

Society of Systematic Biologists Program Chair's Report

David W. Weisrock
December 28, 2018

Meeting preparations for Evolution 2019, Providence RI

SSB Symposia

We have two symposia in place for the 2019 meeting:

- 1) “New Measures of Phylogenetic Support for the Genomic Era” organized by Jeremy Brown (Louisiana State University), Robert Lanfear (Australian National University), and Robert Thomson (University of Hawaii).
- 2) “Diversification through time, space and lineages: relationships between data quality and good inferences” organized by Luna Sánchez-Reyes (postdoc at UT-Knoxville).

A full description of these symposia can be found below.

SSB workshop

We have one workshop in place for the 2019 meeting:

“New developments in phylogenetics and evolution” organized by Dan Warren (Senckenberg Biodiversity and Climate Research Center, Germany). Yes, it’s a non-descript title, but it captures the breadth of the topics to be addressed. A full description of the presenters and topics can be found below.

SSB Spotlight Sessions

We have two symposia in place for the 2019 meeting. We don’t have official titles for these yet, but the general topics are set. Organizers are currently working on building the speaker lineups, which will be in place by February 1.

- 1) General topic is “The bright side of phylogenetics”, organized by Michael Landis (postdoc at Yale University) and Rosana Zenil-Fergesun (postdoc at University of Minnesota).
- 2) General topic is “Choosing the appropriate molecular data set for your phylogenetic study”, organized by Brant Faircloth (Louisiana State University).

Ad hoc funding updates

SSB recently provided ad hoc funding to PhyloPic (phylopic.org) run by Mike Keeseey. SSB's \$2000 donation pushed the crowdsourcing campaign over its \$12,000 goal, which will provide funds for an updated version of the website.

- I'm still confused on the dates of SSB's fiscal year. Is it July 1 to June 30? Or October 1 to September 30? I want to clarify this as we allocate \$8000 per fiscal year and I'm not sure which fiscal year to allocate the ad hoc awards to.

SSB Table at Providence

We are currently working on the possibility of staffing a table in the exhibition hall during poster sessions. This has not been confirmed; however, I am in discussion with the Kelly Zamudio and the SSB student representatives regarding how best to make this happen. It'll need effort from more than just the student reps and me to make it happen. More on this soon.

Title: New Measures of Phylogenetic Support for the Genomic Era

Organizers: Jeremy M. Brown, Robert Lanfear, Robert C. Thomson

Purpose and Relevance:

High-throughput sequencing has revolutionized the nature of genetic datasets used for phylogenetic inference, both in terms of the amount of sequence obtained per sample and the number of tips in the inferred trees. Many studies have now shown that traditional approaches (e.g., nonparametric bootstrapping, posterior probabilities, etc.) for assessing support across branches and trees have limited utility for modern datasets. Due to the amount of sequence data now common in phylogenomic studies, these measures often reach their maximum values and limit meaningful comparisons across genes, datasets, and analyses.

Recently, a variety of alternative approaches have been proposed to more meaningfully assess support in the context of studies utilizing high-throughput sequencing. Creative application and comparison of these approaches has the potential to resolve long-standing phylogenetic debates and to clarify enigmatic relationships. To our knowledge, no concerted effort has been made to discuss and compare these approaches in a unified context, despite their importance across a wide variety of biological disciplines. In this symposium, we will bring together researchers from around the world who have been developing new approaches to assessing phylogenetic support. We aim to discuss the relative merits and drawbacks of these approaches and to highlight common themes.

Potential Speakers:

Dahiana Arcila, Assistant Professor, University of Oklahoma [Confirmed]
Genome-wide gene genealogy interrogation advances resolution of recalcitrant groups in the Tree of Life

Minh Bui, Postdoc, Australian National University [Confirmed]
Site- and gene-concordance measures of branch support for phylogenomic datasets

Genevieve Mount, PhD Candidate, Louisiana State University [Confirmed]
Comparing genome wide measures of phylogenetic support in squamates

John Rhodes, Professor, University of Alaska [Confirmed]
New graphical and statistical tools for testing the source of gene tree discordance

Xing-Xing Shen, Postdoc, Vanderbilt University [Confirmed pending visa]
Can phylogenomic data end incongruence in the tree of life?

Joseph Walker, PhD Candidate, University of Michigan [Confirmed]
Using gene tree conflict to infer and analyze support for contentious relationships

Diversification through time, space and lineages: relationships between data quality and good inferences.

The widespread interest to understand and predict patterns of species diversification has fostered the development and tuning of new tools. The adequacy of Birth-Death models and all derived developments to accurately estimate diversification rates (**DR**) from dated phylogenies and fossil information has been tested profoundly in relation to the shape and size of trees. However, the effect of uncertainty underlying the data used to study the diversification process has seldom been considered. The analysis of different topologies from phylogenies available for the same organism has revealed that diversification inferences are not coherent across phylogenies, probably due to inconsistencies in the ages of clades (Title & Rabosky, 2017, doi: 10.1093/sysbio/syw102), but no more work has been done in that sense. Moreover, the sensitivity of widely used **DR** estimators (such as State dependent Speciation and Extinction, Fossilized Birth-Death, and Bayesian Analysis of Macroevolutionary Mixtures, etc.) to uncertainty in divergence time estimates has not particularly been assessed and remains unknown.

In this symposium, the speakers will specifically address the effect of uncertainty from divergence time estimates on **DR** expectations in methods used to test diversification hypothesis within a temporal (change-through-time), spatial (biogeographic) and phylogenetic (lineage-specific) context, through the analyses of both empirically derived dated phylogenies and simulations. The speakers will try to detect general trends on divergence time uncertainty and to relate these trends to the quantified sensitivity and robustness of **DR** estimators, so that a broader sense on the stability of diversification inferences from various types of uncertainty from divergence time estimates can be established for the general use of the field.

Chair/Organizer:

Luna L. Sánchez-Reyes <sanchez.reyes.luna@gmail.com>; +1 (917) 891 7599

Postdoc, Department of Ecology & Evolutionary Biology, University of Tennessee, Knoxville

Invited speakers:

Rebeca Hernández-Gutiérrez <rebecahdezgtz@gmail.com>; **Confirmed**

PhD student, Departamento de Botánica, Instituto de Biología, Universidad Nacional Autónoma de México (UNAM). Mexico

“Age uncertainty estimates from the fossilized birth-death and its effect on diversification rates inferences in the Angiosperm family of chocolate, Malvaceae.”

Itzi Fragoso-Martínez <i.fragoso@ciencias.unam.mx>; **Confirmed**

PhD student, Departamento de Botánica, Instituto de Biología, Universidad Nacional Autónoma de México (UNAM). Mexico

“Inferring divergence times from high throughput sequencing genomic data: implications for the diversification process of *Salvia*.”

Orlando Schwery <oschwery@vols.utk.edu>; **Confirmed**

PhD student, Ecology & Evolutionary Biology, University of Tennessee, Knoxville. USA

“A sensitivity analysis of age uncertainty estimates on diversification rates: a numerical approach.”

Dave Bapst <dwbpast@gmail.com>; **In process**

Assistant Research Professor, Geology & Geophysics, Texas A & M University

Postdoc, Ecology & Evolutionary Biology, University of Tennessee Knoxville. USA

Invited topic: “Effect of uncertainty from fossil derived lineage ages on diversification rate estimates”

April Wright <april.wright@selu.edu>; **Confirmed**

Researcher, Biology Department, Southeastern Louisiana University. USA

“Effect of incorporating life history information as informative priors of preservation rates on diversification rate analyses with the fossilized birth-death in ants”

Renske Onstein <onsteinre@gmail.com>; **In process**

Junior Researcher, German Centre for Integrative Biodiversity Research (iDiv). Germany

Invited topic: “Effect of uncertainty from divergence time estimates on state dependent diversification models.”

Fabien Condamine <fabien.condamine@gmail.com>; **Confirmed**

Researcher, Institut des Sciences de l'Évolution de Montpellier (ISEM). France

Invited topic: “Divergence time estimates uncertainty effect on inferences from diversification models in biogeographical analyses.”

Luna L. Sánchez-Reyes <sanchez.reyes.luna@gmail.com>; **Confirmed**

Postdoc, Ecology & Evolutionary Biology, University of Tennessee Knoxville. USA

“Leveraging databases to reveal the dated Tree of Life: how much of it can we use to understand the diversification of life on Earth?”

All speakers have been contacted and are 100% confirmed or in process of being confirmed. In the case the speakers that are not fully confirmed yet decide to decline, **alternative speakers** that could potentially present something related to the original topic **are being contacted** (Laura Soul, Lena Cole, Andrea S Meseguer).

New developments in phylogenetics and evolution

Workshop Description

Phylogenies form the foundation of our understanding of both the pattern and process of evolution on Earth. Methods for inferring phylogenies and using them in comparative and macroevolutionary analyses are constantly improving, and it can prove difficult for even seasoned investigators in the field to keep pace. In this workshop we will offer a collection of short (approximately one hour per topic) courses on a diverse array of new analytical methods.

This workshop will be suitable for graduate students, postdocs, and senior faculty. It is intended for users who are already familiar with R and have a good working knowledge of phylogenetics. Attendees will be expected to bring a laptop with R and RStudio installed, and will be provided with a list of necessary R packages beforehand.

Participants and Presentation Titles (all participants confirmed)

Klaus Schliep

University of Massachusetts

Phylogenetic analysis with phangorn and ape

Liam Revell

University of Massachusetts

Phylogenetic comparative biology with phytools

April Wright

Southeastern Louisiana University

Reproducible workflows for total-evidence dating analyses

Luke Harmon

University of Idaho

Investigating evolutionary radiations with Geiger and Arbor

Samantha Price

Clemson University

Macroevolutionary experimental design and how to use simulations to improve your phylogenetic comparative analyses.

Tara Pelletier

Radford University

Conducting posterior predictive checks in Bayesian phylogenetics

Graeme Lloyd

University of Leeds, Leeds UK

Plotting trees against geologic time and generating phylomorphospaces from discrete character data using the R packages Claddis and strap

Dan Warren

Senckenberg Biodiversity and Climate Research Center, Frankfurt Germany

R We There Yet: an R package for diagnosing and visualizing the performance of MCMC chains in Bayesian phylogenetics