Resource Summary Report

Generated by RRID on Apr 8, 2025

seaborn

RRID:SCR_018132

Type: Tool

Proper Citation

seaborn (RRID:SCR_018132)

Resource Information

URL: https://seaborn.pydata.org/

Proper Citation: seaborn (RRID:SCR_018132)

Description: Software Python tool as data visualization library based on matplotlib. Provides interface for drawing attractive and informative statistical graphics. Statistical data visualization using matplotlib.

Pasource Type: software library software application

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

Keywords: Data visualization library, statistical graphic, statistical data visualization

Funding:

Availability: Free, Available for download, Freely available

Resource Name: seaborn

Resource ID: SCR_018132

Alternate URLs: https://github.com/mwaskom/seaborn/tree/v0.10.0

License: BSD 3-Clause "New" or "Revised" License

Record Creation Time: 20220129T080338+0000

Record Last Update: 20250407T220444+0000

Ratings and Alerts

No rating or validation information has been found for seaborn.

No alerts have been found for seaborn.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 302 mentions in open access literature.

Listed below are recent publications. The full list is available at RRID.

Li S, et al. (2025) Quantum and complex-valued hybrid networks for multi-principal element alloys phase prediction. iScience, 28(1), 111582.

Shevchenko V, et al. (2025) A comparative machine learning study of schizophrenia biomarkers derived from functional connectivity. Scientific reports, 15(1), 2849.

Agrawal P, et al. (2024) Network-based approach elucidates critical genes in BRCA subtypes and chemotherapy response in triple negative breast cancer. iScience, 27(5), 109752.

Welzel M, et al. (2024) Turbo autoencoders for the DNA data storage channel with Autoturbo-DNA. iScience, 27(5), 109575.

Suárez LE, et al. (2024) Connectome-based reservoir computing with the conn2res toolbox. Nature communications, 15(1), 656.

Shakhova ES, et al. (2024) An improved pathway for autonomous bioluminescence imaging in eukaryotes. Nature methods, 21(3), 406.

van de Haar J, et al. (2024) Combining Genomic Biomarkers to Guide Immunotherapy in Non-Small Cell Lung Cancer. Clinical cancer research: an official journal of the American Association for Cancer Research, 30(7), 1307.

Wakasugi N, et al. (2024) Harmonizing multisite data with the ComBat method for enhanced Parkinson's disease diagnosis via DAT-SPECT. Frontiers in neurology, 15, 1306546.

Karakose E, et al. (2024) Cycling alpha cells in regenerative drug-treated human pancreatic islets may serve as key beta cell progenitors. Cell reports. Medicine, 5(12), 101832.

Wei L, et al. (2024) Systems-level reconstruction of kinase phosphosignaling networks regulating endothelial barrier integrity using temporal data. NPJ systems biology and applications, 10(1), 134.

Wu Y, et al. (2024) STARDUST: A pipeline for the unbiased analysis of astrocyte regional calcium dynamics. STAR protocols, 5(3), 103305.

Zhai Y, et al. (2024) Machine learning-enhanced assessment of potential probiotics from healthy calves for the treatment of neonatal calf diarrhea. Frontiers in microbiology, 15, 1507537.

Sunderaraman P, et al. (2024) Design and Feasibility Analysis of a Smartphone-Based Digital Cognitive Assessment Study in the Framingham Heart Study. Journal of the American Heart Association, 13(2), e031348.

Goldman AL, et al. (2024) Microbial sensor variation across biogeochemical conditions in the terrestrial deep subsurface. mSystems, 9(1), e0096623.

Zvirblyte J, et al. (2024) Single-cell transcriptional profiling of clear cell renal cell carcinoma reveals a tumor-associated endothelial tip cell phenotype. Communications biology, 7(1), 780.

Huffer K, et al. (2024) Conservation of the cooling agent binding pocket within the TRPM subfamily. eLife, 13.

Sami A, et al. (2024) A deep learning based hybrid recommendation model for internet users. Scientific reports, 14(1), 29390.

Peter CJ, et al. (2024) Single chromatin fiber profiling and nucleosome position mapping in the human brain. Cell reports methods, 4(12), 100911.

Tam R, et al. (2024) Centrosome-organized plasma membrane infoldings linked to growth of a cortical actin domain. The Journal of cell biology, 223(10).

Ramirez Sierra MA, et al. (2024) Al-powered simulation-based inference of a genuinely spatial-stochastic gene regulation model of early mouse embryogenesis. PLoS computational biology, 20(11), e1012473.