Resource Summary Report

Generated by NIF on Apr 8, 2025

A statistical framework for genomic data fusion

RRID:SCR_007219
Type: Tool

Proper Citation

A statistical framework for genomic data fusion (RRID:SCR_007219)

Resource Information

URL: http://noble.gs.washington.edu/proj/sdp-svm/

Proper Citation: A statistical framework for genomic data fusion (RRID:SCR_007219)

Description: A statistical framework for genomic data fusion is a computational framework for integrating and drawing inferences from a collection of genome-wide measurements. Each dataset is represented via a kernel function, which defines generalized similarity relationships between pairs of entities, such as genes or proteins. The kernel representation is both flexible and efficient, and can be applied to many different types of data. Furthermore, kernel functions derived from different types of data can be combined in a straightforward fashion. Recent advances in the theory of kernel methods have provided efficient algorithms to perform such combinations in a way that minimizes a statistical loss function. These methods exploit semidefinite programming techniques to reduce the problem of finding optimizing kernel combinations to a convex optimization problem. Computational experiments performed using yeast genome-wide datasets, including amino acid sequences, hydropathy profiles, gene expression data and known protein-protein interactions, demonstrate the utility of this approach. A statistical learning algorithm trained from all of these data to recognize particular classes of proteins--membrane proteins and ribosomal proteins--performs significantly better than the same algorithm trained on any single type of data. Matlab code to center a kernel matrix and Matlab code for normalization are available.

Resource Type: source code, data or information resource, data set, software resource

Defining Citation: PMID:15130933

Keywords: kernel matrix, random, gene expression, blast, smith-waterman, pfam hmm, hydrophobicity fft, linear interaction, diffusion kernel, protein, membrane, ribosomal

Funding:

Resource Name: A statistical framework for genomic data fusion

Resource ID: SCR_007219

Alternate IDs: nlx_149420

Record Creation Time: 20220129T080240+0000

Record Last Update: 20250407T215633+0000

Ratings and Alerts

No rating or validation information has been found for A statistical framework for genomic data fusion.

No alerts have been found for A statistical framework for genomic data fusion.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 155 mentions in open access literature.

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

Singh S, et al. (2018) Humoral Immunity Profiling of Subjects with Myalgic Encephalomyelitis Using a Random Peptide Microarray Differentiates Cases from Controls with High Specificity and Sensitivity. Molecular neurobiology, 55(1), 633.

Ceglia N, et al. (2018) CircadiOmics: circadian omic web portal. Nucleic acids research, 46(W1), W157.

Burkholder AB, et al. (2018) Muver, a computational framework for accurately calling accumulated mutations. BMC genomics, 19(1), 345.

Wang L, et al. (2017) Integrating genome and transcriptome profiling for elucidating the mechanism of muscle growth and lipid deposition in Pekin ducks. Scientific reports, 7(1), 3837.

Mularoni L, et al. (2017) The Pancreatic Islet Regulome Browser. Frontiers in genetics, 8, 13.

Cayrol F, et al. (2017) THZ1 targeting CDK7 suppresses STAT transcriptional activity and

sensitizes T-cell lymphomas to BCL2 inhibitors. Nature communications, 8, 14290.

Neave MJ, et al. (2017) Transcriptomic analysis of common carp anterior kidney during Cyprinid herpesvirus 3 infection: Immunoglobulin repertoire and homologue functional divergence. Scientific reports, 7, 41531.

Schall KA, et al. (2017) Short bowel syndrome results in increased gene expression associated with proliferation, inflammation, bile acid synthesis and immune system activation: RNA sequencing a zebrafish SBS model. BMC genomics, 18(1), 23.

Baud A, et al. (2017) Genetic Variation in the Social Environment Contributes to Health and Disease. PLoS genetics, 13(1), e1006498.

Cui Z, et al. (2017) KANK1 inhibits cell growth by inducing apoptosis through regulating CXXC5 in human malignant peripheral nerve sheath tumors. Scientific reports, 7, 40325.

Fonseca Costa SS, et al. (2017) Normalisation against Circadian and Age-Related Disturbances Enables Robust Detection of Gene Expression Changes in Liver of Aged Mice. PloS one, 12(1), e0169615.

Overman J, et al. (2017) Pharmacological targeting of the transcription factor SOX18 delays breast cancer in mice. eLife, 6.

Amrein BA, et al. (2017) CADEE: Computer-Aided Directed Evolution of Enzymes. IUCrJ, 4(Pt 1), 50.

Harlen KM, et al. (2017) Subgenic Pol II interactomes identify region-specific transcription elongation regulators. Molecular systems biology, 13(1), 900.

Rhee JS, et al. (2017) Diversity, distribution, and significance of transposable elements in the genome of the only selfing hermaphroditic vertebrate Kryptolebias marmoratus. Scientific reports, 7, 40121.

Loy A, et al. (2017) Lifestyle and Horizontal Gene Transfer-Mediated Evolution of Mucispirillum schaedleri, a Core Member of the Murine Gut Microbiota. mSystems, 2(1).

Liu D, et al. (2017) Decoding of Self-paced Lower-Limb Movement Intention: A Case Study on the Influence Factors. Frontiers in human neuroscience, 11, 560.

Orringer DA, et al. (2017) Rapid intraoperative histology of unprocessed surgical specimens via fibre-laser-based stimulated Raman scattering microscopy. Nature biomedical engineering, 1.

Mayrhofer M, et al. (2017) A novel brain tumour model in zebrafish reveals the role of YAP activation in MAPK- and PI3K-induced malignant growth. Disease models & mechanisms, 10(1), 15.

Nanou A, et al. (2017) The dual role of LSD1 and HDAC3 in STAT5-dependent transcription is determined by protein interactions, binding affinities, motifs and genomic positions. Nucleic acids research, 45(1), 142.