Resource Summary Report

Generated by NIF on May 28, 2025

machine learning open source software

RRID:SCR_013990
Type: Tool

Proper Citation

machine learning open source software (RRID:SCR_013990)

Resource Information

URL: http://mloss.org/software/

Proper Citation: machine learning open source software (RRID:SCR_013990)

Description: A software repository which provides open source software for machine learning. Software entries include information such as author, license, data format, and programming language. The ultimate goal of mloss.org is to create a comprehensive open source machine learning environment where open source machine learning software can compete with comercial closed source solutions.

Abbreviations: mloss

Synonyms: mloss.org

Resource Type: software repository, software resource

Keywords: software repository, machine learning, machine learning software

Funding:

Availability: Open source, The community can contribute to this resource

Resource Name: machine learning open source software

Resource ID: SCR_013990

Record Creation Time: 20220129T080318+0000

Record Last Update: 20250527T055340+0000

Ratings and Alerts

No rating or validation information has been found for machine learning open source software.

No alerts have been found for machine learning open source software.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 14 mentions in open access literature.

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

Feher da Silva C, et al. (2018) A note on the analysis of two-stage task results: How changes in task structure affect what model-free and model-based strategies predict about the effects of reward and transition on the stay probability. PloS one, 13(4), e0195328.

Belk A, et al. (2018) Microbiome Data Accurately Predicts the Postmortem Interval Using Random Forest Regression Models. Genes, 9(2).

Tong KJ, et al. (2017) The impacts of drift and selection on genomic evolution in insects. PeerJ, 5, e3241.

Hernandez-Armenta C, et al. (2017) Benchmarking substrate-based kinase activity inference using phosphoproteomic data. Bioinformatics (Oxford, England), 33(12), 1845.

Wells BS, et al. (2017) Parallel Activin and BMP signaling coordinates R7/R8 photoreceptor subtype pairing in the stochastic Drosophila retina. eLife, 6.

Song HF, et al. (2017) Reward-based training of recurrent neural networks for cognitive and value-based tasks. eLife, 6.

Badet T, et al. (2017) Codon optimization underpins generalist parasitism in fungi. eLife, 6.

Luo W, et al. (2017) New Martian valley network volume estimate consistent with ancient ocean and warm and wet climate. Nature communications, 8, 15766.

Song HF, et al. (2016) Training Excitatory-Inhibitory Recurrent Neural Networks for Cognitive Tasks: A Simple and Flexible Framework. PLoS computational biology, 12(2), e1004792.

Macaulay IC, et al. (2016) Single-Cell RNA-Sequencing Reveals a Continuous Spectrum of Differentiation in Hematopoietic Cells. Cell reports, 14(4), 966.

Roche-Lima A, et al. (2016) Implementation and comparison of kernel-based learning methods to predict metabolic networks. Network modeling and analysis in health informatics and bioinformatics, 5(1), 26.

Winslow BD, et al. (2015) Identification of resilient individuals and those at risk for performance deficits under stress. Frontiers in neuroscience, 9, 328.

Wieneke AE, et al. (2015) Validation of natural language processing to extract breast cancer pathology procedures and results. Journal of pathology informatics, 6, 38.

Ho ES, et al. (2013) A multispecies polyadenylation site model. BMC bioinformatics, 14 Suppl 2(Suppl 2), S9.