Resource Summary Report

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Weka

RRID:SCR_001214
Type: Tool

Proper Citation

Weka (RRID:SCR_001214)

Resource Information

URL: http://www.cs.waikato.ac.nz/ml/weka/

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Description: A collection of machine learning algorithms for data mining tasks. The algorithms can either be applied directly to a dataset or called from your own Java code. Weka contains tools for data pre-processing, classification, regression, clustering, association rules, and visualization. It is also well-suited for developing new machine learning schemes.

Abbreviations: Weka

Synonyms: Weka 3: Data Mining Software in Java, WEKA Data Mining Software

Resource Type: data processing software, software resource, software application, text-mining software

Defining Citation: PMID:15073010

Keywords: data mining, java, machine learning, pre-processing, classification, regression, clustering, feature selection, visualization

Funding:

Availability: GNU General Public License, v3, Acknowledgement requested

Resource Name: Weka

Resource ID: SCR_001214

Alternate IDs: SciRes_000174

Record Creation Time: 20220129T080206+0000

Record Last Update: 20250417T065039+0000

Ratings and Alerts

No rating or validation information has been found for Weka.

No alerts have been found for Weka.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 68 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Chen YW, et al. (2023) Predicting Arm Nonuse in Individuals with Good Arm Motor Function after Stroke Rehabilitation: A Machine Learning Study. International journal of environmental research and public health, 20(5).

Walls S, et al. (2020) Prolonged Exposure to Microgravity Reduces Cardiac Contractility and Initiates Remodeling in Drosophila. Cell reports, 33(10), 108445.

Taujale R, et al. (2020) Deep evolutionary analysis reveals the design principles of fold A glycosyltransferases. eLife, 9.

Hernández-Pérez LA, et al. (2019) New Features for Neuron Classification. Neuroinformatics, 17(1), 5.

Libby ARG, et al. (2019) Automated Design of Pluripotent Stem Cell Self-Organization. Cell systems, 9(5), 483.

Glaab E, et al. (2018) Computational systems biology approaches for Parkinson's disease. Cell and tissue research, 373(1), 91.

Toth T, et al. (2018) Environmental properties of cells improve machine learning-based phenotype recognition accuracy. Scientific reports, 8(1), 10085.

Tang TY, et al. (2018) Development and validation of a penumbra-based predictive model for thrombolysis outcome in acute ischemic stroke patients. EBioMedicine, 35, 251.

Sakr S, et al. (2018) Using machine learning on cardiorespiratory fitness data for predicting hypertension: The Henry Ford ExercIse Testing (FIT) Project. PloS one, 13(4), e0195344.

Wang XH, et al. (2018) Identifying individuals with attention deficit hyperactivity disorder based on temporal variability of dynamic functional connectivity. Scientific reports, 8(1), 11789.

Hu YH, et al. (2018) Improvement of Adequate Digoxin Dosage: An Application of Machine Learning Approach. Journal of healthcare engineering, 2018, 3948245.

Vanneste S, et al. (2018) Thalamocortical dysrhythmia detected by machine learning. Nature communications, 9(1), 1103.

Riganello F, et al. (2018) A Heartbeat Away From Consciousness: Heart Rate Variability Entropy Can Discriminate Disorders of Consciousness and Is Correlated With Resting-State fMRI Brain Connectivity of the Central Autonomic Network. Frontiers in neurology, 9, 769.

Perez-Sanz F, et al. (2017) Plant phenomics: an overview of image acquisition technologies and image data analysis algorithms. GigaScience, 6(11), 1.

Johnson ML, et al. (2017) A Bayesian view of murine seminal cytokine networks. PloS one, 12(11), e0188897.

Burnap P, et al. (2017) Multi-class machine classification of suicide-related communication on Twitter. Online social networks and media, 2, 32.

Choi D, et al. (2017) Predicting protein-binding regions in RNA using nucleotide profiles and compositions. BMC systems biology, 11(Suppl 2), 16.

Ohsuga T, et al. (2017) Distinct preoperative clinical features predict four histopathological subtypes of high-grade serous carcinoma of the ovary, fallopian tube, and peritoneum. BMC cancer, 17(1), 580.

Rojas Sánchez P, et al. (2017) Impact of lopinavir-ritonavir exposure in HIV-1 infected children and adolescents in Madrid, Spain during 2000-2014. PloS one, 12(3), e0173168.

Fusco R, et al. (2017) Breast DCE-MRI: lesion classification using dynamic and morphological features by means of a multiple classifier system. European radiology experimental, 1(1), 10.