

Resource Summary Report

Generated by [kravitz2](#) on Aug 25, 2026

UpSet

RRID:SCR_022731

Type: Tool

Proper Citation

UpSet (RRID:SCR_022731)

Resource Information

URL:

<https://upset.app/#:~:text=UpSet%20plots%20the%20intersections%20of,is%20part%20of%20an%20>

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Description: Software tool to visualize set intersections in matrix layout. Interactive, web based visualization technique designed to analyze set based data. Visualizes both, set intersections and their properties, and elements in dataset. Used for quantitative analysis of data with more than three sets.

Synonyms: UpSet Plot

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

Defining Citation: [PMID:26356912](#)

Keywords: visualize set intersections, matrix layout, intersecting sets, more than three sets quantitative data analysis

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

Availability: Free, Available for download, Freely available

Resource Name: UpSet

Resource ID: SCR_022731

Alternate URLs: <https://github.com/VCG/upset>

License: MIT License

Record Creation Time: 20220913T050150+0000

Record Last Update: 20260821T194239+0000

Ratings and Alerts

No rating or validation information has been found for UpSet.

No alerts have been found for UpSet.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 16 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Wills L, et al. (2025) Assessing the burden of severe nausea and vomiting of pregnancy or hyperemesis gravidarum and the associated use and experiences of medication treatments: An Australian consumer survey. PloS one, 20(9), e0329687.

Potts C, et al. (2025) Digital Mental Health Interventions for Young People Aged 16-25 Years: Scoping Review. Journal of medical Internet research, 27, e72892.

Wang Y, et al. (2025) Telomere-to-telomere genome of common bean (*Phaseolus vulgaris* L., YP4). GigaScience, 14.

Dou Z, et al. (2025) Exploring the mechanism of *Schisandra rubriflora* in the treatment of polycystic ovary syndrome based on network pharmacology and molecular docking. Journal of ovarian research, 18(1), 16.

Pu Y, et al. (2024) A high-quality chromosomal genome assembly of the sea cucumber *Chiridota heheva* and its hydrothermal adaptation. GigaScience, 13.

Yelina NE, et al. (2024) Streamlined regulation of chloroplast development in the liverwort *Marchantia polymorpha*. Cell reports, 43(9), 114696.

Liu Z, et al. (2023) Localized cardiac small molecule trajectories and persistent chemical sequelae in experimental Chagas disease. Nature communications, 14(1), 6769.

Youn K, et al. (2023) Investigating the Potential Anti-Alzheimer's Disease Mechanism of Marine Polyphenols: Insights from Network Pharmacology and Molecular Docking. Marine drugs, 21(11).

Esquivel-Hernández DA, et al. (2023) A network perspective on the ecology of gut microbiota and progression of type 2 diabetes: Linkages to keystone taxa in a Mexican cohort. Frontiers in endocrinology, 14, 1128767.

Savi? R, et al. (2023) Integration of transcriptomes of senescent cell models with multi-tissue patient samples reveals reduced COL6A3 as an inducer of senescence. *Cell reports*, 42(11), 113371.

Busso-Lopes AF, et al. (2022) Connecting multiple microenvironment proteomes uncovers the biology in head and neck cancer. *Nature communications*, 13(1), 6725.

Hernández EG, et al. (2020) Salt Marsh Elevation Drives Root Microbial Composition of the Native Invasive Grass *Elytrigia atherica*. *Microorganisms*, 8(10).

Contador CA, et al. (2019) Use of genome-scale models to get new insights into the marine actinomycete genus *Salinispora*. *BMC systems biology*, 13(1), 11.

Buti M, et al. (2019) A Meta-Analysis of Comparative Transcriptomic Data Reveals a Set of Key Genes Involved in the Tolerance to Abiotic Stresses in Rice. *International journal of molecular sciences*, 20(22).

Crysnanto D, et al. (2019) Accurate sequence variant genotyping in cattle using variation-aware genome graphs. *Genetics, selection, evolution : GSE*, 51(1), 21.

Feng T, et al. (2019) Gene Expression Pattern and Regulatory Network of β -Toxin Treatment in *Bombyx mori*. *International journal of genomics*, 2019, 7859121.