IB200A - R packages for evolutionary biology

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

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| [ade4](http://ie.archive.ubuntu.com/CRAN/web/packages/ade4/index.html) | Analysis of Ecological Data : Exploratory and Euclidean methods in Environmental sciences |
| [adegenet](http://ie.archive.ubuntu.com/CRAN/web/packages/adegenet/index.html) | an R package for the exploratory analysis of genetic and genomic data |
| [adephylo](http://ie.archive.ubuntu.com/CRAN/web/packages/adephylo/index.html) | exploratory analyses for the phylogenetic comparative method |
| [aqp](http://ie.archive.ubuntu.com/CRAN/web/packages/aqp/index.html) | Algorithms for Quantitative Pedology |
| [auteur](http://ie.archive.ubuntu.com/CRAN/web/packages/auteur/index.html) | Bayesian sampler of the trait-evolutionary process |
| [bcool](http://ie.archive.ubuntu.com/CRAN/web/packages/bcool/index.html) | Bringing to light significant Columns correlated with Organism Labels |
| [BoSSA](http://ie.archive.ubuntu.com/CRAN/web/packages/BoSSA/index.html) | a Bunch of Structure and Sequence Analysis |
| [caper](http://ie.archive.ubuntu.com/CRAN/web/packages/caper/index.html) | Comparative Analyses of Phylogenetics and Evolution in R |
| [clue](http://ie.archive.ubuntu.com/CRAN/web/packages/clue/index.html) | Cluster ensembles |
| [distory](http://ie.archive.ubuntu.com/CRAN/web/packages/distory/index.html) | Distance Between Phylogenetic Histories |
| [diversitree](http://ie.archive.ubuntu.com/CRAN/web/packages/diversitree/index.html) | Comparative phylogenetic analyses of diversification |
| [FD](http://ie.archive.ubuntu.com/CRAN/web/packages/FD/index.html) | Measuring functional diversity (FD) from multiple traits, and other tools for functional ecology |
| [geiger](http://ie.archive.ubuntu.com/CRAN/web/packages/geiger/index.html) | Analysis of evolutionary diversification |
| [hierfstat](http://ie.archive.ubuntu.com/CRAN/web/packages/hierfstat/index.html) | Estimation and tests of hierarchical F-statistics |
| [HMPTrees](http://ie.archive.ubuntu.com/CRAN/web/packages/HMPTrees/index.html) | Statistical Object Oriented Data Analysis of RDP-based Taxonomic trees from Human Microbiome Data: Modeling, Visualization, and Two-Group Comparison |
| [iteRates](http://ie.archive.ubuntu.com/CRAN/web/packages/iteRates/index.html) | Parametric rate comparison |
| [kernelPop](http://ie.archive.ubuntu.com/CRAN/web/packages/kernelPop/index.html) | Spatially explicit population genetic simulations |
| [laser](http://ie.archive.ubuntu.com/CRAN/web/packages/laser/index.html) | Likelihood Analysis of Speciation/Extinction Rates from Phylogenies |
| [motmot](http://ie.archive.ubuntu.com/CRAN/web/packages/motmot/index.html) | Models of Trait Macroevolution on Trees |
| [oposSOM](http://ie.archive.ubuntu.com/CRAN/web/packages/oposSOM/index.html) | Package for analysis and visualization of metagenes |
| [ouch](http://ie.archive.ubuntu.com/CRAN/web/packages/ouch/index.html) | Ornstein-Uhlenbeck models for phylogenetic comparative hypotheses |
| [OUwie](http://ie.archive.ubuntu.com/CRAN/web/packages/OUwie/index.html) | Analysis of evolutionary rates in an OU framework |
| [paleotree](http://ie.archive.ubuntu.com/CRAN/web/packages/paleotree/index.html) | Paleontological and Phylogenetic Analyses of Evolution |
| [pcrcoal](http://ie.archive.ubuntu.com/CRAN/web/packages/pcrcoal/index.html) | A package implementing the coalescent approach to PCR simulation developed by Weiss and von Haeseler (NAR, 1997) |
| [pegas](http://ie.archive.ubuntu.com/CRAN/web/packages/pegas/index.html) | Population and Evolutionary Genetics Analysis System |
| [phangorn](http://ie.archive.ubuntu.com/CRAN/web/packages/phangorn/index.html) | Phylogenetic analysis in R |
| [phybase](http://ie.archive.ubuntu.com/CRAN/web/packages/phybase/index.html) | Basic functions for phylogenetic analysis |
| [phyclust](http://ie.archive.ubuntu.com/CRAN/web/packages/phyclust/index.html) | Phylogenetic Clustering (Phyloclustering) |
| [phyext](http://ie.archive.ubuntu.com/CRAN/web/packages/phyext/index.html) | An extension of some of the classes in phylobase. Tree objects now support subnodes on branches |
| [phylobase](http://ie.archive.ubuntu.com/CRAN/web/packages/phylobase/index.html) | Base package for phylogenetic structures and comparative data |
| [phyloclim](http://ie.archive.ubuntu.com/CRAN/web/packages/phyloclim/index.html) | Integrating phylogenetics and climatic niche modeling |
| [phylosim](http://ie.archive.ubuntu.com/CRAN/web/packages/phylosim/index.html) | R package for simulating biological sequence evolution |
| [phylotools](http://ie.archive.ubuntu.com/CRAN/web/packages/phylotools/index.html) | Phylogenetic tools for Eco-phylogenetics |
| [phytools](http://ie.archive.ubuntu.com/CRAN/web/packages/phytools/index.html) | Phylogenetic Tools for comparative biology (and other things) |
| [picante](http://ie.archive.ubuntu.com/CRAN/web/packages/picante/index.html) | R tools for integrating phylogenies and ecology |
| [pmc](http://ie.archive.ubuntu.com/CRAN/web/packages/pmc/index.html) | Phylogenetic Monte Carlo |
| [rdryad](http://ie.archive.ubuntu.com/CRAN/web/packages/rdryad/index.html) | Dryad API interface |
| [rmetasim](http://ie.archive.ubuntu.com/CRAN/web/packages/rmetasim/index.html) | An individual-based population genetic simulation environment |
| [rphast](http://ie.archive.ubuntu.com/CRAN/web/packages/rphast/index.html) | R interface to PHAST software for comparative genomics |
| [spider](http://ie.archive.ubuntu.com/CRAN/web/packages/spider/index.html) | Species Identity and Evolution in R |
| [treebase](http://ie.archive.ubuntu.com/CRAN/web/packages/treebase/index.html) | R interface to TreeBASE |
| [treelet](http://ie.archive.ubuntu.com/CRAN/web/packages/treelet/index.html) | Treelet |
| [TreePar](http://ie.archive.ubuntu.com/CRAN/web/packages/TreePar/index.html) | Estimating speciation and extinction rates based on phylogenies |
| [TreeSim](http://ie.archive.ubuntu.com/CRAN/web/packages/TreeSim/index.html) | Simulating trees under the birth-death model |