

# Resource Summary Report

Generated by [ASWG](#) on Aug 2, 2026

## Inferelator

RRID:SCR\_000218

Type: Tool

---

### Proper Citation

Inferelator (RRID:SCR\_000218)

---

### Resource Information

**URL:** <http://bonneaulab.bio.nyu.edu/networks.html>

**Proper Citation:** Inferelator (RRID:SCR\_000218)

**Description:** THIS RESOURCE IS NO LONGER IN SERVICE. Documented on July 31,2025. Algorithm for learning parsimonious regulatory networks from systems biology data sets de novo. Software that utilizes inference algorithm to model genetic regulatory networks.Inferelator 2.0 is scalable framework for reconstruction of dynamic regulatory network models., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

**Resource Type:** software resource

**Defining Citation:** [PMID:23525069](#), [PMID:16686963](#), [PMID:19964678](#)

**Keywords:** modeling, inference algorithm, halobacterium, genetic regulatory network, learning regulatory network, model gene regulatory network

**Availability:** THIS RESOURCE IS NO LONGER IN SERVICE

**Resource Name:** Inferelator

**Resource ID:** SCR\_000218

**Alternate IDs:** OMICS\_01684

**Record Creation Time:** 20220129T080200+0000

**Record Last Update:** 20260801T190113+0000

---

### Ratings and Alerts

No rating or validation information has been found for Inferelator.

No alerts have been found for Inferelator.

---

## Data and Source Information

**Source:** [SciCrunch Registry](#)

---

## Usage and Citation Metrics

We found 3 mentions in open access literature.

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

Dong X, et al. (2015) Reverse enGENEering of Regulatory Networks from Big Data: A Roadmap for Biologists. Bioinformatics and biology insights, 9, 61.

Arrieta-Ortiz ML, et al. (2015) An experimentally supported model of the Bacillus subtilis global transcriptional regulatory network. Molecular systems biology, 11(11), 839.

Greenfield A, et al. (2013) Robust data-driven incorporation of prior knowledge into the inference of dynamic regulatory networks. Bioinformatics (Oxford, England), 29(8), 1060.