Resource Summary Report

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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: source code, software application, software resource

Defining Citation: PMID:16679334, PMID:33677478

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

Funding:

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: 20250412T060615+0000

Ratings and Alerts

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

No alerts have been found for BAli-Phy.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We have not found any literature mentions for this resource.