Resource Summary Report

Generated by dkNET on May 20, 2025

PhyDyn

RRID:SCR_018544
Type: Tool

Proper Citation

PhyDyn (RRID:SCR_018544)

Resource Information

URL: https://github.com/mrc-ide/PhyDyn

Proper Citation: PhyDyn (RRID:SCR_018544)

Description: Sofware package for performing Bayesian phylogenetic inference under models that deal with structured populations with complex population dynamics. Enables simultaneous estimation of epidemiological parameters and pathogen phylogenies. Epidemiological modelling in BEAST.

Resource Type: software resource, software application, simulation software

Defining Citation: PMID:30422979

Keywords: Bayesian phylogenetic inference, epidemiological modelling, epidemiological parameter estimation, pathogen phylogeny estimation

Funding: NIGMS U01 GM110749;
MRC Centre for Global Infectious Disease Analysis

Availability: Free, Available for download, Freely available

Resource Name: PhyDyn

Resource ID: SCR_018544

Record Creation Time: 20220129T080340+0000

Record Last Update: 20250519T204038+0000

Ratings and Alerts

No rating or validation information has been found for PhyDyn.

No alerts have been found for PhyDyn.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 10 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

Wilinski M, et al. (2024) Congruity of genomic and epidemiological data in modelling of local cholera outbreaks. Proceedings. Biological sciences, 291(2019), 20232805.

Park Y, et al. (2023) Epidemiological inference for emerging viruses using segregating sites. Nature communications, 14(1), 3105.

Volz E, et al. (2021) Evaluating the Effects of SARS-CoV-2 Spike Mutation D614G on Transmissibility and Pathogenicity. Cell, 184(1), 64.

Ragonnet-Cronin M, et al. (2021) Genetic evidence for the association between COVID-19 epidemic severity and timing of non-pharmaceutical interventions. Nature communications, 12(1), 2188.

Geidelberg L, et al. (2021) Genomic epidemiology of a densely sampled COVID-19 outbreak in China. Virus evolution, 7(1), veaa102.

Wu H, et al. (2021) Nucleocapsid mutations R203K/G204R increase the infectivity, fitness, and virulence of SARS-CoV-2. Cell host & microbe, 29(12), 1788.

Hicks JT, et al. (2020) Agricultural and geographic factors shaped the North American 2015 highly pathogenic avian influenza H5N2 outbreak. PLoS pathogens, 16(1), e1007857.

Miller D, et al. (2020) Full genome viral sequences inform patterns of SARS-CoV-2 spread into and within Israel. Nature communications, 11(1), 5518.

Moreno GK, et al. (2020) Distinct patterns of SARS-CoV-2 transmission in two nearby communities in Wisconsin, USA. medRxiv : the preprint server for health sciences.

Moreno GK, et al. (2020) Revealing fine-scale spatiotemporal differences in SARS-CoV-2 introduction and spread. Nature communications, 11(1), 5558.