Guane: A flexible Shiny platform for learning, teaching, and analyses in phylogenetic comparative biology

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Our main goal

Develop a shiny platform to perform interactive evolutive analysis in R language

What is new?

Users will not need to know R scripting to perform their analyses

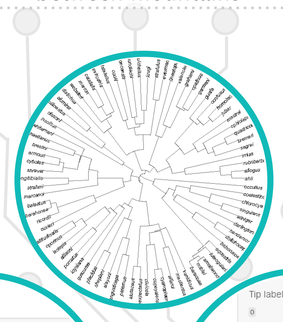


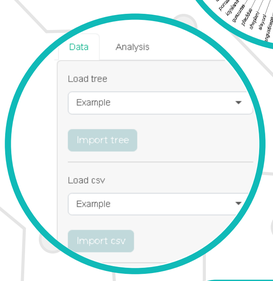
Why this names?



GUANE (in Chibcha) means tree ...

"a tree (*Cavanilesia chicamochae*) that looks how a silver thread (Chicamocha river) create a desert between mountains"





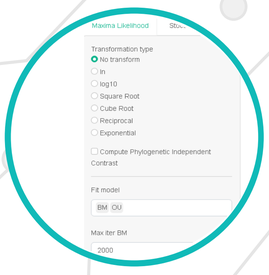


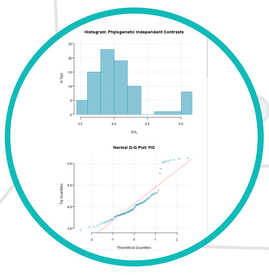
What is Shiny?

Shiny is an R package that makes it easy to build interactive web apps straight from R[1]

How does Shiny work?

Shiny = R + HTML + JS + CSS







Loading data

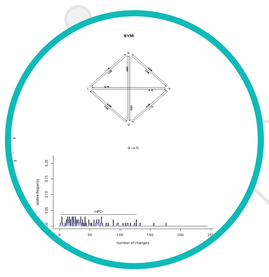
Analysis
Discrete characters:
Maximum Likelihood

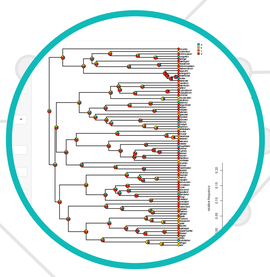
Analysis
Continuous characters:
Maximum Likelihood

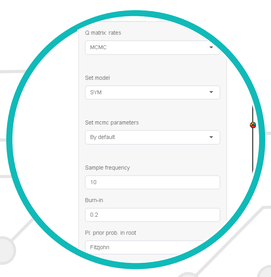
Analysis
Discrete characters:
Bayesian MCMC

Analysis
Continuous characters:
Bayesian MCMC

Extra tools

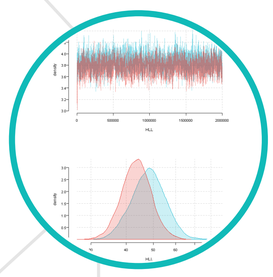


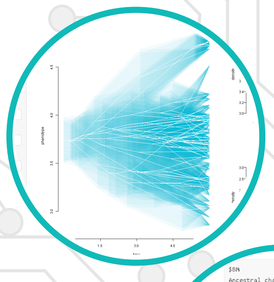




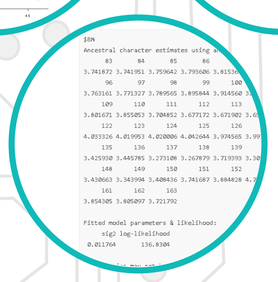












Guane: Version 1.0

- **Ancestral character estimation**[2, 3, 4, 5]
- **Discrete states**
  - Maximum Likelihood estimation (Marginal and joint reconstruction)
  - Estimation under standard (ER, SYM, ARD) and custom models
  - Model averaged ancestral states
  - Constumizable bayesian MCMC analysis
  - Visualization of posterior probabilities in nodes or for a single state.
  - Visualization of number of changes between two states.
- **Continuous states**
  - Variable transformation and visualization of phylogenetic independent contrasts (PIC)
  - Maximum Likelihood estimation under models such as BM, EB, OU
  - Model comparison by AIC
  - Costumizable bayesian ancestral state estimation
  - Visualization of ancestral states and stochastic mapping
- **Load data and extra tools**
  - Input in Newick/Nexus format
  - Export outcome in RDS or TXT format
  - Every panel has a console to get information about the process
  - For continuous characters, user can plot the result as a traitgram or as a phenogram

Where do you find the app?

What is it coming?

- Include analyses such as diversification with phylogenies, time and density dependent diversification, SSE models, among other.
- Create a module to teaching and/or self-instructing of basic analyses of phylogenetic reconstruction and comparative biology.
- Create a panel where users can edit all plots from the analyses to undertaken in this platform
- Create a panel where users can download a script with the functions and parameters used to improve reproducibility and replicability in phylogenetic research.
- Create a multilingual platform (English and Spanish)

Resources

- 1 RStudio, Inc. 2014. Shiny. https://CRAN.R-project.org/package=shiny
- 2 Revell, L. J. 2012. Phytools. https://CRAN.R-project.org/package=phytools
- 3 Paradis, E. et al. 2004. Ape. https://CRAN.R-project.org/package=ape
- 4 Beauieu J. et al. 2012. corHMM. https://CRAN.R-project.org/package=corHMM

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