

Resource Summary Report

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LinDA

RRID:SCR_025966

Type: Tool

Proper Citation

LinDA (RRID:SCR_025966)

Resource Information

URL: <https://github.com/zhouhj1994/LinDA>

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Description: Software linear models for differential abundance analysis of microbiome compositional data. Used to tackle compositional effects in differential abundance analysis. It fits linear regression models on centered log2-ratio transformed data, identifies bias term due to transformation and compositional effect, and corrects bias using mode of regression coefficients. It could fit mixed-effect models.

Synonyms: Linear models for differential abundance analysis of microbiome compositional data (LinDA), Linear models for differential abundance analysis of microbiome compositional data

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

Defining Citation: [PMID:35421994](#)

Keywords: differential abundance analysis, microbiome compositional data, differential abundance analysis,

Funding: Mayo Clinic Center for Individualized Medicine ;
NIGMS R01GM144351;
NSF

Resource Name: LinDA

Resource ID: SCR_025966

Record Creation Time: 20241023T053303+0000

Record Last Update: 20260905T133510+0000

Ratings and Alerts

No rating or validation information has been found for LinDA.

No alerts have been found for LinDA.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 4 mentions in open access literature.

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

Stang A, et al. (2026) Lowered Abundance of Gut Bacteriophage Species Is Associated With Human Cancer Cachexia. Journal of cachexia, sarcopenia and muscle, 17(3), e70324.

Ovaska M, et al. (2026) The role of human milk oligosaccharides in shaping and restoring infant gut microbiota: population-based cohort study. The American journal of clinical nutrition, 123(6), 101318.

von Ameln Lovison O, et al. (2025) Unveiling the role of the upper respiratory tract microbiome in susceptibility and severity to COVID-19. Frontiers in cellular and infection microbiology, 15, 1531084.

Zhou H, et al. (2022) LinDA: linear models for differential abundance analysis of microbiome compositional data. Genome biology, 23(1), 95.