Resource Summary Report

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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.

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

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: 20250411T060022+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 FDI Lab - SciCrunch.org.

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.

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.

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.

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.

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.

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

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.

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.

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

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.

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

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.

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).

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.

Pflughaupt P, et al. (2024) Towards the genomic sequence code of DNA fragility for machine learning. Nucleic acids research, 52(21), 12798.

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

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