

Resource Summary Report

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eulerr

RRID:SCR_022753

Type: Tool

Proper Citation

eulerr (RRID:SCR_022753)

Resource Information

URL: <https://CRAN.R-project.org/package=eulerr>

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Description: Software package to generate area proportional Euler diagrams using numerical optimization that display set relationships (intersections, unions, and disjoint) with circles or ellipses. Area Proportional Euler and Venn Diagrams with Ellipses.

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

Keywords: Euler, Venn Diagrams, Ellipses, generate area proportional Euler diagrams, display set relationships with circles or ellipses, intersections, unions, and disjoint,

Availability: Free, Available for download, Freely available

Resource Name: eulerr

Resource ID: SCR_022753

Alternate URLs: <https://github.com/jolars/eulerr>

License: GPL v3

Record Creation Time: 20220917T050153+0000

Record Last Update: 20260821T194224+0000

Ratings and Alerts

No rating or validation information has been found for eulerr.

No alerts have been found for eulerr.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 30 mentions in open access literature.

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

Franciosa G, et al. (2026) The proteomics and phosphoproteomics landscape of melanoma under T cell attack. Cell reports. Medicine, 7(6), 102829.

Wierbi?owicz K, et al. (2025) Parp7 generates an ADP-ribosyl degron that controls negative feedback of androgen signaling. The EMBO journal, 44(17), 4720.

Jennrich J, et al. (2025) The formation of chaperone-rich GET bodies depends on the tetratricopeptide repeat region of Sgt2 and is reversed by NADH. Journal of cell science, 138(6).

Ophey A, et al. (2025) Being Prodromal: Current Criteria in the Context of Isolated REM Sleep Behavior Disorder. Movement disorders clinical practice, 12(6), 828.

Rauch DA, et al. (2025) Single-Cell Transcriptomic Analysis of Kaposi Sarcoma. PLoS pathogens, 21(4), e1012233.

Eickhoff N, et al. (2025) TRIM33 loss reduces androgen receptor transcriptional output and H2BK120 ubiquitination. Communications biology, 8(1), 1043.

Bensberg M, et al. (2025) Exposing the DNA methylation-responsive compartment of the leukaemic genome in T-ALL cell lines support its potential as a novel therapeutic target in T-ALL. Clinical epigenetics, 17(1), 114.

Simões-Sousa S, et al. (2025) ARID1A stabilizes non-homologous end joining factors at DNA breaks induced by the G4 ligand pyridostatin. Cell reports, 44(9), 116277.

Rask GC, et al. (2025) Seclidemstat (SP-2577) Induces Transcriptomic Reprogramming and Cytotoxicity in Multiple Fusion-Positive Sarcomas. Cancer research communications, 5(9), 1584.

Paras KI, et al. (2025) PAX3-FOXO1 Drives Targetable Cell State-Dependent Metabolic Vulnerabilities in Rhabdomyosarcoma. Cancer research, 85(23), 4718.

Köhne M, et al. (2025) Satb1 directs the differentiation of TH17 cells through suppression of IL-2 expression. Cell reports, 44(7), 115866.

McIntyre TI, et al. (2025) KDM6B-dependent epigenetic programming of uterine fibroblasts in early pregnancy regulates parturition timing in mice. Cell, 188(5), 1265.

Scialò C, et al. (2025) Seeded aggregation of TDP-43 induces its loss of function and reveals early pathological signatures. Neuron, 113(10), 1614.

Reichel M, et al. (2024) ALBA proteins facilitate cytoplasmic YTHDF-mediated reading of m6A in Arabidopsis. *The EMBO journal*, 43(24), 6626.

Schendel V, et al. (2024) The venom and telopodal defence systems of the centipede *Lithobius forficatus* are functionally convergent serial homologues. *BMC biology*, 22(1), 135.

Conrad WS, et al. (2024) Proportion and distribution of neurotransmitter-defined cell types in the ventral tegmental area and substantia nigra pars compacta. *Addiction neuroscience*, 13.

Lu Y, et al. (2024) ALDH1A3-acetaldehyde metabolism potentiates transcriptional heterogeneity in melanoma. *Cell reports*, 43(7), 114406.

Golov AK, et al. (2024) A genome-wide nucleosome-resolution map of promoter-centered interactions in human cells corroborates the enhancer-promoter looping model. *eLife*, 12.

Bortel P, et al. (2024) Systematic Optimization of Automated Phosphopeptide Enrichment for High-Sensitivity Phosphoproteomics. *Molecular & cellular proteomics : MCP*, 23(5), 100754.

Weinberger S, et al. (2024) Mapping the Protein Phosphatase 1 Interactome in Human Cytomegalovirus Infection. *Viruses*, 16(12).