Resource Summary Report

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Amsterdam Decoding And Modeling

RRID:SCR_022172
Type: Tool

Proper Citation

Amsterdam Decoding And Modeling (RRID:SCR_022172)

Resource Information

URL: https://github.com/fahrenfort/ADAM

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Description: Software Matlab based MVPA toolbox for EEG analyses. Allows direct comparison of ERP/ERF results to MVPA results using any dataset in standard EEGLAB or Fieldtrip format. Performs and visualizes multiple comparison corrected group decoding and forward encoding results in variety of ways, such as classifier performance across time, temporal generalization (time-by-time) matrices of classifier performance, channel tuning functions (CTFs) and topographical maps of (forward-transformed) classifier weights.

Abbreviations: ADAM

Synonyms: ADAM toolbox

Resource Type: data analysis software, software toolkit, data processing software, software resource, software application

Defining Citation: PMID:30018529

Keywords: multivariate pattern analysis, electroencephalography (EEG), magnetoencephalography (MEG)

Funding: CO European Research Council Consolidator

Availability: Free, Available for download, Freely available

Resource Name: Amsterdam Decoding And Modeling

Resource ID: SCR_022172

License: GNU GPL v3.0

Record Creation Time: 20220421T050139+0000

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Ratings and Alerts

No rating or validation information has been found for Amsterdam Decoding And Modeling.

No alerts have been found for Amsterdam Decoding And Modeling.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 21 mentions in open access literature.

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

Aydin A, et al. (2024) ADAM19 cleaves the PTH receptor and associates with brachydactyly type E. Life science alliance, 7(4).

Alnaji L, et al. (2024) Machine learning in epidemiology: Neural networks forecasting of monkeypox cases. PloS one, 19(5), e0300216.

Zondag AGM, et al. (2024) The Effect of Artificial Intelligence on Patient-Physician Trust: Cross-Sectional Vignette Study. Journal of medical Internet research, 26, e50853.

Xu J, et al. (2023) iAMPCN: a deep-learning approach for identifying antimicrobial peptides and their functional activities. Briefings in bioinformatics, 24(4).

Takács Á, et al. (2022) Protocol to decode representations from EEG data with intermixed signals using temporal signal decomposition and multivariate pattern-analysis. STAR protocols, 3(2), 101399.

Takacs A, et al. (2021) Neurophysiological mechanisms underlying motor feature binding processes and representations. Human brain mapping, 42(5), 1313.

Lee KW, et al. (2021) Utilizing Red Spotted Apollo Butterfly Transcriptome to Identify Antimicrobial Peptide Candidates against Porphyromonas gingivalis. Insects, 12(5).

Fu Z, et al. (2020) A residual dense network assisted sparse view reconstruction for breast computed tomography. Scientific reports, 10(1), 21111.

Tessema BB, et al. (2020) Strategies Using Genomic Selection to Increase Genetic Gain in Breeding Programs for Wheat. Frontiers in genetics, 11, 578123.

Wang L, et al. (2020) Effect of genomic selection and genotyping strategy on estimation of variance components in animal models using different relationship matrices. Genetics, selection, evolution : GSE, 52(1), 31.

Bevilacqua V, et al. (2019) A comparison between two semantic deep learning frameworks for the autosomal dominant polycystic kidney disease segmentation based on magnetic resonance images. BMC medical informatics and decision making, 19(Suppl 9), 244.

Gao H, et al. (2019) Bias in estimates of variance components in populations undergoing genomic selection: a simulation study. BMC genomics, 20(1), 956.

Mobiny A, et al. (2019) Risk-Aware Machine Learning Classifier for Skin Lesion Diagnosis. Journal of clinical medicine, 8(8).

Chu TT, et al. (2018) Benefits of testing in both bio-secure and production environments in genomic selection breeding programs for commercial broiler chicken. Genetics, selection, evolution : GSE, 50(1), 52.

Expósito RR, et al. (2018) HSRA: Hadoop-based spliced read aligner for RNA sequencing data. PloS one, 13(7), e0201483.

Melnik S, et al. (2018) Cancer cell specific inhibition of Wnt/?-catenin signaling by forced intracellular acidification. Cell discovery, 4, 37.

Yang X, et al. (2017) ChemTS: an efficient python library for de novo molecular generation. Science and technology of advanced materials, 18(1), 972.

Huang KY, et al. (2017) Identification of natural antimicrobial peptides from bacteria through metagenomic and metatranscriptomic analysis of high-throughput transcriptome data of Taiwanese oolong teas. BMC systems biology, 11(Suppl 7), 131.

Schneider MA, et al. (2016) Glycodelin is a potential novel follow-up biomarker for malignant pleural mesothelioma. Oncotarget, 7(44), 71285.

Georges R, et al. (2012) Sequential biphasic changes in claudin1 and claudin4 expression are correlated to colorectal cancer progression and liver metastasis. Journal of cellular and molecular medicine, 16(2), 260.