ARCHIPELAGO

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November 1, 2015

1 Introduction

"Archipelago" is the name of a generative phylogeny-based model that simultaneously incorporates the diversification processes of speciation and extinction nad the biogeographical processes of area gain ("dispersal") and area loss ("extirpation"), with these processes being differentially regulated by ecological or other traits that are themselves co-evolving on the phylogeny. The theory and background to this model and its usage is described in the following paper:

This software project, "archipelago" presents a suite of programs to generate and analyze data under the Archipelago model. The primary objective of the analysis is *model selection*: i.e., statistically identifying the model that generated a particular set of data. "archipelago" is, thus, a computational biogeographical model selection analysis package that exploits the power and flexibility of the Archipelago model to allow you to ask and answer historical biogeographical questions of a nature and complexity that are not possible under any other approach. In particular, instead of asking questions about ancestral area patterns, you can ask questions about processes, and how some processes (e.g., ecology) affect other processes (e.g., dispersal or speciation).

2 Installation

2.1 Pre-requisites

- Python 2.7 or higher
- DendroPy Phylogenetic Computing Library, version 4 or above (http://dendropy.org).

- R (http://www.r-project.org/)
- The following R packages:
  - adegenet
  - picante
  - BioGeoBears
  - GEIGER

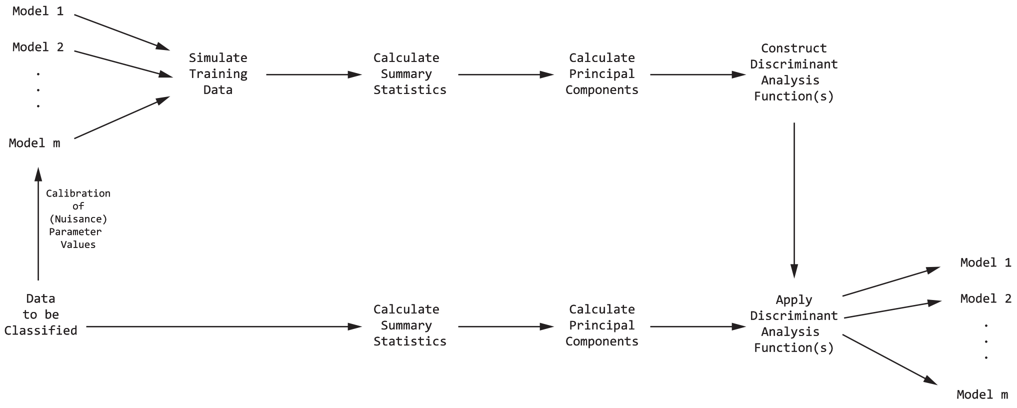
2.2 Installation from Source

Run the following in the top-level directory of the project:

```
python setup.py install
```

3 Usage

4 Overview of Workflow


Model 1
Model 2
.
.
.
Model m
Simulate Training Data
Calculate Summary Statistics
Calculate Principal Components
Construct Discriminant Analysis Function(s)
Calibration of (Nuisance) Parameter Values
Data to be Classified
Calculate Summary Statistics
Calculate Principal Components
Apply Discriminant Analysis Function(s)
Model 1
Model 2
.
.
.
Model m

Let D be the *target* data, consisting of an ultrametric phylogeny with each of the tips associated with a geographic range (presence/absence over one or more areas) as well as with set of trait states. Let $\mathbf{M} = \{M_1, M_2, ...M_m\}$ be a set of k models that we are interested in studying. Let $S(\cdot)$ be a function that takes a set of data returns a set of summary statistics. Our analytical objective is, for each $M_i, M_i \in \mathbf{M}$, estimate the probability that it generated the target data D, relative to all the other models in $\mathbf{M}$. The operational procedure consists of the following steps:

1. **Training Data Simulation**: For each $M_i, M_i \in \mathbf{M}$, simulate n replicates of data, D^{*i}. We label each replicate of this data with the name of the model that generated it (e.g., "Model i"). The set of all data so generated constitutes the training data, $\mathbf{D}^*$.

2. **Summary Statistic Calculation**: Calculate summary statistics on the training data to yield, $S(\mathbf{D}^*)$, and summary statistics on the target data to yield $S(D)$.

3. **Classification**: Construct a Discriminant Analysis (DA) function on principal components (PC) calculated on the training data set summary statistics, $S(\mathbf{D}^*)$; apply the discriminant analysis function to principal components calculated on the summary statistics of the target data, $S(D)$.