package_notes

library(dplyr) library(plyr) library(ggplot2) library(knitr) library(cluster) library(klaR)

Analyses of Phylogenetics and Evolution

- call: library(ape)

- description: ape provides functions for reading and manipulating phylogenetic trees and DNA sequences, computing DNA distances, estimating trees with distance-based methods, and a range of methods for comparative analyses and analysis of diversification.

- use: visualization of clusters

- note: The complete list of functions can be displayed with library(help = ape).