

Resource Summary Report

Generated by [kravitz2](#) on Sep 18, 2026

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: 20260912T195524+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 [kravitz2](#) .

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.