

Resource Summary Report

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FARMS

RRID:SCR_001344

Type: Tool

Proper Citation

FARMS (RRID:SCR_001344)

Resource Information

URL: <http://www.bioinf.jku.at/software/farms/farms.html>

Proper Citation: FARMS (RRID:SCR_001344)

Description: Software using a model-based technique for summarizing high-density oligonucleotide array data at probe level for Affymetrix GeneChips. It is based on a factor analysis model for which a Bayesian maximum a posteriori method optimizes the model parameters under the assumption of Gaussian measurement noise.

Abbreviations: FARMS

Synonyms: Factor Analysis for Robust Microarray Summarization

Resource Type: software resource

Defining Citation: [PMID:16473874](#)

Keywords: oligonucleotide array, probe, affymetrix genechip, r, unix, windows, microarray, summarization, bio.tools

Availability: Free, Freely Available

Resource Name: FARMS

Resource ID: SCR_001344

Alternate IDs: OMICS_01995, biotools:farms

Alternate URLs: <https://bio.tools/farms>

Record Creation Time: 20220129T080207+0000

Record Last Update: 20260815T182156+0000

Ratings and Alerts

No rating or validation information has been found for FARMS.

No alerts have been found for FARMS.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 28 mentions in open access literature.

Listed below are recent publications. The full list is available at [dkNET](#) .

Corwin KA, et al. (2025) Solar energy resource availability under extreme and historical wildfire smoke conditions. Nature communications, 16(1), 245.

Snyder KP, et al. (2025) Sexual Signaling and Sociosexual Behaviors in Relation to Rank, Parasites, Hormones, and Age in Male Vervet Monkeys (*Chlorocebus pygerythrus*) in Uganda. American journal of primatology, 87(1), e23711.

KalantarMotamedi Y, et al. (2021) Transcriptional drug repositioning and cheminformatics approach for differentiation therapy of leukaemia cells. Scientific reports, 11(1), 12537.

Obeidat M, et al. (2017) Network-based analysis reveals novel gene signatures in peripheral blood of patients with chronic obstructive pulmonary disease. Respiratory research, 18(1), 72.

Eigner K, et al. (2017) The unfolded protein response impacts melanoma progression by enhancing FGF expression and can be antagonized by a chemical chaperone. Scientific reports, 7(1), 17498.

Yu J, et al. (2016) Environmental Enteric Dysfunction Includes a Broad Spectrum of Inflammatory Responses and Epithelial Repair Processes. Cellular and molecular gastroenterology and hepatology, 2(2), 158.

Lee M, et al. (2016) Application of dynamic topic models to toxicogenomics data. BMC bioinformatics, 17(Suppl 13), 368.

Shannon CP, et al. (2016) SABRE: a method for assessing the stability of gene modules in complex tissues and subject populations. BMC bioinformatics, 17(1), 460.

Chun S, et al. (2016) A High Phosphorus Diet Affects Lipid Metabolism in Rat Liver: A DNA Microarray Analysis. PloS one, 11(5), e0155386.

Brinza L, et al. (2016) Immune signatures of protective spleen memory CD8 T cells. Scientific reports, 6, 37651.

Sweeney T, et al. (2016) The application of transcriptomic data in the authentication of beef derived from contrasting production systems. BMC genomics, 17(1), 746.

Anderson C, et al. (2016) A strategy to discover new organizers identifies a putative heart organizer. *Nature communications*, 7, 12656.

Smith J, et al. (2015) The early immune response to infection of chickens with Infectious Bronchitis Virus (IBV) in susceptible and resistant birds. *BMC veterinary research*, 11, 256.

Obeidat M, et al. (2015) The Effect of Statins on Blood Gene Expression in COPD. *PloS one*, 10(10), e0140022.

Smith J, et al. (2015) Analysis of the early immune response to infection by infectious bursal disease virus in chickens differing in their resistance to the disease. *Journal of virology*, 89(5), 2469.

Perez-Alvarez S, et al. (2015) FARMS: A New Algorithm for Variable Selection. *BioMed research international*, 2015, 319797.

Lee M, et al. (2014) Of text and gene--using text mining methods to uncover hidden knowledge in toxicogenomics. *BMC systems biology*, 8, 93.

Killick KE, et al. (2014) Key Hub and Bottleneck Genes Differentiate the Macrophage Response to Virulent and Attenuated *Mycobacterium bovis*. *Frontiers in immunology*, 5, 422.

Bökenkamp R, et al. (2014) Dlx1 and Rgs5 in the ductus arteriosus: vessel-specific genes identified by transcriptional profiling of laser-capture microdissected endothelial and smooth muscle cells. *PloS one*, 9(1), e86892.

Cun Y, et al. (2013) Network and data integration for biomarker signature discovery via network smoothed T-statistics. *PloS one*, 8(9), e73074.