

Inference software

pyABC	Python framework for efficient distributed ABC-SMC (Sequential Monte Carlo).
PyMC	A Python package for Bayesian statistical modeling and probabilistic machine learning.
DIY-ABC	Software for fit of genetic data to complex situations. Comparison of competing models. Parameter estimation. Computation of bias and precision measures for a given model and known parameters values.
abc R package	Several ABC algorithms for performing parameter estimation and model selection. Nonlinear heteroscedastic regression methods for ABC. Cross-validation tool.
EasyABC R package	Several algorithms for performing efficient ABC sampling schemes, including 4 sequential sampling schemes and 3 MCMC schemes.
ABC-SysBio	Python package. Parameter inference and model selection for dynamical systems. Combines ABC rejection sampler, ABC SMC for parameter inference, and ABC SMC for model selection. Compatible with models written in Systems Biology Markup Language (SBML). Deterministic and stochastic models.
ABCtoolbox	Open source programs for various ABC algorithms including rejection sampling, MCMC without likelihood, a particle-based sampler, and ABC-GLM. Compatibility with most simulation and summary statistics computation programs.
msBayes	Open source software package consisting of several C and R programs that are run with a Perl "front-end". Hierarchical coalescent models. Population genetic data from multiple co-distributed species.
PopABC	Software package for inference of the pattern of demographic divergence. Coalescent simulation. Bayesian model choice.
ONeSAMP	Web-based program to estimate the effective population size from a sample of microsatellite genotypes. Estimates of effective population size, together with 95% credible limits.
ABC4F	Software for estimation of F-statistics for dominant data.
2BAD	2-event Bayesian Admixture. Software allowing up to two independent admixture events with up to three parental populations. Estimation of several parameters (admixture, effective sizes, etc.). Comparison of pairs of admixture models.
ELFI	Engine for Likelihood-Free Inference. ELFI is a statistical software package written in Python for Approximate Bayesian Computation (ABC), also known e.g. as likelihood-free inference, simulator-based inference, approximative Bayesian inference etc.
ABCPy	Python package for ABC and other likelihood-free inference schemes. Several state-of-the-art algorithms available. Provides quick way to integrate existing generative (from C++, R etc.), user-friendly parallelization using MPI or Spark and summary statistics learning (with neural network or linear regression).
sbi	A Python toolbox for simulation-based inference.



- Open-source Python library for LFI
 - `pip install elfi`
 - `conda install elfi`
 - <http://github.com/elfi-dev/elfi>
- Practitioners:
 - Library of LFI-methods
- Methodologists:
 - Platform for new methods
 - parallelisation, data storing, random number seeding
 - ELFI-models

ELFI: Engine for Likelihood-Free Inference

Jarno Lintusaari
Henri Vuollekoski
Antti Kangasrääsiö
Kusti Skytén
Marko Järvenpää
Pekka Marttinen

*Department of Computer Science
Aalto University
00076 Aalto, Finland*

Michael U. Gutmann
*School of Informatics
The University of Edinburgh
Edinburgh, EH8 9AB, UK*

Aki Vehtari *
*Department of Computer Science
Aalto University
00076 Aalto, Finland*

Jukka Corander *
*Department of Biostatistics
University of Oslo
0317 OSLO, Norway*

Samuel Kaski *
*Department of Computer Science
Aalto University
00076 Aalto, Finland*

JARNO.LINTUSAARI@AALTO.FI
HENRI.VUOLLEKOSKI@AALTO.FI
ANTTI.KANGASRAASIO@AALTO.FI
KUSTI.SKYTEN@AALTO.FI
MARKO.J.JARVENPAA@AALTO.FI
PEKKA.MARTTINEN@AALTO.FI

MICHAEL.GUTMANN@ED.AC.UK

AKI.VEHTARI@AALTO.FI

JUKKA.CORANDER@MEDISIN.UIO.NO

SAMUEL.KASKI@AALTO.FI

Editor: Alexandre Gramfort

Abstract

Engine for Likelihood-Free Inference (ELFI) is a Python software library for performing likelihood-free inference (LFI). ELFI provides a convenient syntax for arranging components in LFI, such as priors, simulators, summaries or distances, to a network called ELFI graph. The components can be implemented in a wide variety of languages. The stand-alone ELFI graph can be used with any of the available inference methods without modifications. A central method implemented in ELFI is Bayesian Optimization for Likelihood-Free Inference (BOLFI), which has recently been shown to accelerate likelihood-free inference up to several orders of magnitude by surrogate-modelling the distance. ELFI also has an inbuilt support for output data storing for reuse and analysis, and supports parallelization of computation from multiple cores up to a cluster environment. ELFI is designed to be extensible and provides interfaces for widening its functionality. This makes the adding of new inference methods to ELFI straightforward and automatically compatible with the inbuilt features.

*. Equal contribution