverse Covariance Estimation for Ecological Association Inference

Resource ID: SCR_022646

Record Creation Time: 20220805T050153+0000

Record Last Update: 20260803T040841+0000

Ratings and Alerts

No rating or validation information has been found for Sparse Inverse Covariance Estimation for Ecological Association Inference.

No alerts have been found for Sparse Inverse Covariance Estimation for Ecological Association Inference.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 12 mentions in open access literature.

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

Schmidt SK, et al. (2025) Biological soil crust microcolonies reveal how microbial communities assemble following retreat of a High Arctic glacier. FEMS microbes, 6, xtaf007.

Jiao X, et al. (2025) Progressive gut microbiota shifts and functional alterations across aging stages and frailty in mice. iScience, 28(7), 112985.

Zhou J, et al. (2024) Identifying stationary microbial interaction networks based on irregularly spaced longitudinal 16S rRNA gene sequencing data. Frontiers in microbiomes, 3.

Tan CCS, et al. (2023) No evidence for a common blood microbiome based on a population study of 9,770 healthy humans. Nature microbiology, 8(5), 973.

Binh Tran TD, et al. (2023) Microbial glutamate metabolism predicts intravenous cocaine self-administration in diversity outbred mice. Neuropharmacology, 226, 109409.

Kim MJ, et al. (2021) Effect of a bioconverted product of Lotus corniculatus seed on the axillary microbiome and body odor. Scientific reports, 11(1), 10138.

Kiledal EA, et al. (2021) Bacterial Communities in Concrete Reflect Its Composite Nature and Change with Weathering. mSystems, 6(3).

Ahmed B, et al. (2021) Phytate and Microbial Suspension Amendments Increased Soybean Growth and Shifted Microbial Community Structure. Microorganisms, 9(9).

Petersen A??, et al. (2021) Conjugated C-6 hydroxylated bile acids in serum relate to human metabolic health and gut Clostridia species. Scientific reports, 11(1), 13252.

Floc'h JB, et al. (2020) Bacterial Communities of the Canola Rhizosphere: Network Analysis Reveals a Core Bacterium Shaping Microbial Interactions. *Frontiers in microbiology*, 11, 1587.

Alvarez AS, et al. (2020) Safety and functional enrichment of gut microbiome in healthy subjects consuming a multi-strain fermented milk product: a randomised controlled trial. *Scientific reports*, 10(1), 15974.

Klimenko NS, et al. (2020) Co-occurrence patterns of bacteria within microbiome of Moscow subway. *Computational and structural biotechnology journal*, 18, 314.