

## IB200A - R packages for evolutionary biology

*Last updated: 04/10/12*

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Each link contains a summary and the .pdf documentation of the package contents.

<a href="#">ade4</a>	Analysis of Ecological Data : Exploratory and Euclidean methods in Environmental sciences
<a href="#">adegenet</a>	an R package for the exploratory analysis of genetic and genomic data
<a href="#">adephylo</a>	exploratory analyses for the phylogenetic comparative method
<a href="#">aqp</a>	Algorithms for Quantitative Pedology
<a href="#">auteur</a>	Bayesian sampler of the trait-evolutionary process
<a href="#">bcool</a>	Bringing to light significant Columns correlated with Organism Labels
<a href="#">BoSSA</a>	a Bunch of Structure and Sequence Analysis
<a href="#">caper</a>	Comparative Analyses of Phylogenetics and Evolution in R
<a href="#">clue</a>	Cluster ensembles
<a href="#">distory</a>	Distance Between Phylogenetic Histories
<a href="#">diversitree</a>	Comparative phylogenetic analyses of diversification
<a href="#">FD</a>	Measuring functional diversity (FD) from multiple traits, and other tools for functional ecology
<a href="#">geiger</a>	Analysis of evolutionary diversification
<a href="#">hierfstat</a>	Estimation and tests of hierarchical F-statistics
<a href="#">HMPTrees</a>	Statistical Object Oriented Data Analysis of RDP-based Taxonomic trees from Human Microbiome Data: Modeling, Visualization, and Two-Group Comparison
<a href="#">iteRates</a>	Parametric rate comparison
<a href="#">kernelPop</a>	Spatially explicit population genetic simulations
<a href="#">laser</a>	Likelihood Analysis of Speciation/Extinction Rates from Phylogenies
<a href="#">motmot</a>	Models of Trait Macroevolution on Trees
<a href="#">oposSOM</a>	Package for analysis and visualization of metagenes
<a href="#">ouch</a>	Ornstein-Uhlenbeck models for phylogenetic comparative hypotheses
<a href="#">OUwie</a>	Analysis of evolutionary rates in an OU framework
<a href="#">paleotree</a>	Paleontological and Phylogenetic Analyses of Evolution

<a href="#"><u>pcrcoal</u></a>	A package implementing the coalescent approach to PCR simulation developed by Weiss and von Haeseler (NAR, 1997)
<a href="#"><u>pegas</u></a>	Population and Evolutionary Genetics Analysis System
<a href="#"><u>phangorn</u></a>	Phylogenetic analysis in R
<a href="#"><u>phybase</u></a>	Basic functions for phylogenetic analysis
<a href="#"><u>phyclust</u></a>	Phylogenetic Clustering (Phyloclustering)
<a href="#"><u>phyext</u></a>	An extension of some of the classes in phylobase. Tree objects now support subnodes on branches
<a href="#"><u>phylobase</u></a>	Base package for phylogenetic structures and comparative data
<a href="#"><u>phyloclim</u></a>	Integrating phylogenetics and climatic niche modeling
<a href="#"><u>phylosim</u></a>	R package for simulating biological sequence evolution
<a href="#"><u>phylotools</u></a>	Phylogenetic tools for Eco-phylogenetics
<a href="#"><u>phytools</u></a>	Phylogenetic Tools for comparative biology (and other things)
<a href="#"><u>picante</u></a>	R tools for integrating phylogenies and ecology
<a href="#"><u>pmc</u></a>	Phylogenetic Monte Carlo
<a href="#"><u>rdryad</u></a>	Dryad API interface
<a href="#"><u>rmetasim</u></a>	An individual-based population genetic simulation environment
<a href="#"><u>rphast</u></a>	R interface to PHAST software for comparative genomics
<a href="#"><u>spider</u></a>	Species Identity and Evolution in R
<a href="#"><u>treebase</u></a>	R interface to TreeBASE
<a href="#"><u>treelet</u></a>	Treelet
<a href="#"><u>TreePar</u></a>	Estimating speciation and extinction rates based on phylogenies
<a href="#"><u>TreeSim</u></a>	Simulating trees under the birth-death model