Resource Summary Report

Generated by NIF on May 8, 2025

Gist

RRID:SCR_007192
Type: Tool

Proper Citation

Gist (RRID:SCR_007192)

Resource Information

URL: http://bioinformatics.ubc.ca/gist/

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Description: Gist contains software tools for support vector machine classification and for kernel principal components analysis. The SVM portion of Gist is available via an interactive web server. The Gist package contains the following programs: * gist-train-svm trains a support vector machine based upon a given set of labeled training examples, permitting feature selection and leave-one-out cross-validation, * gist-classify applies a trained support vector machine to unlabeled data to produce predicted binary classifications. * gist-fast-classify does the same thing as gist-classify, but uses less time and memory. However, this program only works in conjunction with a linear kernel function. * gist-kpca performs kernel principal components analysis on a given data set, and * gist-project projects a data set onto the components discovered by gist-kpca. In addition to the primary programs, the following auxiliary programs are included: * gist-fselect performs linear feature selection on a given data set, using binary classification labels, * gist-matrix performs basic manipulations of matrices, * gist-score-svm computes performance statistics from the outputs of gist-train-svm and gist-classify, * gist-rfe performs SVM recursive feature elimination on a given data set, * gist-sigmoid converts the discriminant values produced by gist-train-svm into probabilities, * gist2html converts an output file from one of the Gist programs into HTML format, and * gist-kernel computes a square kernel matrix from a given data file, using a user-specified list of kernel transformations. Gist is written in ANSI C. Source code, as well as some pre-compiled versions for popular platforms (Linux, Cygwin) can be downloaded.

Resource Type: source code, service resource, software resource

Funding:

Resource Name: Gist

Resource ID: SCR_007192

Alternate IDs: nlx_68451

Record Creation Time: 20220129T080240+0000

Record Last Update: 20250508T065058+0000

Ratings and Alerts

No rating or validation information has been found for Gist.

No alerts have been found for Gist.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 18 mentions in open access literature.

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

van Strien-Knippenberg IS, et al. (2024) Presenting decision-relevant numerical information to Dutch women aged 50-70 with varying levels of health literacy: Case example of adjuvant systemic therapy for breast cancer. PloS one, 19(9), e0309668.

Lira B, et al. (2022) Large studies reveal how reference bias limits policy applications of self-report measures. Scientific reports, 12(1), 19189.

Gandomkar Z, et al. (2021) Global processing provides malignancy evidence complementary to the information captured by humans or machines following detailed mammogram inspection. Scientific reports, 11(1), 20122.

Y?lmaz NG, et al. (2020) Testing the Effects of Modality and Narration Style on Patients' Information Use in a Lung Cancer Treatment Decision Aid. Medical decision making : an international journal of the Society for Medical Decision Making, 40(8), 990.

Mitsakakis N, et al. (2013) Prediction of Drosophila melanogaster gene function using Support Vector Machines. BioData mining, 6(1), 8.

Sato Y, et al. (2011) Meta-analytic approach to the accurate prediction of secreted virulence effectors in gram-negative bacteria. BMC bioinformatics, 12, 442.

Shazman S, et al. (2011) From face to interface recognition: a differential geometric approach to distinguish DNA from RNA binding surfaces. Nucleic acids research, 39(17), 7390.

Ogawa R, et al. (2010) Computational prediction of nucleosome positioning by calculating the relative fragment frequency index of nucleosomal sequences. FEBS letters, 584(8), 1498.

Le NT, et al. (2010) Sequence-dependent histone variant positioning signatures. BMC genomics, 11 Suppl 4(Suppl 4), S3.

Le NT, et al. (2009) Characterizing nucleosome dynamics from genomic and epigenetic information using rule induction learning. BMC genomics, 10 Suppl 3(Suppl 3), S27.

Skarman A, et al. (2009) Gene set analysis methods applied to chicken microarray expression data. BMC proceedings, 3 Suppl 4(Suppl 4), S8.

Oved K, et al. (2009) Predicting and controlling the reactivity of immune cell populations against cancer. Molecular systems biology, 5, 265.

Fujishima K, et al. (2007) Proteome-wide prediction of novel DNA/RNA-binding proteins using amino acid composition and periodicity in the hyperthermophilic archaeon Pyrococcus furiosus. DNA research : an international journal for rapid publication of reports on genes and genomes, 14(3), 91.

Håndstad T, et al. (2007) Motif kernel generated by genetic programming improves remote homology and fold detection. BMC bioinformatics, 8, 23.

Akerman M, et al. (2007) Does distance matter? Variations in alternative 3' splicing regulation. Nucleic acids research, 35(16), 5487.

Yao Z, et al. (2006) A regression-based K nearest neighbor algorithm for gene function prediction from heterogeneous data. BMC bioinformatics, 7 Suppl 1(Suppl 1), S11.

Kustra R, et al. (2006) A factor analysis model for functional genomics. BMC bioinformatics, 7, 216.

Zhang W, et al. (2004) The functional landscape of mouse gene expression. Journal of biology, 3(5), 21.