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Tony Jhwueng <tony.jhwueng@gmail.com>

Trait evolution on phylogenetic networks

1 message

Paul Bastide <paul.bastide@m4x.org>   Fri, Oct 6, 2017 at 4:18 PM
To: Brian O'Meara <bomeara@utk.edu>, dcjhwueng@fcu.edu.tw

Dear Drs. Jhwueng and O'Meara,

I'm writing to you about the paper "Trait evolution on phylogenetic networks", that you submitted for the same special issue as us. I have been asked to be one of the reviewers for it. I will sign my review, so I don't think there is any conflict for me to write to you directly. I thought (and Cécile agreed) that it might speed up the process. However, if you'd would prefer to wait for the information to go through the official canals of the journal, please just let me know and ignore this e-mail.

The reason I'm writing you is that I did not manage to make a correct use of your R package BMhyb. I tried to compute variance matrices with your function `GetVModified` on simple examples, but I did not get the results expected from a manual computation.

I am going to open two separate issues on GitHub (for two example networks), so that the problems I encountered might be more easy to track down. However, all my attempts are already summarized in the attached R script, that is maybe more convenient for you to browse.

The problem might be that I did not understand correctly the way you encoded the network (through your flow matrix). If that is the case, I'd be grateful if you could point me to the correct direction.

Thank you for your help,
Best regards,
Paul

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📄 **test_BMhyb.R**
    10K