-----Original Message-----

From: R-sig-phylo [<mailto:r-sig-phylo-bounces@r-project.org>] On Behalf Of David Bapst

Sent: Monday, March 16, 2015 3:05 PM

To: William Gearty

Cc: r-sig-phylo

Subject: Re: [R-sig-phylo] (P)GLS (nlme) vs. PGLS (caper)

William,

Yes, the different PCM models make very different statements about what is happening biologically in your data. Additionally, the three Pagel parameters are not always easy to interpret biologically. Carl Boettiger has some particularly lucid thoughts on Pagel's lambda:

<http://www.carlboettiger.info/2013/10/11/is-it-time-to-retire-pagels-lambda.html>

In general, model choice is much more satisfying if you have strong prior expectations for the models you are choosing between being realistic descriptions of the actual process.

My advice would be to carefully choose a priori models of trait evolution that seem like defensible biologically-reasonable hypotheses of how these traits might be evolving in your group, and then either

(a) use some sort of model choice criteria to choose between those different PGLS models and interpret the parameters of this best-fit model or (b) examine the parameter values estimated by the different models for insights into the biological implications for your dataset.

For example, OU often fits better than BM, but sometimes the 'pull'

parameter in OU is so small that the best-fit OU model is not describing a process of trait change that is distinguishable from BM.

> I've come to accept my dataset isn't representing brownian evolution,

> so I've discarded those results, leaving me with the OU results

Hmm... William, is your dataset a time-scaled tree of fossil taxa?

Just curious, as these trees sometimes show an unfortunate bias toward OU. This is in addition to the general ever-present bias toward OU, see this recent paper by Ho and Ane:

<http://onlinelibrary.wiley.com/doi/10.1111/2041-210X.12285/abstract>

I hope this helps,

-Dave Bapst

On Sun, Mar 15, 2015 at 6:24 PM, William Gearty <[wgearty@stanford.edu](mailto:wgearty@stanford.edu)> wrote:

> Hi all,

> I'm looking for some advice on and thoughts regarding performing a

> phylogenetic generalized least squares analysis in R.

> I've tried GLS from the nlme package using corBrownian and corMartins

> from the ape package and get one set of results (I've come to accept

> my dataset isn't representing brownian evolution, so I've discarded

> those results, leaving me with the OU results).

> I've also tried PGLS from the cape package, having it estimate the 3

> different Pagel parameters. After optimizing these parameters, I get

> different results from those of the OU (corMartins) GLS analysis.

> I'm wondering what is to blame for these drastically different results?

> The different parameters that the two methods are estimating?

> Is it the difference between using REML in the GLS vs. ML in the PGLS?

> Do people have particular preferences for running these types of analyses?

> Should I feel okay about estimating all three Pagel parameters at the

> same time with PGLS?

> Any insight or thoughts would be greatly appreciated.

> Thanks,

> Will

>

> --

> William Gearty

> PhD Student, Paleobiology

> Department of Geological and Environmental Sciences Stanford School of

> Earth, Energy & Environmental Sciences people.stanford.edu/wgearty

>

> [[alternative HTML version deleted]]

>

> \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

> R-sig-phylo mailing list - [R-sig-phylo@r-project.org](mailto:R-sig-phylo@r-project.org)

> <https://stat.ethz.ch/mailman/listinfo/r-sig-phylo>

> Searchable archive at

> <http://www.mail-archive.com/r-sig-phylo@r-project.org/>

--

David W. Bapst, PhD

Adjunct Asst. Professor, Geology and Geol. Eng.

South Dakota School of Mines and Technology

501 E. St. Joseph

Rapid City, SD 57701

<http://webpages.sdsmt.edu/~dbapst/>

<http://cran.r-project.org/web/packages/paleotree/index.html>

\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

R-sig-phylo mailing list - [R-sig-phylo@r-project.org](mailto:R-sig-phylo@r-project.org) <https://stat.ethz.ch/mailman/listinfo/r-sig-phylo>

Searchable archive at <http://www.mail-archive.com/r-sig-phylo@r-project.org/>