K/A

Kevin Amses, Ph.D.

COMPUTATIONAL BIOLOGIST

<email first please>
amsesk@oregonstate.edu
Corvallis, OR, USA
github.com/amsesk
linkedin.com/in/amsesk
amsesk.github.io

FLUENCIES

Level	Skill
Advanced	python
Advanced	R
Advanced	Unix shell
Intermediate	rust
Proficient	git and GitHub

EDUCATION

Ph.D. Ecology and Evolutionary Biology

"Single cell sequencing facilitates genome-enabled biology in uncultured fungi and resolves deep branches on the fungal tree of life."
University of Michigan
2015 – 2021

M.S. Ecology and Evolutionary Biology

University of Michigan
2015 – 2017

B.S. Botany, minor Organic Chemistry

Humboldt State University
2009 – 2015

ABOUT ME

I pair a broad set of self-taught computational fluencies with a strong theoretical foundation in biology. I have successfully used these skills to study microbial evolution.

Specific skills and experience in:

- metagenomics
- single-cell genomics
- genome-scale phylogenetics
- genomic variation
- *de novo* genome assembly and annotation
- comparative genomics
- transcriptomics
- data visualization
- biological software development

EXPERIENCE

Postdoctoral Scholar

Oregon State University / Corvallis, OR / June 2021 – present

Lead researcher on government-funded project to study the evolution and distribution of bacterial endosymbionts of soil fungi in the Mortierellomycotina.

- Design and deploy bioinformatics tools and pipelines for analyzing NGS data.
- Manage shared computational resources for working group, including HPC.
- Conduct phylogenomic analyses, metagenomic filtering, *de novo* genome assembly and annotation, comparative genomics, etc. of host-endosymbiont pairs.
- Cultivate microbes for purification and sequencing of biological molecules.
- Provide mentorship in bioinformatic and molecular wet lab techniques.

SELECTED PUBLICATIONS

Amses, K.R., *R. Simmons, J.E. Longcore, S.J. Mondo, K. Seto, G. Jeronimo, A. Bonds, C.A. Quandt, W. Davis, Y. Chang, B.A. Federici, A. Kuo, K. LaButti, J. Pangilinan, W. Andreopoulos, A.J. Tritt, R. Riley, H. Hundley, J. Johnson, A. Lipzen, K. Barry, B.F. Lang, C.A. Cuomo, N.E. Buchler, I.V. Grigoriev, J.W. Spatafora, J.E. Stajich, T.Y. James. 2022. Phylogenomic analysis of zoosporic taxa suggests diploid-dominant life cycles characterized the early evolution of Fungi. Proc Natl Acad Sci USA. 119(36):e2116841119. doi: 10.1073/pnas.2116841119.*

Amses, K.R., W.J. Davis and T.Y. James. 2020. *SCGid: a consensus approach to contig filtering and genome prediction from single cell sequencing libraries of uncultured eukaryotes. Bioinform. 36(7): 1994–2000. doi: 10.1093/bioinformatics/btz866.*

Davis, W.J., ***K.R. Amses****, G.L. Benny, D. Carter-House, Y. Chang, I. Grigoriev, M.E. Smith, J.W. Spatafora, J.E. Stajich, T.Y. James. 2019. Genome-scale phylogenetics reveals and monophyletic Zoopagales (Zoopagomycota, Fungi). Mol Phylogenet Evol. 133:152–163. doi: 10.1016/j.ympev.2019.01.006.*