## **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 resource, software application

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

#### **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 12 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>dkNET</u>.

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.

Malacrinò A, et al. (2024) Soil microbiota and herbivory drive the assembly of tomato plantassociated 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.

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

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.

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.

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).