Resource Summary Report

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PILGRM

RRID:SCR_004749
Type: Tool

Proper Citation

PILGRM (RRID:SCR_004749)

Resource Information

URL: http://pilgrm.princeton.edu

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Description: PILGRM (the platform for interactive learning by genomics results mining) puts advanced supervised analysis techniques applied to enormous gene expression compendia into the hands of bench biologists. This flexible system empowers its users to answer diverse biological questions that are often outside of the scope of common databases in a data-driven manner. This capability allows domain experts to quickly and easily generate hypotheses about biological processes, tissues or diseases of interest. Specifically PILGRM helps biologists generate these hypotheses by analyzing the expression levels of known relevant genes in large compendia of microarray data. PILGRM is for the biologist with a set of proteins relevant to a disease, biological function or tissue of interest who wants to find additional players in that process. It uses a data driven method that provides added value for literature search results by mining compendia of publicly available gene expression datasets using lists of relevant and irrelevant genes (standards). PILGRM produces publication quality PDFs usable as supplementary material to describe the computational approach, standards and datasets. Each PILGRM analysis starts with an important biological question (e.g. What genes are relevant for breast cancer but not mammary tissue in general?). For PILGRM to discover relevant genes, it needs examples of both genes that you would (positive) and would not (negative) find interesting. Lists of these genes are what we call standards and in PILGRM you can build your own standards or you can use standards from common sources that we pre-load for your convenience. PILGRM lets you build your own literature-documented standards so that processes, disease, and tissues that are not well covered in databases of tissue expression, disease, or function can still be used for an analysis.

Abbreviations: PILGRIM

Synonyms: Platform for Interactive Learning by Genomics Results Mining

Resource Type: production service resource, service resource, analysis service resource, data analysis service

Defining Citation: PMID:21653547

Keywords: data mining, gene expression, user directed data mining, bio.tools

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NIGMS R01 GM071966;
NIGMS P50 GM071508;
NCI T32 CA005928

Resource Name: PILGRM

Resource ID: SCR_004749

Alternate IDs: nlx_75372, biotools:pilgrm

Alternate URLs: https://bio.tools/pilgrm

Record Creation Time: 20220129T080226+0000

Record Last Update: 20250412T054919+0000

Ratings and Alerts

No rating or validation information has been found for PILGRM.

No alerts have been found for PILGRM.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 1 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Kacsoh BZ, et al. (2017) Machine Learning Analysis Identifies Drosophila Grunge/Atrophin as an Important Learning and Memory Gene Required for Memory Retention and Social Learning. G3 (Bethesda, Md.), 7(11), 3705.