

# Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 7, 2026

## [BAli-Phy](#)

RRID:SCR\_023976

Type: Tool

### Proper Citation

BAli-Phy (RRID:SCR\_023976)

### Resource Information

**URL:** <http://www.bali-phy.org>

**Proper Citation:** BAli-Phy (RRID:SCR\_023976)

**Description:** Software application as simultaneous Bayesian inference of alignment and phylogeny. Used to estimate multiple sequence alignments and evolutionary trees from DNA, amino acid, or codon sequences. to explore the joint space of alignment and phylogeny given molecular sequence data. BAli-Phy version 3 is model based co-estimation of alignment and phylogeny. Version 3 is substantially faster for large trees, and implements covarion models, additional codon models and other new models. Implements ancestral state reconstruction, allows prior selection for all model parameters, and can also analyze multiple genes simultaneously.

**Synonyms:** bali-phy, BAli-Phy version 3

**Resource Type:** software application, software resource, source code

**Defining Citation:** [PMID:16679334](#), [PMID:33677478](#)

**Keywords:** estimate multiple sequence alignments, estimate evolutionary trees, DNA sequences, amino acid sequences, codon sequences,

**Availability:** Free, Available for download, Freely available

**Resource Name:** BAli-Phy

**Resource ID:** SCR\_023976

**Alternate IDs:** OMICS\_03734

**Alternate URLs:** <https://sources.debian.org/src/bali-phy/>

**Record Creation Time:** 20230824T050211+0000

**Record Last Update:** 20260905T133102+0000

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## Ratings and Alerts

No rating or validation information has been found for BALi-Phy.

No alerts have been found for BALi-Phy.

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## Data and Source Information

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

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## Usage and Citation Metrics

We have not found any literature mentions for this resource.