

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

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: Air Force Research Laboratory and DARPA ;
Austrian Science Fund ;
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: 20260821T194239+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 25 mentions in open access literature.

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

Liu XX, et al. (2026) SARS-CoV-2 infection during the first trimester leads to profound immune dysregulation at the maternal-fetal interface despite limited virus detection in placental tissues. *Nature communications*, 17(1).

Piquer-Esteban S, et al. (2026) *Blattella germanica* Selects Microbiota Taxa from Feces and Environmental Inputs. *Insects*, 17(6).

Francette AM, et al. (2026) Evolutionary analysis of transcription elongation factors reveals conserved and lineage-specific regulatory domains. *PLoS biology*, 24(6), e3003855.

Matthys L, et al. (2026) Cost-effective DNA extraction method optimized for high yield and long fragments from coastal sediments. *PloS one*, 21(2), e0343743.

Amin MHF, et al. (2026) Haplotype-level analysis of environmental DNA metabarcoding revealed the biogeography and phylogeography of freshwater fishes in Korean Peninsula. *Scientific reports*, 16(1), 6955.

Monavarian M, et al. (2026) Anoikis resistance and metastasis of ovarian cancer can be overcome by CDK8/19 mediator kinase inhibition. *JCI insight*, 11(4).

Antony F, et al. (2026) Comparative Evaluation of Solid-phase and Membrane Mimetic Strategies in Membrane Proteome Coverage and Disease-State Analysis. *Molecular & cellular proteomics : MCP*, 25(2), 101496.

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

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.

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

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.

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.

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.

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.

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.

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*.

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.