NESCent Call for Users of Comparative Methods

The R statistical analysis package has emerged as a popular platform for implementation of powerful comparative phylogenetic methods to understand the evolution of organismal traits. The National Evolutionary Synthesis Center (NESCent) is organizing a hackathon focused on the **integration of comparative phylogenetic methods** within **R**. The event will take place on Dec 10-14, 2007, at NESCent in Durham, North Carolina. Having largely identified the set of developers to do the actual hacking, we are 1) soliciting applications for end-user participation and 2) comments and suggestions from the community. More information about the event is available at http://hackathon.nescent.org/R_Hackathon_1.

We are actively seeking applications from end-users of comparative methods: biologists familiar with comparative phylogenetic methods who are interested in working face-to-face with developers to help prioritize needs, document and test the code being developed, provide feedback regarding usability, and ensure the community value of the code being written at the event. End-users need not be experienced programmers.

LOGISTICS & ORGANIZATION
The event will take place on Dec 10-14, 2007, at NESCent in Durham, North Carolina. Travel, accommodation, expenses for meals, etc, will be paid by NESCent. Logistical and travel details will be communicated once participation is confirmed.

CALL FOR INPUT

We are soliciting input from the community at large regarding the priorities and objectives of the hackathon. If you are a user of comparative phylogenetic software and have any ideas that you would like the community of developers to be aware of, please submit your input directly through the hackathon wiki (http://hackathon.nescent.org; click on 'Forum') or by email to hackathon2@nescent.org.

CALL FOR END-USER PARTICIPATION

We invite all individuals interested in attending to respond by email to the questions below. We encourage applications from:
- Members of underrepresented groups, specifically women and members of minorities.
- Graduate students and postdocs.

Please email your responses and, if possible, a CV to hackathon2@nescent.org by October 25. Also, please be aware that the funds, as well as the space, for this event are limited, and the organizers need to balance the skills of the attendees, so not all qualified applicants can be guaranteed acceptance.

1. Please indicate if you would be available for all or only for part of the Dec 10-14 time period.
2. Briefly describe your qualifications (e.g. your familiarity with comparative phylogenetic methods, particularly those implemented in R). How you would like to contribute and how you would expect to benefit?
3. Please state what you would most like to see accomplished at the hackathon.

4. Please indicate if you are a member of an underrepresented group (including women, persons with disabilities, and any of the following minorities: African American, Hispanic, American Indian, Alaska Native, Native Hawaiian, and Pacific Islander).

The Organizing Committee
From NESCent: Hilmar Lapp, Brian O'Meara, Samantha Price, Todd Vision, Amy Zanne
From UC Berkeley: Steven Kembel