subject: Last call for applications (due March 4): Phylotastic! hackathon at NESCent (June 4 to 8)

February 28, 2012

Dear Colleague,

This is the final call for applications to the Phylotastic! hackathon planned at NESCent in June. The application (see below) should take about 15 minutes (deadline: March 4 at midnight EST). We especially encourage women and members of traditionally under-represented minorities to apply.

Every year, the number and size of available species phylogenies grows, with the largest trees now exceeding 10^5 tips. The information contained in these megatrees is tremendous, but there is no easy way to access and use it.

To address this issue, a NESCent working group, named HIP (Hackathons, Interoperability, Phylogenies), has planned a hackathon (<http://en.wikipedia.org/wiki/Hackathon>) in which scientist-programmers will design and implement Phylotastic!, an open software system to extract a phylogeny for a named set of species from available megatrees, and optionally create mash-ups with data from online services. Phylotastic is envisioned as a set of web services that collectively provides the operations— pruning, grafting, name-reconciliation, branch estimation, translation— that will democratize using the Tree of Life, making it accessible and computable for researchers throughout the life sciences, from community ecology to comparative genomics

Applications are now being accepted to participate in the Phylotastic hackathon, which will take place June 4 to 8 at NESCent headquarters in Durham, NC (see below, How to Apply). Support for travel and meal expenses will be available to each successful applicant, according to his or her stated needs.

We urge you to apply if you are enthusiastic about the goals of the project, and you have one or more of the following skills:

* development, adaptation and use of software for megatree informatics,
* grafting & pruning trees,
* branch length estimation,
* NeXML support,
* provenance annotation,
* mashups (semantic integration),
* taxonomic name resolution,
* phylogenetic visualization,
* construction of and programming with web service interfaces, and
* assembling web-services into executable workflows .

We also welcome your application if you can envision a role for yourself based on other attributes not listed, including non-programming skills (e.g., generating documentation) and expert knowledge of use-cases (i.e., real-world problems).

To understand how you might be able to contribute, please review a brief slide presentation (ppt format, [http://bit.ly/xGvwRr](http://www.google.com/url?q=http%3A%2F%2Fbit.ly%2FxGvwRr&sa=D&sntz=1&usg=AFQjCNGqrbYWLJKK7XHtexhT3OASS2T92A), or PDF format, http://bit.ly/wcQzMI). If further information is needed, consult the Phylotastic project wiki (<http://www.evoio.org/wiki/Phylotastic>), or contact a member of the HIP leadership team (listed below).

Sincerely,

<your name> \*

<your email address>

\* on behalf of the HIP (Hackathons, Interoperability and Phylogenies) Leaderhip Team

1. HOW TO APPLY

You may apply by filling in the online form here <http://tinyurl.com/PhyloTasticForm>. Please note the following:

1. The application deadline is March 4 at midnight, EST
2. Be sure that you understand the project before applying. If needed, review a brief slide presentation (ppt format, <http://bit.ly/xGvwRr>, or PDF format, http://bit.ly/wcQzMI).
3. The application form asks you to describe your qualifications. If possible, cite tangible accomplishments to provide evidence of your skills.
4. All code produced at the event is to be made available immediately under an OSI-approved open-source license, and documentation under a Creative Commons BY license (<http://creativecommons.org/licenses/by/3.0/>). Using the online application, indicate whether this would pose any difficulty for your participation.

Support for travel and meal expenses will be available to each successful applicant, according to his or her stated needs. Please understand that your application is not a guarantee of participation in the event. Funds and space are limited: we may not be able to sponsor every individual who is qualified to participate.

2. SCOPING STATEMENTS

To further clarify the project, consider the following points. In scope:

* Populating data store of existing trees
* Evolution of PhyloWS to support the needs of PhyloTastic
* Taxonomic name resolution (embedding existing TNRS capacities)
* Pruning trees and grafting species on them
* Branch length (existing methods for incorporating branch lengths)
* Integration of data and trees (e.g., mashups) - species-wise integration
* Display of resulting trees (using existing technologies)
* Wrap all these existing tools as web services
* NeXML syntax extensions if needed
* If needed, determine methods for compressing NeXML representations
* user interfaces that are simple (web form) or that adapt existing tools

Not In Scope:

* Constructing new input trees
* New Data Generation
* Arguing or evaluating the correctness of trees
* Design of new TNRS systems
* Debates about which naming system is best
* Developing new techniques to derive branch lengths

Uncertain:

* Phylo-referencing
* satisfying any particular standard of provenance annotation

3. HIP (Hackathons, Interoperability, Phylogenetics)

The Phylotastic Hackathon represents the first of three sponsored by a new working group at NESCent called HIP (Hackathons, Interoperability, Phylogenetics). HIP is organized by a Leadership Team consisting of Karen Cranston, Sergei Kosakovsky Pond, Hilmar Lapp, Enrico Pontelli (PI), Michael Rosenberg, Brian Sidlauskas, Arlin Stoltzfus (PI), Rutger Vos (PI), Mark Westneat, and Mark Wilkinson.

More information about HIP, including goals, strategies, and project ideas, can be found here: <http://www.evoio.org/wiki/HIP>.

(end of message about Phylotastic hackathon)