iBPP documentation

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Introduction

iBPP builds on BPP (Rannala and Yang, 2003; Yang and Rannala, 2010) to analyze pheno-typic and molecular data in a common Bayesian framework. The method and its performance are described in Solís-Lemus *et al.* (2014).

Compilation

The source files (bpp.c, paml.h, tools.c, treespace.c, treesub.c) are in the `src/` folder. Go to that folder, then compile with these commands. The first command creates the executable that analyzes data. The second command creates the executable that simulates data.

- To compile for Mac:
  ```
  # cc -o ibpp -O3 bpp.c tools.c -lm
  # cc -o ibpp-simul -DSIMULATION -O3 bpp.c tools.c -lm
  ```

- To compile for Linux:
  ```
  # gcc -o ibpp -O3 bpp.c tools.c -lm
  # gcc -o ibpp-simul -DSIMULATION -O3 bpp.c tools.c -lm
  ```

Trial example

Use the files in the `example` folder to do a test run:
```
# ibpp-simul 5s.simul.ctl
# ibpp 5s.analysis.ctl
```

iBPP analysis control file

The control file for iBPP is very similar to the one for BPP (see BPP documentation for more details). Only the following lines are added:

`traitfile = 5s.morph.txt`	replace with name of file with the trait data
`useseqdata = 1`	0 if sequence data should not be used in the analysis, and 1 if it should
`usetraitdata = 1`	0 if trait data should not be used in the analysis, and 1 if it should
`ntraits = 10`	number of traits in the trait file
`nu0 = 0`	prior parameter for σ^2
`kappa0 = 0`	prior parameter for μ given σ^2

Simulation control file

The simulation control file is very similar to the one for MCcoal. Only the following lines are added:

`ntraits = 10`	Number of traits to simulate
`lambda = 1:0.7`	Between-to-within trait variance (Pagel's lambda). The first number is 0 (default) to simulate i.i.d. uniform(0,1) λ's across traits, and 1 if the same λ is used for all traits
`phyloModel = 1:1.0`	The first number is 0 if the model for the species means is Brownian Motion (BM) and 1 if it is Ornstein-Uhlenbeck (OU), followed by the parameter α for the OU model
`OUmuSD = 0.2`	Standard deviation of optimal values for the OU model, across branches and traits, relative to trait scale.
`traitflow = 0.0 0.95`	Probabilities at internal nodes that sister species have equal evolution. This option provides an analog of gene flow (migration) between sister species. It can also be used with an artificially larger tree to model phenotypic plasticity.

Literature Cited

RANNALA, B. and Z. YANG. 2003. Bayes estimation of species divergence times and ancestral population sizes using DNA sequences from multiple loci. Genetics **164**:1645–1656.

SOLÍS-LEMUS, C., L. L. KNOWLES, and C. ANÉ. 2014. Bayesian species delimitation combining multiple genes and traits in a unified framework. Evolution p. In press.

YANG, Z. and B. RANNALA. 2010. Bayesian species delimitation using multilocus sequence data. PNAS **107**:9264–9269.