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# genieR: An R package for inference of demographic history of phylogenies

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## Software

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## Summary

genieR is an R package (R Core Team (2016)) for the inference of demographic history from reconstructed molecular phylogenies (see Dearlove, Xiang, & Frost (2017) for one application), modeled after the C++ package GENIE (Pybus & Rambaut, 2002). The package processes phylogenetic trees in Newick format, in which taxa may be sampled either at the same time (isochronous) or at different times (heterochronous); the latter are particularly common in the analysis of pathogen sequence data. In addition to extracting basic information from a particular phylogeny such as sampling and coalescent times, genieR also fits a coalescent model (Kingman (1982)) under several demographic scenarios, including constant population size, exponential growth, expansion growth, logistic growth, with both continuous and piecewise variants. The fit of different models can be compared using Akaike's Information Criterion (AIC) (Akaike, 1973) values. genieR uses C++ code as an option for better computational performance, and models can be fit either using maximum likelihood or Markov Chain Monte Carlo (Hastings, 1970). genieR can also simulate phylogenies under different demographic models.

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