

Resource Summary Report

Generated by [nidm-terms](#) on Jul 29, 2026

Bayesian Output Analysis Program

RRID:SCR_007141

Type: Tool

Proper Citation

Bayesian Output Analysis Program (RRID:SCR_007141)

Resource Information

URL: <http://www.public-health.uiowa.edu/boa>

Proper Citation: Bayesian Output Analysis Program (RRID:SCR_007141)

Description: BOA is an R/S-PLUS program for carrying out convergence diagnostics and statistical and graphical analysis of Monte Carlo sampling output. It can be used as an output processor for the BUGS software or for any other program which produces sampling output. BOA includes all of the analysis options found in CODA, plus a few others. It is designed to be faster, more efficient, and offer more flexible data management than CODA. BOA can be used at the command-line or with the supplied menu-driven interface. Either way, the program enables the user to focus on the analysis at hand rather than on the manipulation of data. Sponsors: This resource is supported by the University of Iowa. Keywords: Bayesian, Analysis, Program, Diagnostics, Statistical, Graphical, Software,

Synonyms: BOA

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

Resource Name: Bayesian Output Analysis Program

Resource ID: SCR_007141

Alternate IDs: nif-0000-30165

Record Creation Time: 20220129T080240+0000

Record Last Update: 20260727T040422+0000

Ratings and Alerts

No rating or validation information has been found for Bayesian Output Analysis Program.

No alerts have been found for Bayesian Output Analysis Program.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 4 mentions in open access literature.

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

Leil TA, et al. (2014) A bayesian perspective on estimation of variability and uncertainty in mechanism-based models. CPT: pharmacometrics & systems pharmacology, 3(6), e121.

de Maturana EL, et al. (2010) Modeling relationships between calving traits: a comparison between standard and recursive mixed models. Genetics, selection, evolution : GSE, 42(1), 1.

M??rk AK, et al. (2009) Bayesian population analysis of a washin-washout physiologically based pharmacokinetic model for acetone. Toxicology and applied pharmacology, 240(3), 423.

Rosales RA, et al. (2009) Allosteric control of gating mechanisms revisited: the large conductance Ca²⁺-activated K⁺ channel. Biophysical journal, 96(10), 3987.