

Resource Summary Report

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SpiecEasi

RRID:SCR_022712

Type: Tool

Proper Citation

SpiecEasi (RRID:SCR_022712)

Resource Information

URL: <https://github.com/zdk123/SpiecEasi>

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Description: Software R package for microbiome network analysis. Used for inference of microbial ecological networks from amplicon sequencing datasets. Combines data transformations developed for compositional data analysis with graphical model inference framework that assumes underlying ecological association network is sparse.

Abbreviations: SpiecEasi

Synonyms: SParse InverseE Covariance Estimation for Ecological Association Inference

Resource Type: software resource, software application, data processing software, data analysis software

Defining Citation: [PMID:25950956](#)

Keywords: microbiome network analysis, amplicon sequencing datasets, microbial ecological networks inference

Funding: NIAID AI007180;
NIDDK DK103358;
NIGMS GM63270;
Simons Foundation

Availability: Free, Available for download, Freely available

Resource Name: SpiecEasi

Resource ID: SCR_022712

Record Creation Time: 20220830T050156+0000

Record Last Update: 20260817T040652+0000

Ratings and Alerts

No rating or validation information has been found for SpiecEasi.

No alerts have been found for SpiecEasi.

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 [dkNET](#).

Castro-Severyn J, et al. (2026) Distinct taxonomic signatures in the rhizobiome of two native plants from the polyextreme Salar de Huasco ecosystem. *Environmental microbiome*, 21(1).

Ghosh S, et al. (2026) Phyllosphere microbiome responses to spray-induced gene silencing targeting *Phytophthora infestans* in potato. *NPJ biofilms and microbiomes*, 12(1).

Schneeberger PHH, et al. (2026) Profound taxonomic and functional gut microbiota alterations associated with trichuriasis: cross-country and country-specific patterns. *NPJ biofilms and microbiomes*, 12(1), 45.

Boulund U, et al. (2025) Infant gut anellovirus composition associates with early life factors and childhood atopic disease. *Nature communications*, 17(1), 80.

Crevecoeur S, et al. (2025) Spatio-Temporal Resolution of Microbial Functions and Taxa Associated With Cyanobacterial Harmful Algae Blooms Along a 500-Km Aquatic Continuum in the Lake Erie Watershed. *Environmental microbiology*, 27(10), e70183.

Jensen IT, et al. (2024) Compositionally aware estimation of cross-correlations for microbiome data. *PloS one*, 19(6), e0305032.

Mazzarella T, et al. (2024) Effect of exogenous treatment with zaxinone and its mimics on rice root microbiota across different growth stages. *Scientific reports*, 14(1), 31374.

Ahn S, et al. (2024) Differential network connectivity analysis for microbiome data adjusted for clinical covariates using jackknife pseudo-values. *BMC bioinformatics*, 25(1), 117.

Li JD, et al. (2024) Dual stressors of infection and warming can destabilize host microbiomes. *Philosophical transactions of the Royal Society of London. Series B, Biological sciences*, 379(1901), 20230069.

Li J, et al. (2024) Cross-Cohort Gut Microbiome Signatures of Irritable Bowel Syndrome Presentation and Treatment. *Advanced science (Weinheim, Baden-Wurtemberg, Germany)*, 11(41), e2308313.

Chávez-González JD, et al. (2024) Desert plants, arbuscular mycorrhizal fungi and associated bacteria: Exploring the diversity and role of symbiosis under drought. *Environmental microbiology reports*, 16(4), e13300.

Kishore D, et al. (2023) Inferring microbial co-occurrence networks from amplicon data: a systematic evaluation. *mSystems*, 8(4), e0096122.

Bergman O, et al. (2023) Sodium levels and grazing pressure shape natural communities of the intracellular pathogen *Legionella*. *Microbiome*, 11(1), 167.

Mesquita E, et al. (2023) Entomopathogenic fungus treatment changes the gut bacterial diversity of *Rhipicephalus microplus* ticks. *Parasites & vectors*, 16(1), 185.

Wang Q, et al. (2022) Multiomics Analysis Reveals Aberrant Metabolism and Immunity Linked Gut Microbiota with Insomnia. *Microbiology spectrum*, 10(5), e0099822.

Zhang J, et al. (2022) Niche differentiation of comammox *Nitrospira* in sediments of the Three Gorges Reservoir typical tributaries, China. *Scientific reports*, 12(1), 6820.

Reyman M, et al. (2021) Microbial community networks across body sites are associated with susceptibility to respiratory infections in infants. *Communications biology*, 4(1), 1233.

Miragoli F, et al. (2021) A mixture of quebracho and chestnut tannins drives butyrate-producing bacteria populations shift in the gut microbiota of weaned piglets. *PloS one*, 16(4), e0250874.

Kim HJ, et al. (2018) Fragile skin microbiomes in megacities are assembled by a predominantly niche-based process. *Science advances*, 4(3), e1701581.

Yang H, et al. (2018) Evaluating the profound effect of gut microbiome on host appetite in pigs. *BMC microbiology*, 18(1), 215.