spedeSTEM 2.0

New, improved & more fun than ever!

Bryan Carstens, Matthew Demarest, Maxim Kim, Tara Pelletier, Jordan Satler.

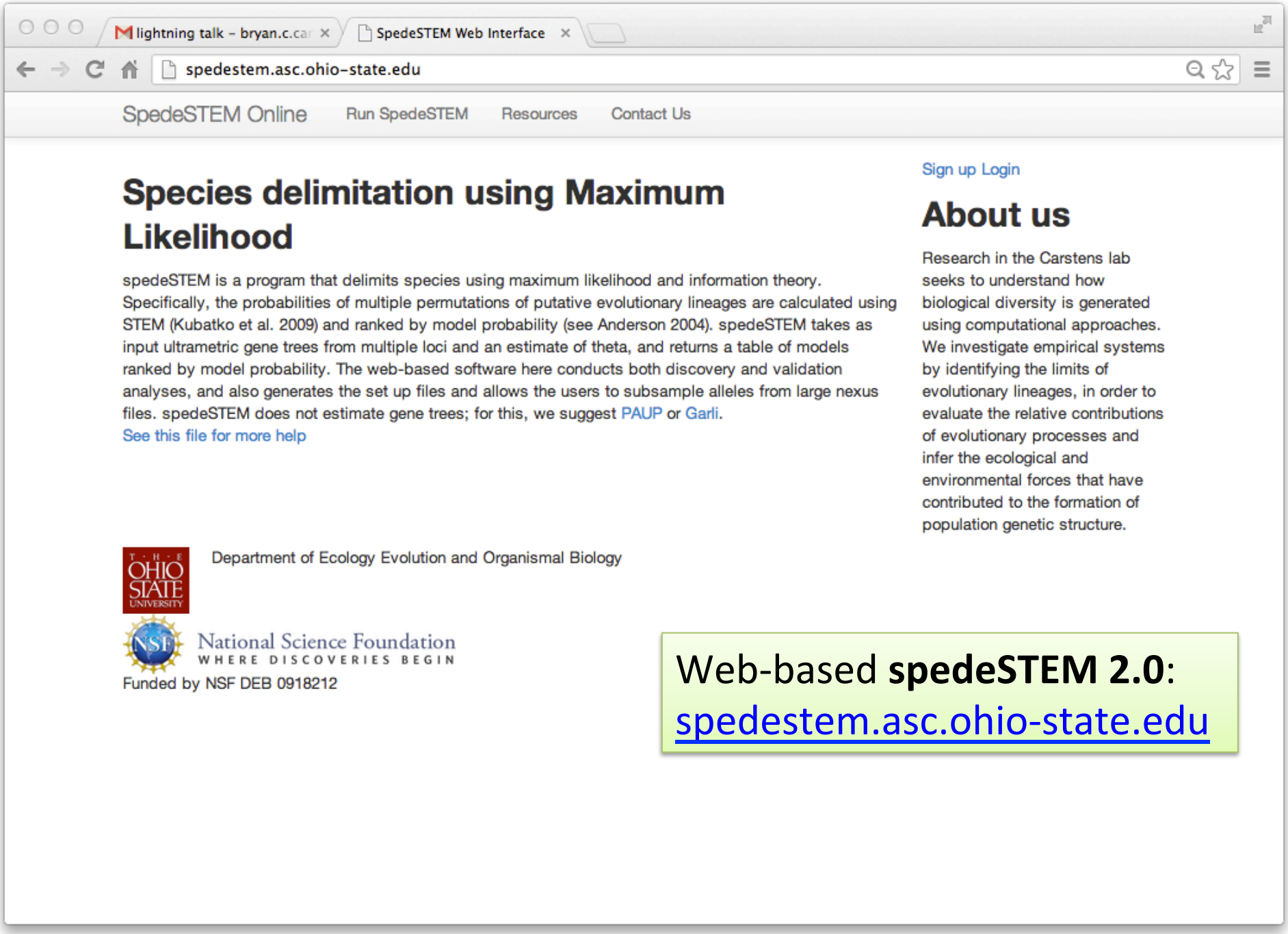
MOLECULAR ECOLOGY
RESOURCES
Molecular Ecology Resources (2011) **11**, 473–480 doi: 10.1111/j.1755-0998.2010.02947.x

TECHNICAL ADVANCES

SpedeSTEM: a rapid and accurate method for species delimitation

DANIEL D. ENCE and BRYAN C. CARSTENS
Department of Biological Sciences, Louisiana State University, 202 Life Sciences Building, Baton Rouge, LA 70803, USA

- takes ultrametric gene trees as input
- calculates the probability of species trees that represent all permutations of *n* putative lineages
- ranks the models using information theory


lightning talk - bryan.c.car
SpedeSTEM Web Interface
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Species delimitation using Maximum Likelihood
spedeSTEM is a program that delimits species using maximum likelihood and information theory. Specifically, the probabilities of multiple permutations of putative evolutionary lineages are calculated using STEM (Kubatko et al. 2009) and ranked by model probability (see Anderson 2004). spedeSTEM takes as input ultrametric gene trees from multiple loci and an estimate of theta, and returns a table of models ranked by model probability. The web-based software here conducts both discovery and validation analyses, and also generates the set up files and allows the users to subsample alleles from large nexus files. spedeSTEM does not estimate gene trees; for this, we suggest PAUP or Garli.
See this file for more help
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About us
Research in the Carstens lab seeks to understand how biological diversity is generated using computational approaches. We investigate empirical systems by identifying the limits of evolutionary lineages, in order to evaluate the relative contributions of evolutionary processes and infer the ecological and environmental forces that have contributed to the formation of population genetic structure.
THE OHIO STATE UNIVERSITY
Department of Ecology Evolution and Organismal Biology
National Science Foundation
WHERE DISCOVERIES BEGIN
Funded by NSF DEB 0918212
Web-based spedeSTEM 2.0:
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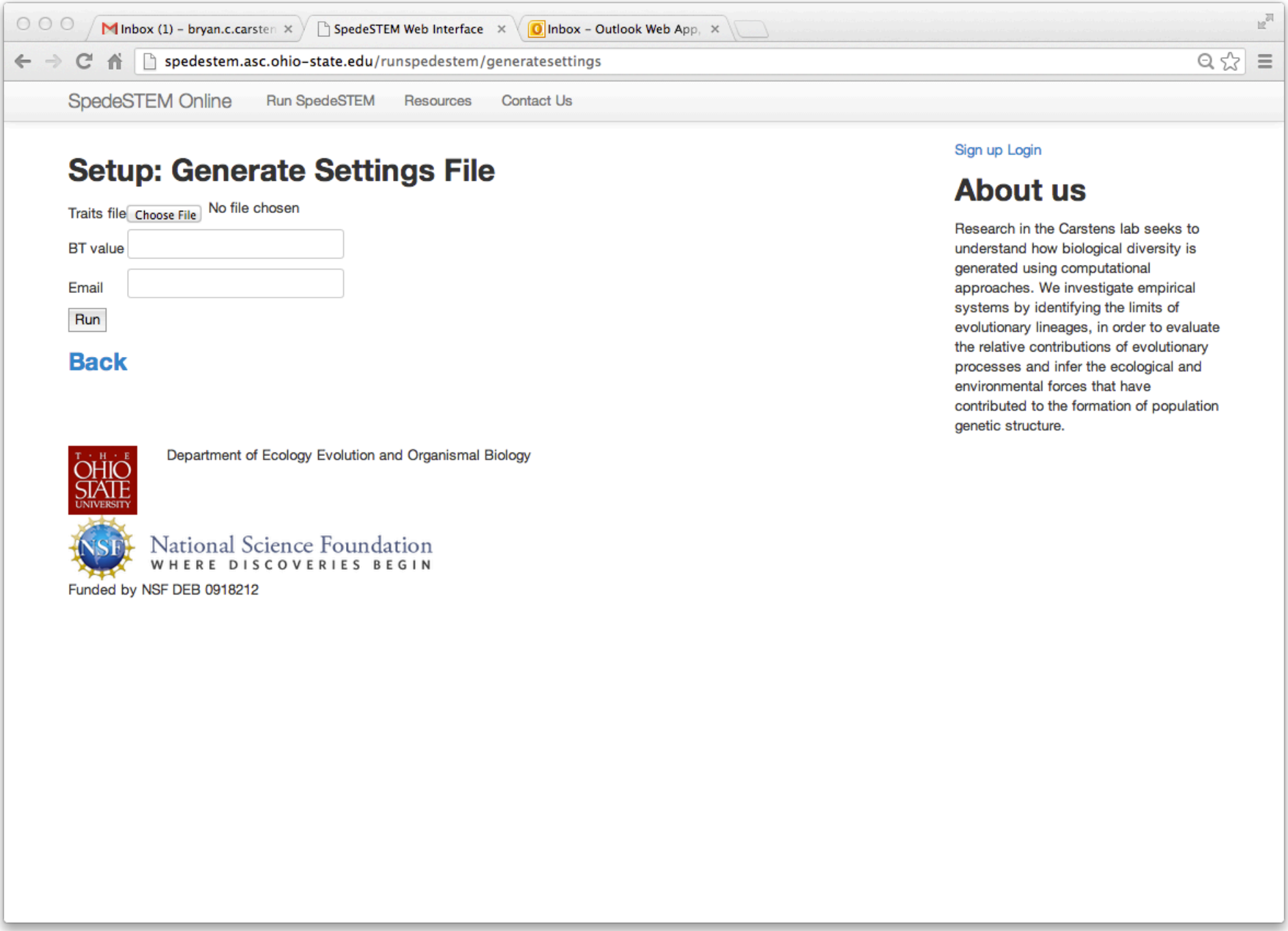
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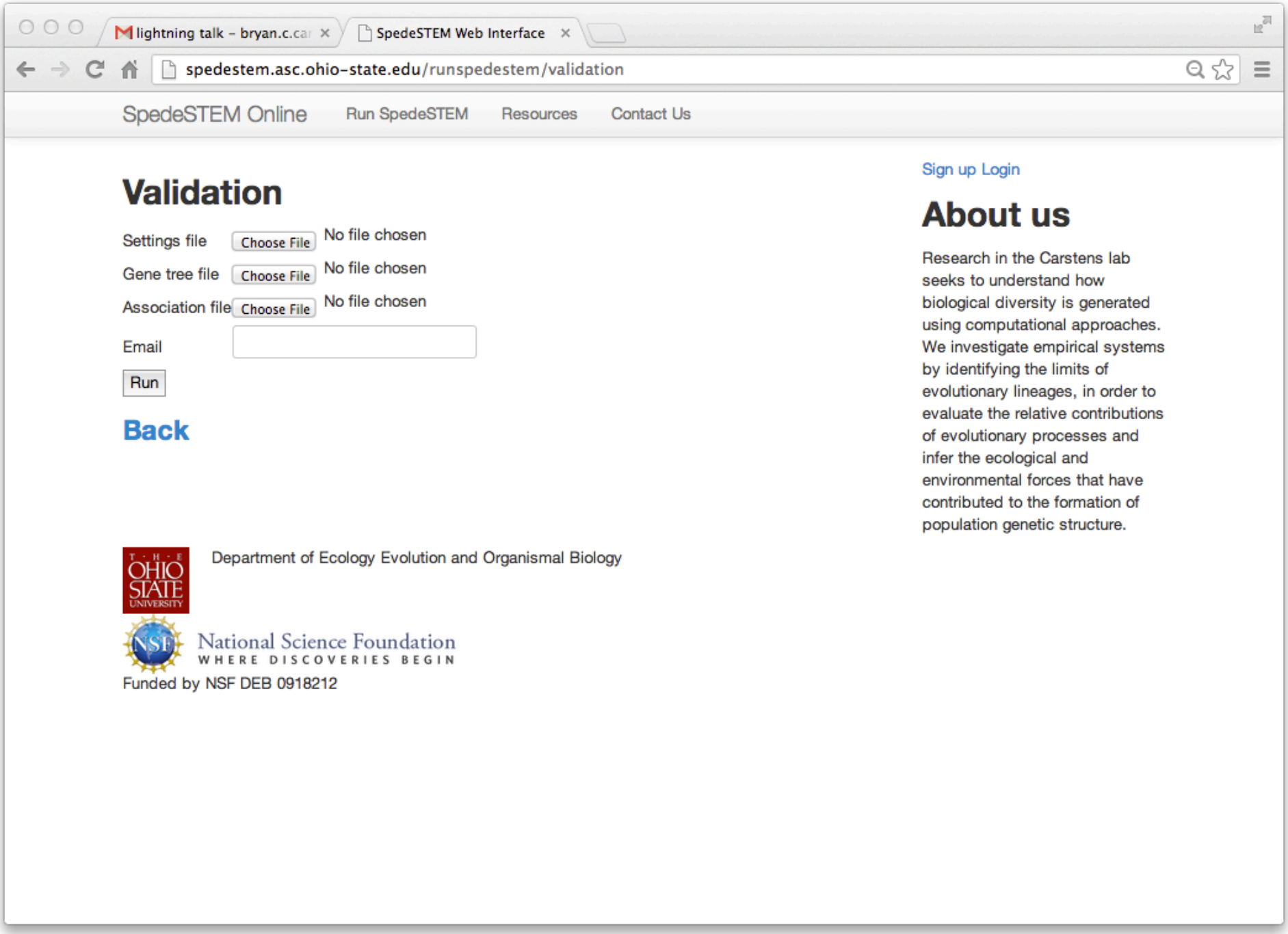
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SpedeSTEM Online
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Validation
Settings file
Choose File
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Association file
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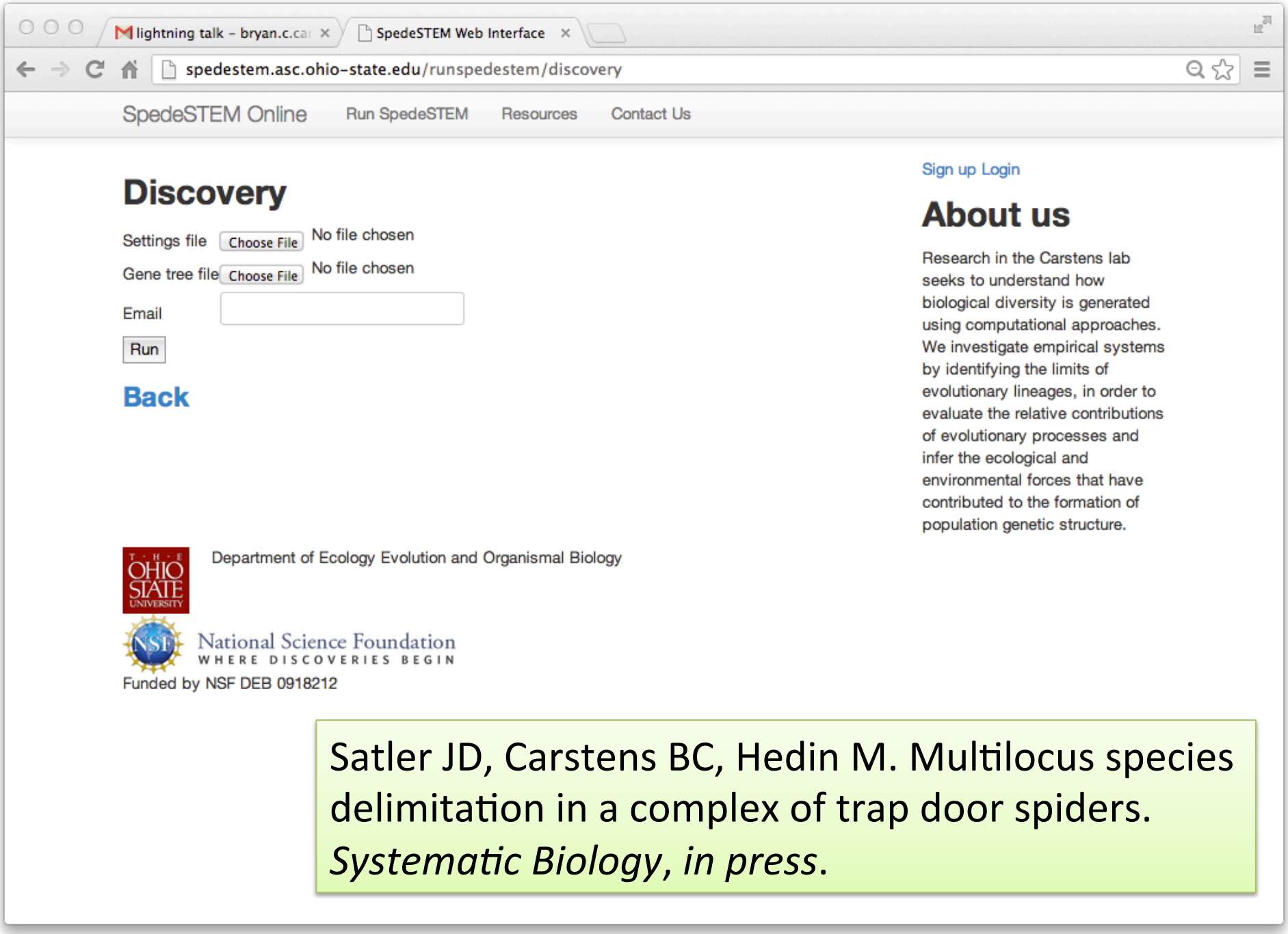

Satler JD, Carstens BC, Hedin M. Multilocus species delimitation in a complex of trap door spiders. *Systematic Biology*, *in press*.

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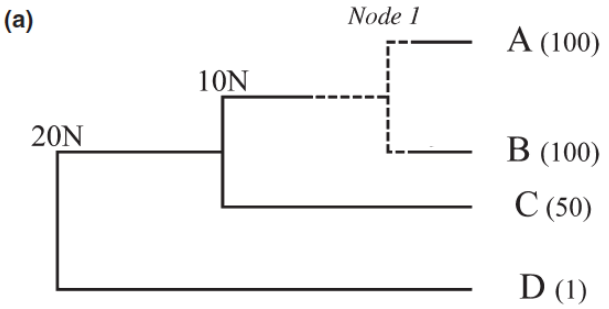

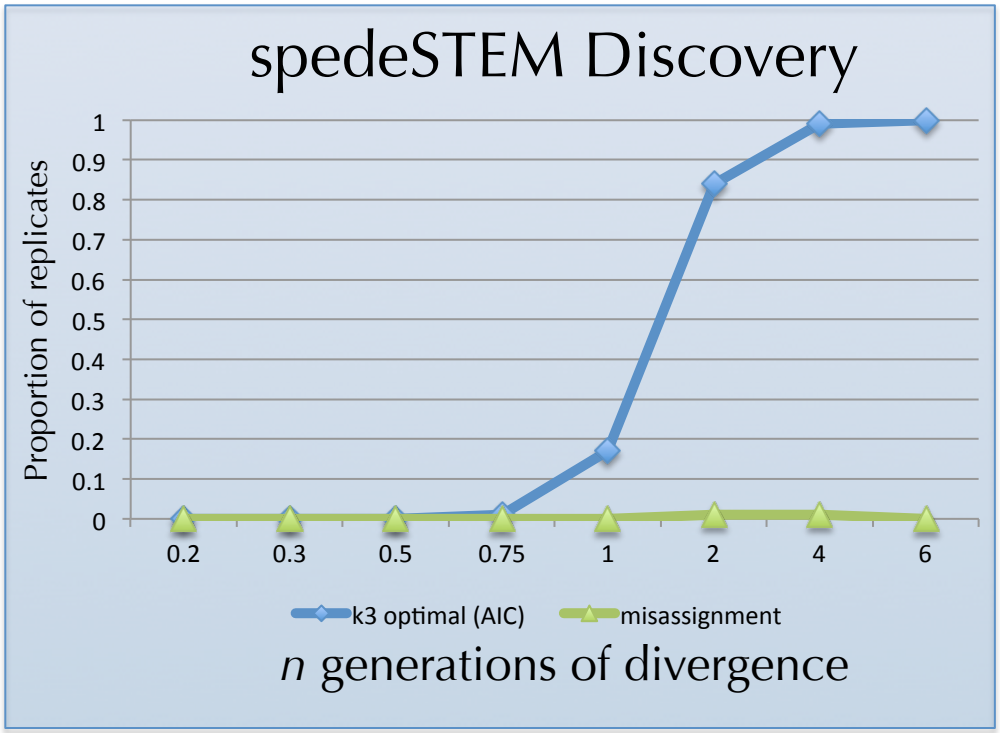

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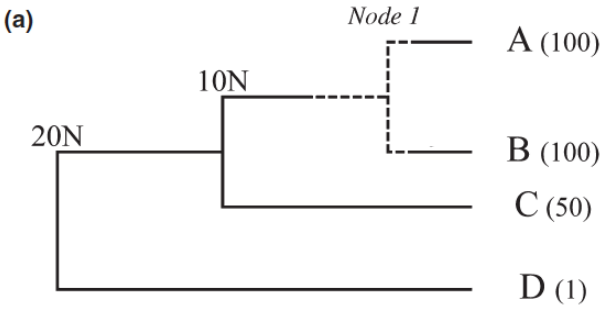

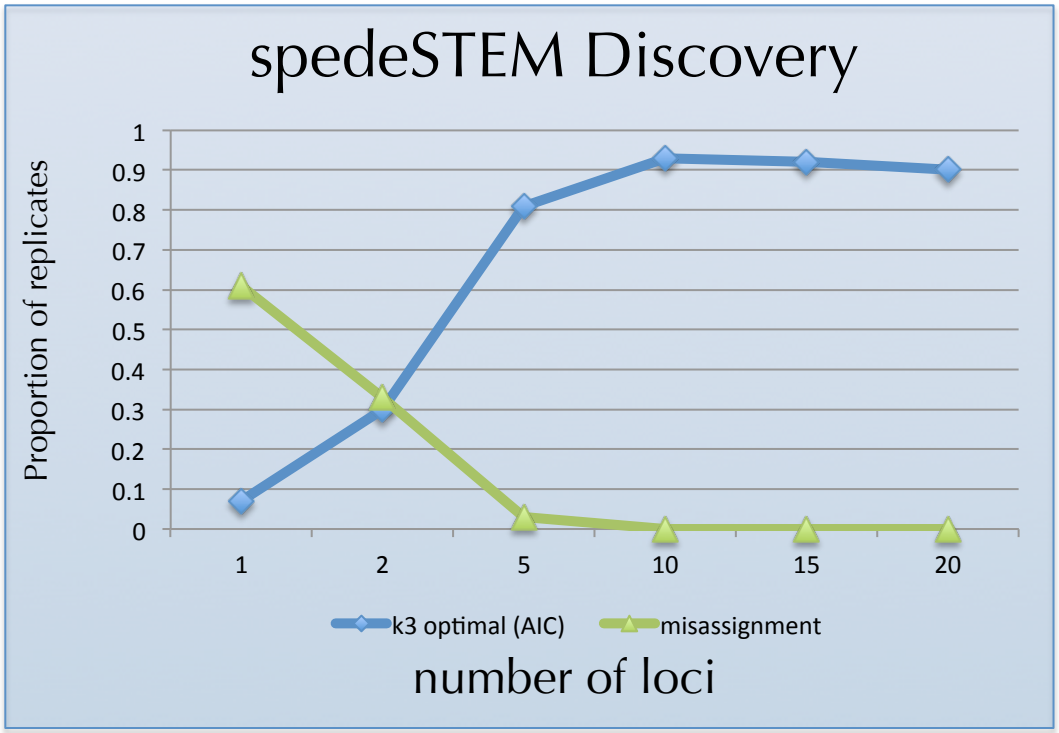

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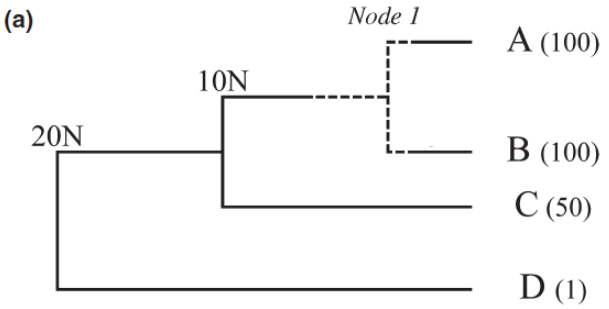

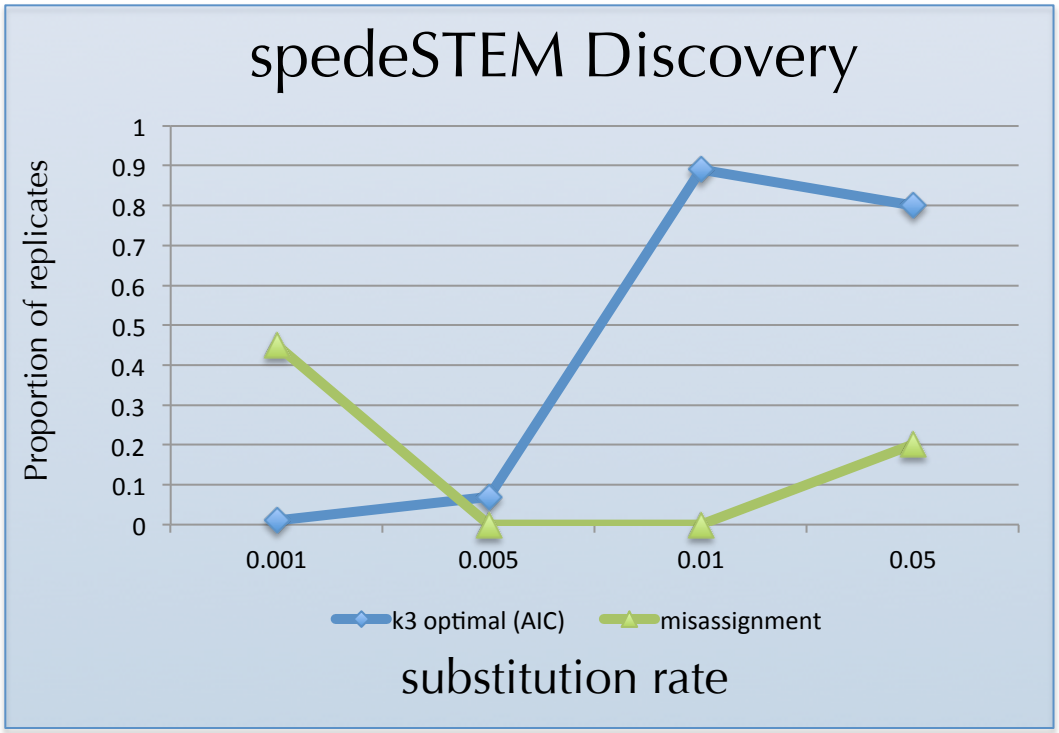

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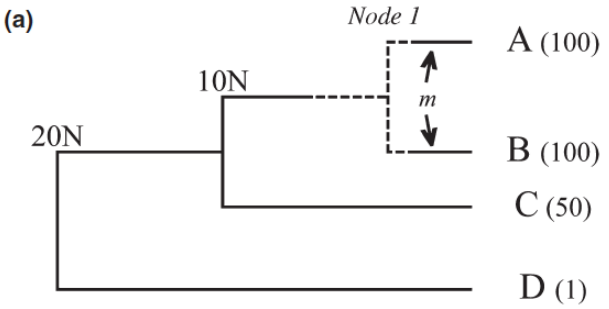

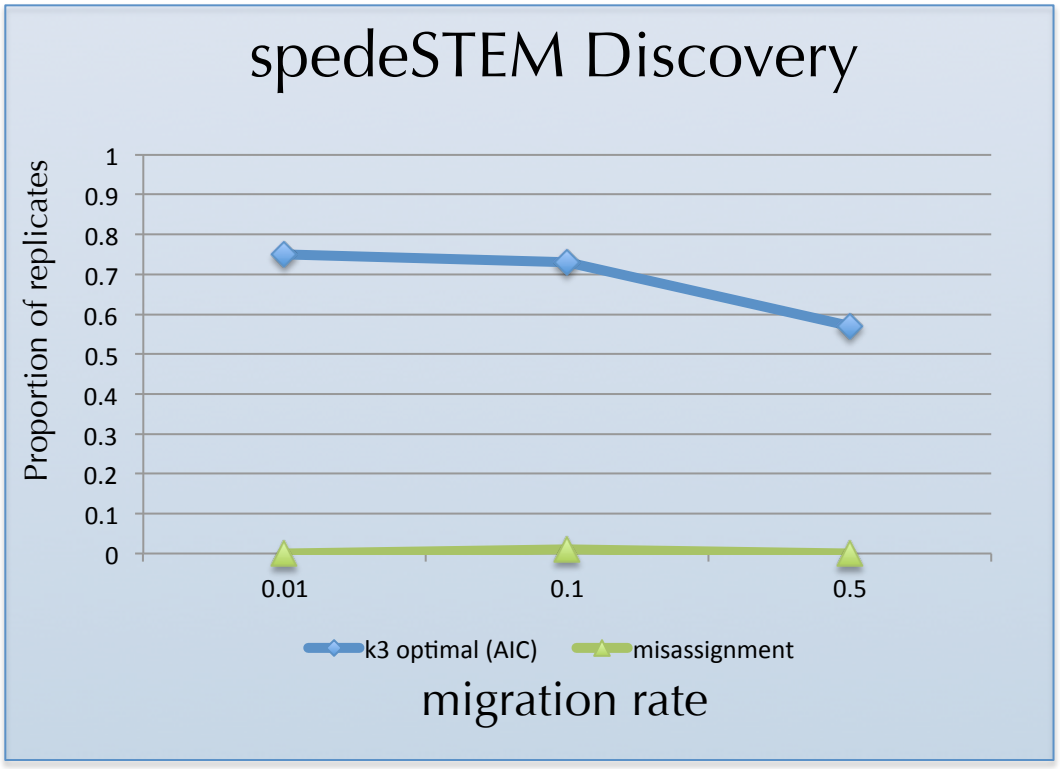

Acknowledgments

- NSF (DEB-0918212; DEB-1257784)
- Past and present members of the Carstens lab
- The *NIMBioS* Species Delimitation Working Group
- The Weisrock Lab at UK

I'm hiring a Post-doc and graduate students for my new lab – let's talk if interested!

Questions?

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Download python version of **spedeSTEM 2.0** from our web-site: carstenslab.org.ohio-state.edu

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