

Provide a brief summary of your professional background (no more than one-half page).

I develop and apply novel phylogenetic methods, generally for investigating trait evolution. I have also worked on beetle and ant empirical systems, though my current work is now mostly theoretical. I got my PhD from UC Davis' population biology program, went on to a postdoc at NESCent, and I am now in my second year an assistant professor in ecology and evolutionary biology at the U. of Tennessee, Knoxville.

What expertise do you bring that is relevant to assembling, visualizing, or carrying out analyses on the tree of life (no more than one-half page).

My main expertise is in developing and applying new comparative methods, so I know the issues involved in this. Through iPlant, I am working to make these methods more accessible and also scale well to tens of thousands of taxa (issues are speed, of course, but also numerical precision issues). I also have created and maintained a database of actual and possible comparative methods and software (Treetapper.org) and a task view of phylogenetics packages in R. In addition to software and analyses for comparative methods, I have done empirical sequencing and tree inference work on ants and beetles, so I know the issues facing systematists. I have also worked, with colleagues in the Sanderson lab, on methods to discover the information about the tree of life present in GenBank. I have also developed a simulated annealing tree search program and a pair of techniques for jointly inferring species limits and a species tree given a set of gene trees.

In fifty words or less, describe a major phylogenetic challenge or a breakthrough needed to advance the field.

The challenge after building the tree of life is using it in a variety of fields. We need ways for ecologists, educators, and other non-systematists to identify proper methods to address their questions using this phylogeny, and ways to communicate their needs for methods to those who can build them.

Page two: Please spend some time considering your answers to the following questions. Your responses (no more than 100 words each) should demonstrate that you have suitable skills and aptitude to participate in the Ideas Lab event (unrelated to your research track record).

What is your personal experience with working in teams?

Extensive. I am scientific lead of iPlant's trait evolution group, where I interact with a variety of scientists, programmers, interface designers, and outreach specialists. I organized a successful "high performance computing for phylogenetics" workshop at NIMBioS, arranging for instructors from across the country (incidentally, half the participants were women). I am a member of several NIMBioS and NESCent working groups. I have co-organized a hackathon in R for comparative methods that has had lasting effects. I organized a team across two departments to create a seminar series on women in science at the interface of community ecology and phylogenetics.

How would you describe your ability to explain your research to non-experts?

Fairly good. I have given talks to community groups about phylogenetics in general as well as taught gentle introductions to phylogenetics to undergraduates in my macroevolution class. I have been invited to write articles or chapters about aspects of phylogenetics for publications targeted at non-experts, such as a textbook for theoretical ecologists or a general review journal. Much of my interaction with iPlant members has been explaining the rationale behind phylogenetic methods to people without biology backgrounds.

The Ideas Lab environment is especially suited to individuals who are willing to step outside their particular area of interest or expertise, who are positively driven, who enjoy creative activity, who can think innovatively and who can settle in easily in the company of strangers. Please describe an experience you have had in a comparable environment.

My postdoc experience at NESCent was a good example of this. Before that, I was a systematist who did solo programming in comparative methods. During my <2 year postdoc, I co-organized a hackathon in comparative methods in R that has resulted in a robust community of programmers, several joint software projects, and resources for the broader community, I interacted with the local informatics team to learn how to create an interactive database and website of present and missing comparative methods, and I remotely mentored a student through the Google Summer of Code program.

What would you personally and professionally gain from participating in this Ideas Lab event?

I am in phylogenetics because I am thrilled with the power to understand biology that a tree provides. I want to extend this power to scientists other than the traditional tree-builders and this is a means to do so. I have also enjoyed interacting with mathematicians, computer scientists, and others who approach phylogenetics from a distinct perspective. On a professional level, contact with potential future collaborators is important. Finally, and perhaps somewhat obviously, the opportunity to apply for and ideally get grants is also crucial for advancing my research and career, especially as a fairly new assistant professor.