Resource Summary Report

Generated by RRID on Apr 11, 2025

ALDEx2

RRID:SCR_003364
Type: Tool

Proper Citation

ALDEx2 (RRID:SCR_003364)

Resource Information

URL: https://github.com/ggloor/ALDEx2

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Description: Software tool to examine compositional high-throughput sequence data with Welch's t-test. A differential relative count abundance analysis for the comparison of two conditions. For example, single-organism and meta-rna-seq high-throughput sequencing assays, or of selected and unselected values from in-vitro sequence selections. Uses a Dirichlet-multinomial model to infer abundance from counts, that has been optimized for three or more experimental replicates. Infers sampling variation and calculates the expected Benjamini-Hochberg false discovery rate given the biological and sampling variation using several parametric and non-parametric tests. Can to glm and Kruskal-Wallace tests on one-way ANOVA style designs.

Resource Type: software resource

Defining Citation: PMID:24910773

Keywords: standalone software, r, bio.tools

Funding:

Availability: GNU Affero General Public License, v3

Resource Name: ALDEx2

Resource ID: SCR_003364

Alternate IDs: biotools:aldex2, OMICS_04634

Alternate URLs: https://bio.tools/aldex2

Record Creation Time: 20220129T080218+0000

Record Last Update: 20250410T065000+0000

Ratings and Alerts

No rating or validation information has been found for ALDEx2.

No alerts have been found for ALDEx2.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 418 mentions in open access literature.

Listed below are recent publications. The full list is available at RRID.

Chao H, et al. (2025) Litter quality modulates changes in bacterial and fungal communities during the gut transit of earthworm species of different ecological groups. ISME communications, 5(1), ycae171.

Grieves LA, et al. (2025) Uropygial gland microbiota of nearctic-neotropical migrants vary with season and migration distance. Animal microbiome, 7(1), 11.

Gregory CL, et al. (2025) Utilizing a novel fecal sampling method to examine resistance of the honey bee (Apis mellifera) gut microbiome to a low dose of tetracycline. PloS one, 20(1), e0317129.

Yunusbayev B, et al. (2025) Gut dysbiosis narrative in psoriasis: matched-pair approach identifies only subtle shifts correlated with elevated fecal calprotectin. Microbiology spectrum, 13(1), e0138224.

Salas-López M, et al. (2025) Human Milk Archaea Associated with Neonatal Gut Colonization and Its Co-Occurrence with Bacteria. Microorganisms, 13(1).

de Freitas AS, et al. (2025) Harnessing the synergy of Urochloa brizantha and Amazonian Dark Earth microbiomes for enhanced pasture recovery. BMC microbiology, 25(1), 27.

Algethamy H, et al. (2025) Distinct relative abundances in pathogens detected in mechanically ventilated patients with suspected pneumonia in the intensive care unit at King Abdulaziz University Hospital. Scientific reports, 15(1), 3291.

Dawson MA, et al. (2024) Early time-restricted eating improves markers of cardiometabolic health but has no impact on intestinal nutrient absorption in healthy adults. Cell reports. Medicine, 5(1), 101363.

Hernandez AR, et al. (2024) Microbiome-driven alterations in metabolic pathways and impaired cognition in aged female TgF344-AD rats. Aging brain, 5, 100119.

Fazzone B, et al. (2024) Short-Term Dietary Restriction Potentiates an Anti-Inflammatory Circulating Mucosal-Associated Invariant T-Cell Response. Nutrients, 16(8).

Mes W, et al. (2024) Feeding strategy and feed protein level affect the gut microbiota of common carp (Cyprinus carpio). Environmental microbiology reports, 16(3), e13262.

Hengist A, et al. (2024) Ketogenic diet but not free-sugar restriction alters glucose tolerance, lipid metabolism, peripheral tissue phenotype, and gut microbiome: RCT. Cell reports. Medicine, 5(8), 101667.

Davies T, et al. (2024) Ecological phage therapy: Can bacteriophages help rapidly restore the soil microbiome? Ecology and evolution, 14(8), e70185.

Erlandson SR, et al. (2024) Sterile sentinels and MinION sequencing capture active soil microbial communities that differentiate crop rotations. Environmental microbiome, 19(1), 30.

Junker R, et al. (2024) Integration of metataxonomic data sets into microbial association networks highlights shared bacterial community dynamics in fermented vegetables. Microbiology spectrum, 12(6), e0031224.

Wong NST, et al. (2024) Characterization of the hoof bacterial communities in feedlot cattle affected with digital dermatitis, foot rot or both using a surface swab technique. Animal microbiome, 6(1), 2.

Ryu EP, et al. (2024) Nepali oral microbiomes reflect a gradient of lifestyles from traditional to industrialized. bioRxiv : the preprint server for biology.

Chen H, et al. (2024) Blood microbial signatures associated with mortality in patients with sepsis: A pilot study. Heliyon, 10(8), e29572.

Shtossel O, et al. (2024) mi-Mic: a novel multi-layer statistical test for microbiota-disease associations. Genome biology, 25(1), 113.

Shu C, et al. (2024) Microbial community characteristics and pathogens detection in Rhipicephalus sanguineus and Haemaphysalis hystricis from Hainan Island, China. Frontiers in microbiology, 15, 1450219.