

Utilizing **maticce** to estimate transitions in continuous character evolution

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1 Introduction

This document provides an overview of the **maticce** package, which serves three primary purposes. First, it implements an information-theoretic approach to estimating where on a phylogeny there has been a transition in a continuous character. As currently implemented, the approach assumes that (1) such transitions are appropriately modeled as shifts in optimum / equilibrium of a character evolving according to an Ornstein-Uhlenbeck process; (2) strength of constraint / rate of evolution toward the optimum is constant over the tree, as is variance; and (3) all branches on which a change could occur are identified. These assumptions can be relaxed in future versions if needed. Second, the package provides helper functions for the **ouch** package, in which all likelihood calculations are performed. For example, the package automates the process of painting regimes for the **hansen** function of **ouch**, specifying nodes at which the regime changes. It also provides functions for identifying most recent common ancestors and all descendents of a particular node. Users of **ouch** who want to handle large numbers of analyses may find the routines for summarizing analyses over trees and over regimes useful as well. Finally, **maticce** provides a flexible set of simulation functions for visualizing how different model parameters affect (i.e., what they 'say' about) our inference of the evolution of a continuous character on a phylogenetic tree.

This document also provides a worked example of analyzing a continuous character dataset that illustrates most of the **maticce** features. Working through this example will I expect address most questions that should come up during a typical analysis.

2 Package Overview

The **maticce** package currently implements functions in the following categories:

- Extracting information from **ouch**-style (S4 class **ouchtree**) trees
- Painting regimes on a batch of **ouch**-style trees

- Performing batch analyses in `ouch` over trees and over regimes
- Summarizing analyses

Functions in the first two categories will be of general utility to `ouch` users; functions in the third category are utilized to perform analyses over trees and over models, and in the fourth to summarize these with regard to the hypothesis that there has been a shift in continuous character on a given branch of a phylogenetic tree. While these latter two categories are more specific, the functions can be easily modified to address other multiple-tree / multiple-model questions.

3 Getting started

In case you aren't familiar with R, the following commands will get you started.

```
> # library(maticce) # load the maticce package into memory; also loads the required ouch pa
> library(ouch)
> data(carex)
> attach(carex)
> ovales.tree <- ape2ouch(ovales.tree) # make the tree an ouchtree object
```

Note that although the sample tree provided (`carex[['ovales.tree']]`) is ultrametric, this is not strictly required.

4 Extracting information from trees

Three functions are available to extract information from an `ouchtree` object:

- `isMonophyletic`: returns a T or F depending on whether the taxa identified are monophyletic on the tree provided
- `nodeDescendents`: identifies all descendents of a given node on a tree
- `mrcaOUCH`: identifies the most recent common ancestor of a given set of taxa

These functions can be used interactively to identify nodes on the tree for analysis. Because the batch-analysis functions in `maticce` identify nodes based on taxa (see explanation in the section on 'Performing batch analyses'), nodes are provided as a list of vectors, each vector containing all taxa descendent from the node of interest. You can generate these lists manually by typing lists of names into vectors, or you could use the following if you want to explicitly designate all taxa for each node by selecting from a list:

```
> nodes <- list(8) # assuming you want 8 nodes}
> for(i in 1:length(nodes)) nodes[[i]] <- select.list(otree@nodelabels, multiple = T)}
```

Alternatively, if you want to designate the node more quickly by just selecting the most recent common ancestor of a set of taxa:

```
> for(i in 1:length(nodes)) {
>   ancestor <- mrcaOUCH(select.list(otree@nodelabels, multiple = T), otree)
>   nodes[[i]] <- nodeDescendants(otree, ancestor)
> }
```

These functions are all documented under `isMonophyletic`.

5 Painting regimes

Two functions are available for painting selective regimes that may be used in the `hansen` function of `ouch`:

- **paintBranches**: returns the single regime for changes occurring at all specified nodes
- **regimeVectors**: returns all possible regimes for specified nodes, up to a maximum of `maxNodes + 1` optima
- **regimeMaker**: returns regimes defined by a matrix, with each row specifying which nodes the optimz change at

The `paintBranches` function is typically called from within `regimeVectors`, but it can be called separately. Nodes can be designated by number or taxa; the function assumes the latter only if it receives a list to evaluate instead of a vector.

```
> ou2 <- paintBranches(list(ovales.nodes[[2]]), ovalues.tree)
```

The regime can be used directly in a call to `hansen` or the `plot` method for an `ouchtree` object (Figure 1).

6 Batch analyses

```
> ha.4.2 <- runBatchHansen(ovales.tree, ovalues.data, ovalues.nodes[1:4], maxNodes = 2, brown
> print(summary(ha.4.2))
```

Summarizing `hansenBatch` analyses over 1 trees and 12 models

ESTIMATED SUPPORT FOR CHANGES OCCURRING AT DESIGNATED NODES

Averaged over all trees:

	1	2	3	4
AIC.weight	0.4306845	0.8848683	0.15490978	0.15202585
AICc.weight	0.4060012	0.8824765	0.14168053	0.13901638
BIC.weight	0.3189039	0.8740303	0.09500061	0.09311196

```
> plot(ovales.tree, regimes = ou2, cex = 1.2)
```

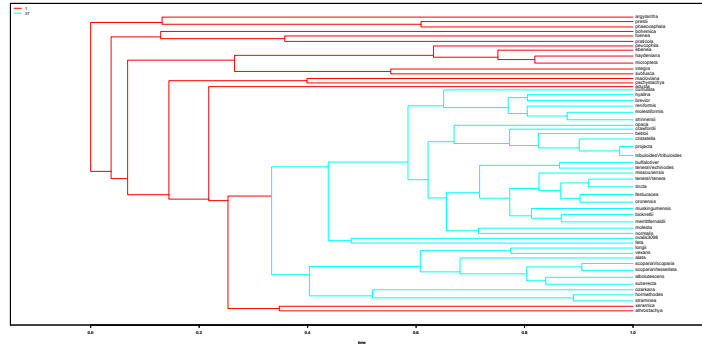


Figure 1: ovalues.tree with coloring according to ou2

Support conditioned on trees that possess the node

	1	2	3	4
AIC.weight	0.4306845	0.8848683	0.15490978	0.15202585
AICc.weight	0.4060012	0.8824765	0.14168053	0.13901638
BIC.weight	0.3189039	0.8740303	0.09500061	0.09311196

MODEL-AVERAGED PARAMETERS

alpha = 312.4266
sigma^2 = 5.192254

What is the relative support for the brownian motion vs. OU-2 model? We find which model has a change only at node 2 by inspecting the regime matrix

```
> ha.4.2[['regMatrix']][['overall']]
```

	1	2	3	4
1	1	1	0	0
2	1	0	1	0
3	1	0	0	1
4	1	0	0	0
5	0	1	1	0
6	0	1	0	1
7	0	1	0	0
8	0	0	1	1
9	0	0	1	0
10	0	0	0	1
11	0	0	0	0

Then we can find the likelihood of these models on a given tree:

```
> ouSim.ha.4.2 <- ouSim(ha.4.2, tree = ovales.tree)
> plot(ouSim.ha.4.2, colors = ou2)
```

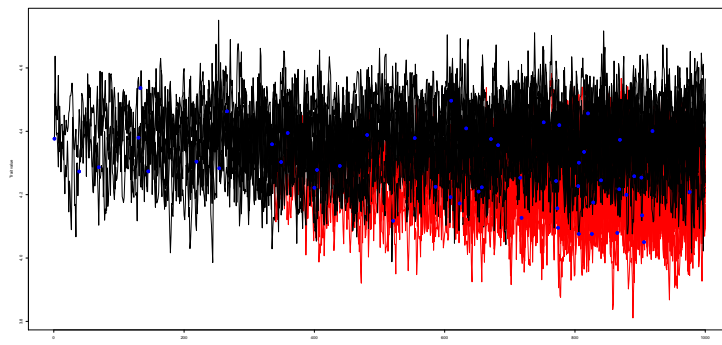


Figure 2: Simulated character on `ovales.tree` at model-averaged theta values, with coloring according to `ou2`

```
> ha.4.2[['hansens']][[1]]
```

	loglik	dof	sigma.squared	theta / alpha
1	52.72744	5	5.31005363	331.626872
2	50.54000	5	5.86424413	337.252821
3	50.21561	5	6.04474990	343.369492
4	49.95720	4	5.14354118	289.387746
5	51.75330	5	5.12434568	308.473054
6	51.81077	5	4.84664447	292.440242
7	51.75142	4	5.16258108	310.762680
8	44.31518	5	6.55448190	297.993592
9	44.17736	4	8.49647580	384.329498
10	42.89766	4	6.87292796	296.238909
11	39.57676	3	0.09810907	3.341806
brown	31.50503	2	0.04205436	4.351195

or the information criterion weights:

```
> summary(ha.4.2)[['modelsMatrix']][[1]]
```

	AICwi	AICcwi	BICwi
1	3.158399e-01	2.887904e-01	1.933452e-01
2	3.543867e-02	3.240359e-02	2.169421e-02
3	2.562102e-02	2.342676e-02	1.568422e-02
4	5.378499e-02	6.138046e-02	8.818021e-02
5	1.192348e-01	1.090232e-01	7.299104e-02
6	1.262885e-01	1.154727e-01	7.730903e-02
7	3.235051e-01	3.691902e-01	5.303850e-01

8	7.015685e-05	6.414841e-05	4.294738e-05
9	1.661543e-04	1.896184e-04	2.724090e-04
10	4.621088e-05	5.273673e-05	7.576248e-05
11	4.537212e-06	6.148318e-06	1.992244e-05
brown	3.851020e-09	5.912695e-09	4.528691e-08