

Resource Summary Report

Generated by SPARC SAWG on Sep 16, 2026

PESTO

RRID:SCR_016891

Type: Tool

Proper Citation

PESTO (RRID:SCR_016891)

Resource Information

URL: <https://github.com/ICB-DCM/PESTO>

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Description: Software customizable toolbox for parameter estimation in MathWorks MATLAB. Offers scalable algorithms for optimization, uncertainty and identifiability analysis which do not depend on any problem-specific assumptions.

Abbreviations: PESTO

Synonyms: Parameter ESTimation TOolbox, PESTO

Resource Type: data analysis software, data processing software, software application, software resource, software toolkit

Defining Citation: [PMID:29069312](https://pubmed.ncbi.nlm.nih.gov/29069312/)

Keywords: parameter, estimation, MATLAB, algorithm, optimization, uncertainty, identifiability, analysis

Funding: European Union's Horizon ;
German Federal Ministry of Education and Research ;
German Research Foundation via the Graduate School of Quantitative Biosciences
Munich

Availability: Free, Available for download, Freely available

Resource Name: PESTO

Resource ID: SCR_016891

Alternate URLs: <https://zenodo.org/record/579890#.XDZvSlxKiM9>

License: BSD license

Record Creation Time: 20220129T080332+0000

Record Last Update: 20260912T195845+0000

Ratings and Alerts

No rating or validation information has been found for PESTO.

No alerts have been found for PESTO.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 11 mentions in open access literature.

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

Schulz M, et al. (2024) Mathematical multi-compartment modeling of chronic lymphocytic leukemia cell kinetics under ibrutinib. *iScience*, 27(12), 111242.

Assadizadeh M, et al. (2023) Oligomer formation of SARS-CoV-2 ORF8 through 73YIDI76 motifs regulates immune response and non-infusion antiviral interactions. *Frontiers in molecular biosciences*, 10, 1270511.

Wang D, et al. (2023) Modeling early treatment response in AML from cell-free tumor DNA. *iScience*, 26(12), 108271.

Eriksson O, et al. (2022) Combining hypothesis- and data-driven neuroscience modeling in FAIR workflows. *eLife*, 11.

Raimúndez E, et al. (2021) COVID-19 outbreak in Wuhan demonstrates the limitations of publicly available case numbers for epidemiological modeling. *Epidemics*, 34, 100439.

Raimúndez E, et al. (2020) Model-based analysis of response and resistance factors of cetuximab treatment in gastric cancer cell lines. *PLoS computational biology*, 16(3), e1007147.

Schuh L, et al. (2020) H4K20 Methylation Is Differently Regulated by Dilution and Demethylation in Proliferating and Cell-Cycle-Arrested *Xenopus* Embryos. *Cell systems*, 11(6), 653.

Alabert C, et al. (2020) Domain Model Explains Propagation Dynamics and Stability of Histone H3K27 and H3K36 Methylation Landscapes. *Cell reports*, 30(4), 1223.

Hross S, et al. (2018) Mechanistic description of spatial processes using integrative modelling of noise-corrupted imaging data. *Journal of the Royal Society, Interface*, 15(149), 20180600.

Fröhlich F, et al. (2018) Efficient Parameter Estimation Enables the Prediction of Drug Response Using a Mechanistic Pan-Cancer Pathway Model. *Cell systems*, 7(6), 567.

Bast L, et al. (2018) Increasing Neural Stem Cell Division Asymmetry and Quiescence Are Predicted to Contribute to the Age-Related Decline in Neurogenesis. *Cell reports*, 25(12), 3231.