

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 application, text-mining software, software resource

Defining Citation: [PMID:15073010](#)

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

Availability: Free, Available for download, Freely available

Resource Name: Weka

Resource ID: SCR_001214

Alternate IDs: SciRes_000174

Record Creation Time: 20220129T080206+0000

Record Last Update: 20260815T182700+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 70 mentions in open access literature.

Listed below are recent publications. The full list is available at [RRID](#) .

Padman BS, et al. (2025) AI-directed voxel extraction and volume EM identify intrusions as sites of mitochondrial contact. *The Journal of cell biology*, 224(10).

Borrelli MJ, et al. (2025) CAMKK γ supports growth and viability of epithelial ovarian cancer in vitro and in vivo. *Scientific reports*, 15(1), 25913.

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.

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.

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

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.

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

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.

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.

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

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.

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

Ohsga 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.