

Resource Summary Report

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[ggalluvial](#)

RRID:SCR_021253

Type: Tool

Proper Citation

ggalluvial (RRID:SCR_021253)

Resource Information

URL: <https://corybrunson.github.io/ggalluvial/>

Proper Citation: ggalluvial (RRID:SCR_021253)

Description: Software tool as ggplot2 extension for alluvial plots. Used to visualize frequency distributions over time or frequency tables involving several categorical variables. Requires user to specify dimensions, either as separate aesthetics or as key-value pairs, relies on separate layers (stats and geoms) to produce strata, alluvia, and alluvial segments called lodes and flows.

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

Keywords: Alluvial plots extension, visualize frequency distributions over time, visualize frequency tables involving several categorical variables,

Availability: Free, Available for download, Freely available

Resource Name: ggalluvial

Resource ID: SCR_021253

Alternate URLs: <https://CRAN.R-project.org/package=ggalluvial>,
<https://github.com/corybrunson/ggalluvial/>

License: GNU General Public License v3.0

Record Creation Time: 20220129T080354+0000

Record Last Update: 20260729T044515+0000

Ratings and Alerts

No rating or validation information has been found for ggalluvial.

No alerts have been found for ggalluvial.

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 [nidm-terms](#) .

Wang T, et al. (2025) Predictive and therapeutic value of the ferroptosis gene C1SD1 in non-small cell lung cancer. *Oncology letters*, 29(5), 235.

Franczak A, et al. (2025) Effect of electromagnetic field radiation on transcriptomic profile and DNA methylation level in pig conceptuses during the peri-implantation period. *Scientific reports*, 15(1), 14025.

Olweny G, et al. (2025) Protocol for identifying *Mycobacterium tuberculosis* infection status through airway microbiome profiling. *STAR protocols*, 6(1), 103574.

Savani MR, et al. (2025) Nitrogen metabolism profiling reveals cell state-specific pyrimidine synthesis pathway choice. *bioRxiv : the preprint server for biology*.

Paloviita P, et al. (2025) Integrated transcriptomic analysis reveals metabolic remodeling and gene expression networks related to human 8-cell-stage embryo-like cells. *Cell reports*, 45(1), 116748.

Cheng Y, et al. (2024) Endosymbiotic Fungal Diversity and Dynamics of the Brown Planthopper across Developmental Stages, Tissues, and Sexes Revealed Using Circular Consensus Sequencing. *Insects*, 15(2).

Shama S, et al. (2024) Mother's milk microbiota is associated with the developing gut microbial consortia in very-low-birth-weight infants. *Cell reports. Medicine*, 5(9), 101729.

Xu P, et al. (2024) Cancer marker TNFRSF1A: From single-cell heterogeneity of renal cell carcinoma to functional validation. *Oncology letters*, 28(3), 425.

Bhat GP, et al. (2024) Structured wound angiogenesis instructs mesenchymal barrier compartments in the regenerating nerve. *Neuron*, 112(2), 209.

Xiao D, et al. (2023) DNA methylation-mediated Rbpjk suppression protects against fracture nonunion caused by systemic inflammation. *The Journal of clinical investigation*, 134(3).

Barreto HC, et al. (2022) Fluctuating selection on bacterial iron regulation in the mammalian gut. *Current biology : CB*, 32(15), 3261.

Wang FX, et al. (2020) Chromatin Accessibility Dynamics and a Hierarchical Transcriptional Regulatory Network Structure for Plant Somatic Embryogenesis. *Developmental cell*, 54(6), 742.