

Running GeoHiSSE

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Getting started

This tutorial gives some basic information on how to set up and execute parameter estimates for a series of models using GeoHiSSE (Caetano et al., in review). The GeoHiSSE models can be used to infer ancestral ranges, rates of dispersion and extirpation as well as testing hypothesis about range-dependent diversification processes.

The main difference between GeoSSE and GeoHiSSE is that here we implement models that allow for diversification rate variation both within and between geographical areas. Such models are more adequate to empirical data than homogeneous diversification rates implied by GeoSSE (as well as BiSSE). The GeoHiSSE models belong to the same category of Hidden-Markov models as HiSSE. Thus, the concepts will be familiar to you if you have some experience with HiSSE (and vice-versa).

Best place to install the package with the new functions provided here is from our github repository using the package devtools:

```
library( devtools )
## At the moment you need to point to the development branch on github.
install_github(repo = "thej022214/hisse", ref = "master")
```

Before getting started, be sure to load the `hisse` and `diversitree` packages:

```
library(hisse)

## Loading required package: ape
## Warning: package 'ape' was built under R version 3.4.4
## Loading required package: deSolve
## Warning: package 'deSolve' was built under R version 3.4.4
## Loading required package: GenSA
## Warning: package 'GenSA' was built under R version 3.4.3
## Loading required package: subplex
## Warning: package 'subplex' was built under R version 3.4.4
## Loading required package: nloptr
library(diversitree)
```

Simulating a range-independent process

Here we will simulate a phylogenetic tree using neutral geographical ranges. We will incorporate three different rates of diversification. Thus, the correct process here is: “rates of diversification vary independently of the geographic ranges”.

We use a simulation here just because it is an easy way to produce data and because we know the underlying diversification process. Otherwise, if you have an empirical dataset, all the steps we show here apply. Just make sure to substitute the phylogeny and data with your dataset.

```
## Generate a list with the parameters of the model:
pars <- SimulateGeoHiSSE(hidden.areas = 1, return.GeoHiSSE_pars = TRUE)
pars
```

```
## $model.pars
##      A B
## s01 0 0
## s0   0 0
## s1   0 0
## x0   0 0
## x1   0 0
## d0   0 0
## d1   0 0
##
## $q.01
##      01A 01B
## 01A  NA   0
## 01B   0  NA
##
## $q.0
##      0A 0B
## 0A  NA   0
## 0B   0  NA
##
## $q.1
##      1A 1B
## 1A  NA   0
## 1B   0  NA
##
## attr(,"class")
## [1] "list"          "GeoHiSSE_pars"
```

The object `pars` is a list with all the parameter values for this model in the correct order and format, but all values are 0. Thus, we need to populate these parameters with numbers in order to perform the simulation.

```
pars$model.pars[,1] <- c(0.1, 0.1, 0.1, 0.03, 0.03, 0.05, 0.05)
pars$model.pars[,2] <- c(0.2, 0.2, 0.2, 0.03, 0.03, 0.05, 0.05)
pars$q.01[1,2] <- pars$q.01[2,1] <- 0.05
pars$q.0[1,2] <- pars$q.0[2,1] <- 0.05
pars$q.1[1,2] <- pars$q.1[2,1] <- 0.05
pars
```

```
## $model.pars
##      A      B
## s01 0.10 0.20
## s0   0.10 0.20
## s1   0.10 0.20
## x0   0.03 0.03
## x1   0.03 0.03
## d0   0.05 0.05
## d1   0.05 0.05
##
## $q.01
##      01A 01B
## 01A   NA 0.05
```

```
## 01B 0.05    NA
##
## $q.0
##      OA    OB
## OA    NA 0.05
## OB 0.05    NA
##
## $q.1
##      1A    1B
## 1A    NA 0.05
## 1B 0.05    NA
##
## attr("class")
## [1] "list"          "GeoHiSSE_pars"
```

Now we can use the parameters with the same function we applied before `SimulateGeoHiSSE` to generate both the data and the phylogeny.

Here we will set the seed for the simulation, so the outcome of the simulation is always the same. Note that you can change the seed or skip this lines to generate a different, random, dataset.

```
set.seed(1234)
sim.geohisse <- SimulateGeoHiSSE(pars=pars, hidden.areas = 1, x0 = "OA", max.taxa = 200)

## [1] "Simulating the phylogeny..."
## [1] "Simulation finished!"
```

Setting up the models

In this tutorial we will fit a total of four models. Two models with a range-independent diversification process and two other models in which the range have an effect on the diversification rate of the lineages (each with either one or two rate classes).

Note that the function to estimate the parameters of the model is commented out below. Just uncomment and run to perform the estimate of the models. Here we will load results from a previous estimate.

Models 1 and 2 below do not include hidden classes. Note that in this case the model will have 3 speciation parameters and 2 extirpation parameters.

```
## Model 1 - Dispersal parameters vary only, no range-dependent diversification.
speciation <- c(1,1,1)
extirpation <- c(1,1)
trans.rate <- TransMatMakerGeoHiSSE(hidden.areas=0)
mod1 <- GeoHiSSE(phy = sim.geohisse$phy, data = sim.geohisse$data, f=c(1,1,1),
                 speciation=speciation, extirpation=extirpation,
                 hidden.areas=FALSE, trans.rate=trans.rate)

## Model 2. Canonical GeoSSE model, range effect on diversification
speciation <- c(1,2,3)
extirpation <- c(1,2)
trans.rate <- TransMatMakerGeoHiSSE(hidden.areas=0)
mod2 <- GeoHiSSE(sim.geohisse$phy, data = sim.geohisse$data, f=c(1,1,1),
                 speciation=speciation, extirpation=extirpation,
                 hidden.areas=FALSE, trans.rate=trans.rate)
```

Models 3 and 4 below have 2 hidden rates each. In this case the models will have twice the number of parameters: 6 speciation parameters and 4 extirpation parameters.

```
## Model 3. GeoHiSSE model with 1 hidden area, no range-dependent diversification.
## Note below how parameters vary among hidden classes but are the same within each
## hidden class.
speciation <- c(1,1,1,2,2,2)
extirpation <- c(1,1,2,2)
trans.rate <- TransMatMakerGeoHiSSE(hidden.areas=1)
mod3 <- GeoHiSSE(sim.geohisse$phy, data = sim.geohisse$data, f=c(1,1,1),
                 speciation=speciation, extirpation=extirpation,
                 hidden.areas=TRUE, trans.rate=trans.rate)

## Model 4. GeoHiSSE model with 1 hidden area, no range-dependent diversification.
speciation <- c(1,2,3,4,5,6)
extirpation <- c(1,2,3,4)
trans.rate <- TransMatMakerGeoHiSSE(hidden.areas=1)
mod4 <- GeoHiSSE(sim.geohisse$phy, data = sim.geohisse$data, f=c(1,1,1),
                 speciation=speciation, extirpation=extirpation,
                 hidden.areas=TRUE, trans.rate=trans.rate)
```

Load the fit of the models:

```
load( "geohisse_vignette.Rsave" )
```

Now that we have the fit for the 4 models we can check their parameter estimates.

First model assumes a homogeneous diversification rate across the tree independent of the ranges.

```
mod1

##
## Fit
##          -lnL          AIC          AICc          n.taxa
##          -803.026      1614.052      1614.257      200.000
## n.hidden.classes
##          1.000
##
## Model parameters:
##
##          s0A          s1A          s01A          x0A          x1A          d0A_01A
## 0.10495443 0.10495443 0.10495443 0.04700056 0.04700056 0.04523465
##          d1A_01A
## 0.06328808
```

Second model assumes a range-dependent diversification process without hidden states. This means that diversification shifts occur across the branches of the tree and are correlated to the ranges.

```
mod2

##
## Fit
##          -lnL          AIC          AICc          n.taxa
##          -802.1938      1618.3876      1618.9709      200.0000
## n.hidden.classes
##          1.0000
##
## Model parameters:
##
##          s0A          s1A          s01A          x0A          x1A          d0A_01A
```

```
## 0.11383796 0.10000999 0.08864935 0.04545565 0.06020702 0.05333405
##      d1A_01A
## 0.05346983
```

Third model incorporates shifts in diversification across the tree but these are independent of the ranges. Note that the parameter estimates vary between hidden classes but are held the same among different ranges within each hidden class. This is an example of our more complex null model in GeoHiSSE. This model can be extended to fit up to 5 hidden classes.

```
mod3
```

```
##
## Fit
##           -lnL           AIC           AICc           n.taxa
##          -810.6062        1639.2124        1640.1597        200.0000
## n.hidden.classes
##           2.0000
##
## Model parameters:
##
##           s0A           s1A           s01A           x0A           x1A
## 4.996388e+00 4.996388e+00 4.996388e+00 7.411601e+02 7.411601e+02
##      d0A_01A      d1A_01A      d0A_0B      d1A_1B      d01A_01B
## 7.983518e-03 9.980557e+01 2.339666e-05 2.339666e-05 2.339666e-05
##           s0B           s1B           s01B           x0B           x1B
## 1.742381e-01 1.742381e-01 1.742381e-01 1.670225e-01 1.670225e-01
##      d0B_01B      d1B_01B      d0B_0A      d1B_1A      d01B_01A
## 6.429553e-02 9.702651e-02 2.339666e-05 2.339666e-05 2.339666e-05
```

Finally, the third model describes a range-dependent diversification process while also accounting for multiple rate classes. This is the most complex model in this set.

```
mod4
```

```
##
## Fit
##           -lnL           AIC           AICc           n.taxa
##          -798.7843        1627.5686        1630.1773        200.0000
## n.hidden.classes
##           2.0000
##
## Model parameters:
##
##           s0A           s1A           s01A           x0A           x1A
## 1.371612e-01 7.618960e-02 1.668092e-01 7.176987e-02 7.841790e-02
##      d0A_01A      d1A_01A      d0A_0B      d1A_1B      d01A_01B
## 6.001005e-02 7.188738e-02 7.811913e-03 7.811913e-03 7.811913e-03
##           s0B           s1B           s01B           x0B           x1B
## 6.434724e-02 1.261423e-01 2.066618e-09 7.637460e-03 4.241552e-02
##      d0B_01B      d1B_01B      d0B_0A      d1B_1A      d01B_01A
## 4.497654e-02 3.689476e-02 7.811913e-03 7.811913e-03 7.811913e-03
```

Computing Akaike Weights.

Akaike weights are important to evaluate the relative importance of each of the models to explain the variation observed in the data. This quantity takes into account penalties associated to the number of free parameters.

Models with higher weight show better fit to the data and, as a result, have more weight when performing model averaging (see below).

To compute model weight we can use one of the functions of the package. This will work with both HiSSE and GeoHiSSE objects.

```
GetModelWeight(model1 = mod1, model2 = mod2, model3 = mod3, model4 = mod4)

##          model1          model2          model3          model4
## 8.963818e-01 1.025742e-01 3.083187e-06 1.040898e-03

## As the number of models in the set grows, naming each model in the set can become hard.
## So one can use a list (created by some automated code) as an input also:
list.geohisse <- list(model1 = mod1, model2 = mod2, model3 = mod3, model4 = mod4)
GetModelWeight(list.geohisse)

##          model1          model2          model3          model4
## 8.963818e-01 1.025742e-01 3.083187e-06 1.040898e-03
```

Model averaging and plotting.

Now we can model average the results. Note that this step will reflect the Akaike model weights that we computed above.

For this we need first to perform a marginal reconstruction for each of the models in the set. This will reconstruct the hidden states at the nodes of the phylogeny. Then we can use this information to compute the model average for the rates.

These can take a while to run. We will load the results of previous analyses. Uncomment the code below to perform the reconstructions.

```
recon.mod1 <- MarginReconGeoSSE(phy = mod1$phy, data = mod1$data, f = mod1$f,
                                pars = mod1$solution, hidden.areas = mod1$hidden.areas,
                                root.type = mod1$root.type, root.p = mod1$root.p,
                                aic = mod1$AIC, n.cores = 4)
recon.mod2 <- MarginReconGeoSSE(phy = mod2$phy, data = mod2$data, f = mod2$f,
                                pars = mod2$solution, hidden.areas = mod2$hidden.areas,
                                root.type = mod2$root.type, root.p = mod2$root.p,
                                aic = mod2$AIC, n.cores = 4)
recon.mod3 <- MarginReconGeoSSE(phy = mod3$phy, data = mod3$data, f = mod3$f,
                                pars = mod3$solution, hidden.areas = mod3$hidden.areas,
                                root.type = mod3$root.type, root.p = mod3$root.p,
                                aic = mod3$AIC, n.cores = 4)
recon.mod4 <- MarginReconGeoSSE(phy = mod4$phy, data = mod4$data, f = mod4$f,
                                pars = mod4$solution, hidden.areas = mod4$hidden.areas,
                                root.type = mod4$root.type, root.p = mod4$root.p,
                                aic = mod4$AIC, n.cores = 4)

## Load previous results:
load( "geohisse_recons_vignette.Rsave" )
```

The results are phylogenetic trees with information on the nodes.

```
recon.mod1

##
## Phylogenetic tree with 200 tips and 199 internal nodes.
##
```

```
## Tip labels:
##  sp14, sp16, sp21, sp23, sp26, sp30, ...
## Node labels:
##  1, 3, 1, 3, 3, 1, ...
##
## Rooted; includes branch lengths.
```

```
recon.mod2
```

```
##
## Phylogenetic tree with 200 tips and 199 internal nodes.
##
## Tip labels:
##  sp14, sp16, sp21, sp23, sp26, sp30, ...
## Node labels:
##  1, 3, 1, 1, 3, 1, ...
##
## Rooted; includes branch lengths.
```

```
recon.mod3
```

```
##
## Phylogenetic tree with 200 tips and 199 internal nodes.
##
## Tip labels:
##  sp14, sp16, sp21, sp23, sp26, sp30, ...
## Node labels:
##  2, 6, 6, 4, 6, 4, ...
##
## Rooted; includes branch lengths.
```

```
recon.mod4
```

```
##
## Phylogenetic tree with 200 tips and 199 internal nodes.
##
## Tip labels:
##  sp14, sp16, sp21, sp23, sp26, sp30, ...
## Node labels:
##  1, 3, 1, 1, 3, 1, ...
##
## Rooted; includes branch lengths.
```

Now that we have the AIC associated with each model and their reconstruction across the nodes of the tree we can compute the model average:

```
recon.models <- list(recon.mod1, recon.mod2, recon.mod3, recon.mod4)
model.ave.rates <- GetModelAveRates(x = recon.models, type = "tips")
```

```
## Warning in CheckReconBounds(x = list(rates.tips.turnover,
## rates.tips.net.div, : Models in position 3 have parameters outside the
## bounds defined by 'bound.matrix' argument. These will NOT be included in
## the reconstruction.
```

The error message appeared here because the function uses the argument `bound.par.matrix` in order to exclude models with parameter estimates outside the pre-defined bounds. You can use these bounds to make sure that models with poor MLE estimates will not influence the model averages.

The result of the reconstruction is a matrix with the parameter estimates for each of the tips species averaged

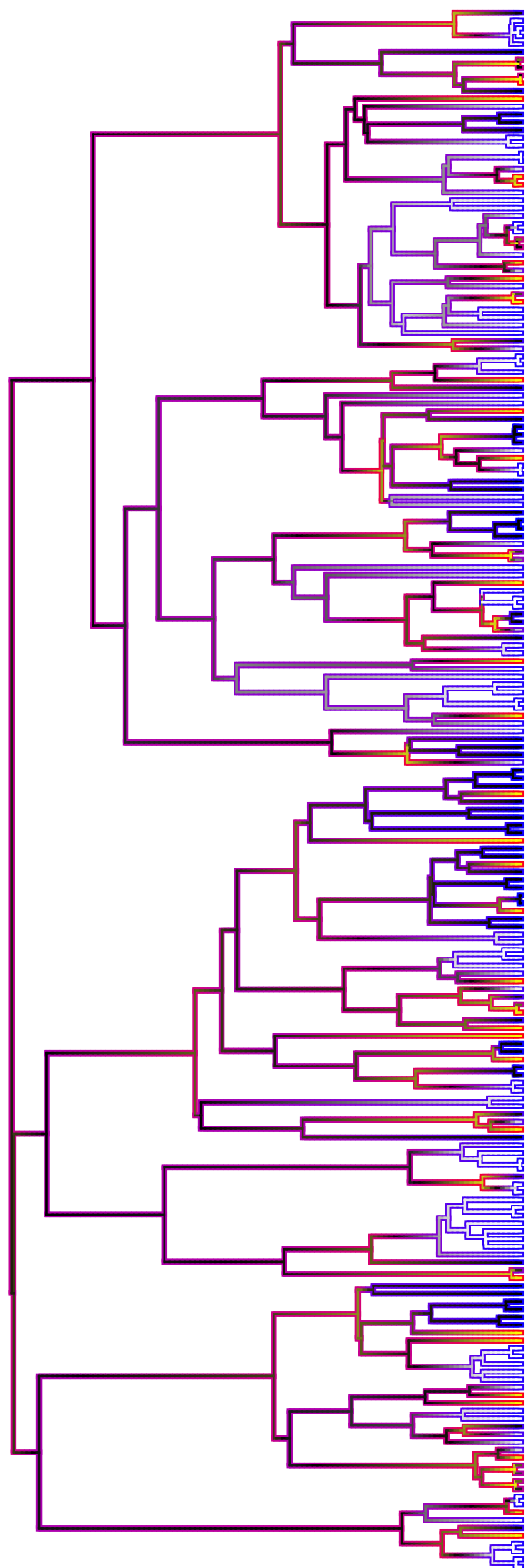
over all models. Note that for the GeoSSE model there is no “extinction” parameter associated with widespread (01) lineages. Also note that one can change the type of model averaging (between tips, nodes, and both) when calling the `GetModelAveRates` function.

```
head( model.ave.rates )
```

```
##   taxon state.0 state.1 state.01  turnover   net.div speciation
## 1  sp14      0      0      1 0.3133588 0.3133588 0.1031989
## 2  sp16      1      0      0 0.1527295 0.1058221 0.1058792
## 3  sp21      1      0      0 0.1527351 0.1058224 0.1058822
## 4  sp23      1      0      0 0.1527147 0.1058211 0.1058713
## 5  sp26      1      0      0 0.1527019 0.1058203 0.1058645
## 6  sp30      0      0      1 0.3137521 0.3137521 0.1033111
##   extinct.frac extinction
## 1    0.0000000 0.00000000
## 2    0.4428098 0.04685031
## 3    0.4428264 0.04685293
## 4    0.4427659 0.04684335
## 5    0.4427281 0.04683735
## 6    0.0000000 0.00000000
```

Finally, we can plot the use the resulting data matrix to make a plot of the results.

```
plot.geohisse.states(x = recon.models, rate.param = "net.div", type = "phylogram",
                     show.tip.label = FALSE, legend = "none")
```

```
## $rate.tree
## Object of class "contMap" containing:
##
## (1) A phylogenetic tree with 200 tips and 199 internal nodes.
##
## (2) A mapped continuous trait on the range (0.104231, 0.318219).
##
##
## $state.tree
## Object of class "contMap" containing:
##
## (1) A phylogenetic tree with 200 tips and 199 internal nodes.
##
## (2) A mapped continuous trait on the range (0, 2.002).
```