Resource Summary Report

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DeRisi Lab

RRID:SCR_008581
Type: Tool

Proper Citation

DeRisi Lab (RRID:SCR_008581)

Resource Information

URL: http://derisilab.ucsf.edu/

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Description: The DeRisi Lab focuses on genomic approaches to the study of infectious disease. Specifically, we are studying Plasmodium falciparum, the causative agent of the most deadly form of human malaria. We are also involved in a major effort for the discovery of new viral pathogens associated with diseases of unknown etiology. Software tools developed in the lab include: HMMSplicer discovers splice sites in high throughput sequencing datasets without using gene models. HMMSplicer can also be used to find non-canonical junctions as well. HMMSplicer was benchmarked on publickly available A. thaliana, H. sapiens, and P. falciparum datasets and performs well on all genomes. Information about the datasets tested, including the exact command parameters and the final results, is provided. HMMSplicer is implemented in Python and is freely available for all. VersaCount is a simple application to assist with the counting of cells by microscopy. When used with a numeric keypad, it can significantly increase counting efficiency when compared with a traditional clicker. Although it was designed for malaria work, it can be customized for a wide variety of cell counting applications. VersaCount was written by Charlie Kim. ExpressionNet is a program written by Jingchun Zhu that uses Bayesian network learning algorithms to explore relationships among random variables to generate network models. The software has been used to study the transcriptional response to environmental perturbations in budding yeast. Details of the program and the study of yeast transcription using Bayesian Networks was published in PLoS ONE. DNA microarrays may be used to identify microbial species present in environmental and clinical samples. However, automated tools for reliable species identification based on observed microarray hybridization patterns are lacking. We present an algorithm, E-Predict, for microarray-based species identification. ArrayOligoSelector (AOS) is an open source program developed by Jingchun Zhu for the purpose of systematically designing gene-specific long oligonucleotide probes for entire genomes. For each open reading frame, the program optimizes oligo selection based upon several parameters, including uniqueness, complexity, secondary structure, GC content, and 3'' end proximity. AOS also is hosted at SourceForge. This site contains documentation and a user-friendly how-to. ArrayMaker 2 provides high performance robotic control of microarrayer robots with an incredibly intuitive, easy to use interface. ArrayMaker 2 is optimized for use with the new generation of ultra fast linear servo driven arrayers, yet it is backwards compatible with the original MGuide style of ball-screw driven arrayers.

Synonyms: DeRisi Lab

Resource Type: portal, data analysis software, simulation software, software application, image processing software, software resource, laboratory portal, data processing software, organization portal, data or information resource

Keywords: model

Funding:

Resource Name: DeRisi Lab

Resource ID: SCR_008581

Alternate IDs: nif-0000-31884

Record Creation Time: 20220129T080248+0000

Record Last Update: 20250503T060024+0000

Ratings and Alerts

No rating or validation information has been found for DeRisi Lab.

No alerts have been found for DeRisi Lab.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 12 mentions in open access literature.

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

Cheemadan S, et al. (2014) Role of calcium signaling in the transcriptional regulation of the apicoplast genome of Plasmodium falciparum. BioMed research international, 2014, 869401.

Dong Z, et al. (2013) Urea transporter UT-B deletion induces DNA damage and apoptosis in mouse bladder urothelium. PloS one, 8(10), e76952.

Li BW, et al. (2012) Transcription profiling reveals stage- and function-dependent expression patterns in the filarial nematode Brugia malayi. BMC genomics, 13, 184.

Runckel C, et al. (2011) Temporal analysis of the honey bee microbiome reveals four novel viruses and seasonal prevalence of known viruses, Nosema, and Crithidia. PloS one, 6(6), e20656.

Li BW, et al. (2011) Gender-associated genes in filarial nematodes are important for reproduction and potential intervention targets. PLoS neglected tropical diseases, 5(1), e947.

Berretta R, et al. (2010) Cancer biomarker discovery: the entropic hallmark. PloS one, 5(8), e12262.

van Haaften RI, et al. (2009) An integrated bioinformatics approach to improve two-color microarray quality-control: impact on biological conclusions. Genes & nutrition, 4(2), 123.

Li BW, et al. (2009) Transcriptomes and pathways associated with infectivity, survival and immunogenicity in Brugia malayi L3. BMC genomics, 10, 267.

Wang J, et al. (2008) Genome-wide expression patterns and the genetic architecture of a fundamental social trait. PLoS genetics, 4(7), e1000127.

Lodovici M, et al. (2007) Smokers and passive smokers gene expression profiles: correlation with the DNA oxidation damage. Free radical biology & medicine, 43(3), 415.

Eshaghi M, et al. (2007) Global profiling of DNA replication timing and efficiency reveals that efficient replication/firing occurs late during S-phase in S. pombe. PloS one, 2(8), e722.

Liu JM, et al. (2007) Discovery of a mRNA mitochondrial localization element in Saccharomyces cerevisiae by nonhomologous random recombination and in vivo selection. Nucleic acids research, 35(20), 6750.