## Using the PCMBase parametrization API

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knitr::opts\_chunk\$set(echo = TRUE)

library(phytools)

## Loading required package: ape

## Loading required package: maps

library(PCMBase)

## Introduction

Model parameters are the key object of interest in every phylogenetic comparative method. PCMBase provides a powerful interface for specifying and manipulating model parameters. This interface is based on the S3 object system (see http://adv-r.had.co.nz/S3.html for an excellent introduction by Hadley Wickham).

In PCMBase, every model is an object of an S3 class, such as "OU", inheriting from the base S3-class "PCM". A PCM object represents a named list. Each element of that list can be one of the following:

- a global parameter shared by all regimes in the model. For example, this would be the case for a non-heritable variance-covariance parameter  $\Sigma_e$  if it is assumed to be the same for every observed species (i.e. tip) in the tree.
- a local stacked parameter that has a different value for each regime in the model. For example, in an OU model, the selection strength matrix H has a diffent value for each of the R regimes in the model. Therefore, an OU model contains a  $k \times k \times R$  array member called "H". The element  $H[_{n}1]$  would correspond to regime 1,  $H[_{n}2]$  to regime 2, etc. As a second example, the long-term optimum parameter of an OU process is a k-dimensional vector  $\vec{\theta_r}$  for each regime in the model. In an OU model with R regimes, this would be represented by a  $k \times R$  array (matrix) called "theta", such that the vector theta[, 1] corresponds to regime 1. Finally, a local scalar parameter (i.e. a number), would be represented by an R-vector.
- a nested PCM object corresponding to a regime. This is the case for a mixed Gaussian phylogenetic
  model, where different types of Gaussian processes can be acting on different parts of the tree, represented
  by different regimes.

, each element being a parameter of the model or, in the case of a mixed Gaussian model, a nested PCM corresponding to a specific regime.