Resource Summary Report

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ComplexUpset

RRID:SCR_022752
Type: Tool

Proper Citation

ComplexUpset (RRID:SCR_022752)

Resource Information

URL: https://CRAN.R-project.org/package=ComplexUpset

Proper Citation: ComplexUpset (RRID:SCR_022752)

Description: Software R package for visualization of intersecting sets. Used for quantitative analysis of sets, their intersections, and aggregates of intersections. Visualizes set intersections in matrix layout and introduces aggregates based on groupings and queries.

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

Defining Citation: PMID:26356912

Keywords: visualization of intersecting sets, set intSections in matrix layout, aggregates based on groupings and queries, quantitative analysis of sets

Funding: Austrian Science Fund ;
Air Force Research Laboratory and DARPA ;
NHGRI K99 HG007583

Availability: Free, Available for download, Freely available

Resource Name: ComplexUpset

Resource ID: SCR_022752

License: MIT

Record Creation Time: 20220917T050153+0000

Record Last Update: 20260728T043647+0000

Ratings and Alerts

No rating or validation information has been found for ComplexUpset.

No alerts have been found for ComplexUpset.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 18 mentions in open access literature.

Listed below are recent publications. The full list is available at nidm-terms .

López-González C, et al. (2025) Species-specific phylloplane responses to changes in external pH. Journal of experimental botany, 76(17), 5102.

Geonczy SE, et al. (2025) Patchy burn severity explains heterogeneous soil viral and prokaryotic responses to fire in a mixed conifer forest. mSystems, 10(6), e0174924.

Glombik M, et al. (2025) Rapid reprogramming and stabilization of homoeolog expression bias in hexaploid wheat biparental populations. Genome biology, 26(1), 147.

Shimada S, et al. (2025) Characterization of Mycobacterium antarcticum sp. nov., a psychrotolerant member of the genus Mycobacterium isolated from Antarctic soil. Scientific reports, 15(1), 34231.

Schwab KH, et al. (2025) Simple 3D-Printed Stirred Bioreactor Enhances Retinal Organoid Production Via Improved Oxygenation. bioRxiv : the preprint server for biology.

Akopyan M, et al. (2025) Reference genome choice compromises population genetic analyses. Cell.

Palos-Fernández R, et al. (2024) Copper acquisition is essential for plant colonization and virulence in a root-infecting vascular wilt fungus. PLoS pathogens, 20(11), e1012671.

Aira M, et al. (2024) Taxonomic and Functional Dynamics of Bacterial Communities During Drift Seaweed Vermicomposting. Microorganisms, 13(1).

Malacrinò A, et al. (2024) Soil microbiota and herbivory drive the assembly of tomato plant-associated microbial communities through different mechanisms. Communications biology, 7(1), 564.

Thakur S, et al. (2024) Genomic epidemiology and phenotypic characterisation of Salmonella enterica serovar Panama in Victoria, Australia. PLoS neglected tropical diseases, 18(11), e0012666.

Moore A, et al. (2023) Evaluating 17 methods incorporating biological function with GWAS summary statistics to accelerate discovery demonstrates a tradeoff between high sensitivity and high positive predictive value. Communications biology, 6(1), 1199.

Monavarian M, et al. (2023) Development of adaptive anoikis resistance promotes metastasis that can be overcome by CDK8/19 Mediator kinase inhibition. bioRxiv : the preprint server for biology.

Valdés-Hernández J, et al. (2023) Global analysis of the association between pig muscle fatty acid composition and gene expression using RNA-Seq. Scientific reports, 13(1), 535.

Zhang Z, et al. (2023) Complete De Novo Assembly of Wolbachia Endosymbiont of Frankliniella intonsa. International journal of molecular sciences, 24(17).

Brivio E, et al. (2023) Sex shapes cell-type-specific transcriptional signatures of stress exposure in the mouse hypothalamus. Cell reports, 42(8), 112874.

Bender FR, et al. (2022) Microbiome of Nodules and Roots of Soybean and Common Bean: Searching for Differences Associated with Contrasting Performances in Symbiotic Nitrogen Fixation. International journal of molecular sciences, 23(19).

Halvarsson P, et al. (2022) Parasitic strongyle nemabiome communities in wild ruminants in Sweden. Parasites & vectors, 15(1), 341.

Bueno de Mesquita CP, et al. (2021) Methanogenesis and Salt Tolerance Genes of a Novel Halophilic Methanosarcinaceae Metagenome-Assembled Genome from a Former Solar Saltern. Genes, 12(10).