Resource Summary Report

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MEFIT

RRID:SCR_010743
Type: Tool

Proper Citation

MEFIT (RRID:SCR_010743)

Resource Information

URL: http://avis.princeton.edu/mefit/

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Description: MEFIT is a Microarray Experiment Functional Integration Technology. Given any amount of microarray data, it predicts the probability of pairwise functional relationship for any gene pair within individual biological functions. This web site makes the results of this evaluation available for download and provides an online view of the test set predictions based on hierarchical clustering. As a framework, MEFIT uses the results of many microarray experiments in combination with known biological process annotations (drawn from the Gene Ontology, KEGG, MIPS, or a biologist''s own pathways of interest) to predict new gene pair functional relationships within the given biological functions. Or in other words, MEFIT is a system that takes microarray results and known functional annotations as inputs and produces predicted gene pair functional relationships as output. To make these predictions, MEFIT uses a Bayesian network that consumes microarray data as input observations and produces predicted functional relationships through a single unobserved (except during training) node. Furthermore, to make predictions within the context of individual biological functions, a single Bayesian network structure is replicated once per function of interest. These networks with identical structure are then trained using known functional annotations such that each function''s network learns its own set of conditional probabilities. These probabilities encode how predictive each microarray experiment is of a particular function; for example, a sporulation time course might be very predictive of meiosis, but not much help in determining which genes perform ATP synthesis. We''ve evaluated this system using a collection of 40 microarray data sets and 200 biological processes. Select a biological function from the menu to view the results of clustering the S. cerevisiae genome using MEFIT''s test set predictions within that function as a similarity metric. Alternatively, enter a gene name or ORF identifier to list only functions in which that gene is predicted to be active. We are currently able to offer for download: The MEFIT README file, a Windows version and Linux version.

Abbreviations: MEFIT

Synonyms: Microarray Experiment Functional Integration Technology

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

Defining Citation: PMID:17005538

Funding:

Resource Name: MEFIT

Resource ID: SCR_010743

Alternate IDs: nlx_97939

Record Creation Time: 20220129T080300+0000

Record Last Update: 20250519T203621+0000

Ratings and Alerts

No rating or validation information has been found for MEFIT.

No alerts have been found for MEFIT.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 23 mentions in open access literature.

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

McCoy ZT, et al. (2024) Antibody Response to the Sneathia vaginalis Cytopathogenic Toxin A during Pregnancy. ImmunoHorizons, 8(1), 114.

Efremova I, et al. (2024) Akkermansia muciniphila is associated with normal muscle mass and Eggerthella is related with sarcopenia in cirrhosis. Frontiers in nutrition, 11, 1438897.

Efremova I, et al. (2023) Gut Dysbiosis and Hemodynamic Changes as Links of the Pathogenesis of Complications of Cirrhosis. Microorganisms, 11(9).

Ivashkin V, et al. (2023) Eubiotic effect of rifaximin is associated with decreasing abdominal pain in symptomatic uncomplicated diverticular disease: results from an observational cohort study. BMC gastroenterology, 23(1), 82.

Huang Z, et al. (2023) The Effect of the Microalgae Chlorella vulgaris on the Gut Microbiota of Juvenile Nile Tilapia (Oreochromis niloticus) Is Feeding-Time Dependent. Microorganisms, 11(4).

Paz EA, et al. (2022) Bacterial communities in the gastrointestinal tract segments of helminth-resistant and helminth-susceptible sheep. Animal microbiome, 4(1), 23.

Sun S, et al. (2022) Race, the Vaginal Microbiome, and Spontaneous Preterm Birth. mSystems, 7(3), e0001722.

Kawser AQMR, et al. (2022) Microbiome data reveal significant differences in the bacterial diversity in freshwater rohu (Labeo rohita) across the supply chain in Dhaka, Bangladesh. Letters in applied microbiology, 75(4), 813.

Maslennikov R, et al. (2021) Gut dysbiosis is associated with poorer long-term prognosis in cirrhosis. World journal of hepatology, 13(5), 557.

Islam SMR, et al. (2021) Insights into the nutritional properties and microbiome diversity in

sweet and sour yogurt manufactured in Bangladesh. Scientific reports, 11(1), 22667.

Meldal BHM, et al. (2021) Analysing the yeast complexome-the Complex Portal rising to the challenge. Nucleic acids research, 49(6), 3156.

Kenna JE, et al. (2021) Changes in the Gut Microbiome and Predicted Functional Metabolic Effects in an Australian Parkinson's Disease Cohort. Frontiers in neuroscience, 15, 756951.

Ivashkin V, et al. (2021) Disruption of the pro-inflammatory, anti-inflammatory cytokines and tight junction proteins expression, associated with changes of the composition of the gut microbiota in patients with irritable bowel syndrome. PloS one, 16(6), e0252930.

van Leeuwen J, et al. (2020) Systematic analysis of bypass suppression of essential genes. Molecular systems biology, 16(9), e9828.

Baldini F, et al. (2020) Parkinson's disease-associated alterations of the gut microbiome predict disease-relevant changes in metabolic functions. BMC biology, 18(1), 62.

Gupta SK, et al. (2020) Impact of varied combinatorial mixture of non-fishmeal ingredients on growth, metabolism, immunity and gut microbiota of Lates calcarifer (Bloch, 1790) fry. Scientific reports, 10(1), 17091.

Semenov MV, et al. (2020) Spatial Changes in Microbial Communities along Different Functional Zones of a Free-Water Surface Wetland. Microorganisms, 8(10).

Foysal MJ, et al. (2019) Marked variations in gut microbiota and some innate immune responses of fresh water crayfish, marron (Cherax cainii, Austin 2002) fed dietary supplementation of Clostridium butyricum. PeerJ, 7, e7553.

Chua EG, et al. (2019) The Influence of Modernization and Disease on the Gastric Microbiome of Orang Asli, Myanmars and Modern Malaysians. Microorganisms, 7(6).

Donowitz JR, et al. (2019) Increased Fecal Lactobacillus Is Associated With a Positive Glucose Hydrogen Breath Test in Bangladeshi Children. Open forum infectious diseases, 6(7), ofz266.