

Andrew Magee

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Education

- 2016–2021 **PhD**, UW Seattle, Biology.
2011–2015 **BS with Highest Honors**, UC Davis, Animal Biology.

Publications

Referreed Publications

- **Magee AF**, Höhna S, Vasylyeva TI, Leaché AD, Minin VN. Locally adaptive Bayesian birth-death model successfully detects slow and rapid rate shifts. *PLoS Computational Biology* 16 (10): e1007999. <https://doi.org/10.1371/journal.pcbi.1007999>
- **Magee AF***, Hilton SK*, DeWitt WD*. Robustness of phylogenetic inference to model misspecification caused by pairwise epistasis. *Molecular Biology and Evolution* 38 (10): 4603-4615. <https://doi.org/10.1093/molbev/msab163> (* indicates co-first-authorship)
- Pekar JE, **Magee AF**, et al. The molecular epidemiology of multiple zoonotic origins of SARS-CoV-2. *Science* 377 (6609): 960-966. <https://doi.org/10.1126/science.abp8337>
- Faulkner JF, **Magee AF**, Shapiro B., Minin VN. Horseshoe-based Bayesian nonparametric estimation of effective population size trajectories. *Biometrics* 76 (3): 677-690. <https://doi.org/10.1111/biom.13276>
- Fourment M, **Magee AF**, Whidden C, Bilge A, Matsen FA, Minin VN. 19 dubious ways to compute the marginal likelihood of a phylogenetic tree topology. *Systematic Biology* 69 (2): 209-220. <https://doi.org/10.1093/sysbio/syz046>
- Whidden C, Claywell B, Fisher T, **Magee AF**, Fourment M, Matsen FA. Systematic exploration of the high likelihood density set of phylogenetic trees. *Systematic Biology* 69 (2): 280-293. <https://doi.org/10.1093/sysbio/syz047>
- **Magee AF**, May MR, Moore BR. The Dawn of Open Access to Phylogenetic Data. *PLoS ONE* 9(10): e110268. <https://doi.org/10.1371/journal.pone.0110268>

Preprints

- Höhna, S, Kopperud, BT, **Magee, AF** (2022). CRABS: Congruent Rate Analyses in Birth-death Scenarios. In press at *Methods in Ecology and Evolution* [bioRxiv:476142v1](https://doi.org/10.1111/2041-210X.14444)
- **Magee AF**, Karcher MD, Matsen FA, Minin VN. How trustworthy is your tree? Bayesian phylogenetic effective sample size through the lens of Monte Carlo error. In revisions at *Bayesian Analysis* [aRxiv:2109.07629](https://doi.org/10.1214/20-BA1009)
- Kopperud, BT, **Magee, AF**, Höhna, S, (2022). Rapidly changing speciation and extinction rates can be inferred in spite of non-identifiability. In revisions at *PNAS* [bioRxiv:491456v1](https://doi.org/10.1073/pnas.2111111119)
- **Magee AF**, Höhna S Impact of K-Pg Mass Extinction Event on Crocodylomorpha Inferred from Phylogeny of Extinct and Extant Taxa. [bioRxiv:426715v1](https://doi.org/10.1101/2021.09.15.456151)

Non-refereed Publications

- Faulkner JF, **Magee AF**, Shapiro B., Minin VN. Rejoinder for discussion on “Horseshoe-based Bayesian nonparametric estimation of effective population size trajectories.” *Biometrics* 76 (3): 695-699. <https://doi.org/10.1111/biom.13273>
- Matsen FA, Karcher MD, Fourment M, **Magee AF**, Swanepoel, C, Zhang, C. Learning, using, and extending variational distributions of phylogenetic trees. 14th Conference on Machine Learning in Computational Biology. [Link](#).
- **Magee AF**. The Makings of a Meta-Analysis, or: How I Wasted Dozens of Hours Obtaining Publicly Available Data. [Essay for DNAdigest](#)

Conference Presentations and Posters

- Scalable random-effects substitution models for phylogenetics. *Talk* presented at: 29th International Dynamics & Evolution of Human Viruses. June 2022; San Diego, California.
- A prelude to “how trustworthy is your tree?”, or, why is phylogenetic inference difficult? *Invited talk* presented at: BayesComp-ISBA Workshop “Measuring the quality of MCMC output.” October 2021; online.
- Fossilized birth-death models, crocodiles, and the K-Pg mass extinction. *Talk* presented in Mayr Award Symposium at: Evolution 2021. June 2021; online.
- Flexible birth-death tree models with Markov random fields. *Talk* presented at: WNAR IBS Conference 2019. June 2019; Portland, Oregon.
- Horseshoes and hand grenades: shrinking models with exploding numbers of parameters using horseshoe priors. *Talk* presented at: Evolution 2017. June 2017; Portland, Oregon.
- Diversity-dependent diversification: fact or artifact? *Poster* presented at: Evolution 2016. June 2016; Austin, Texas.
- A meta-analysis exploring the prevalence of density-dependent diversification. *Poster* presented at: New Frontiers in Botany: Botany 2014. July 2014; Boise, Idaho.

Other Presentations

- Birth-death congruence classes can be collapsed using Bayesian shrinkage priors. *Talk* co-presented with Bjørn Kopperud as part of the online phyloseminar series. February 2021; online. [Link](#).

Awards and Honors

- 2021 **Outstanding Contribution Prize**, Awarded for presentation and participation at 2021 BayesComp-ISBA workshop “Measuring the quality of MCMC output.”
- 2021 **Ernst Mayr Award**, Award for outstanding graduate student talk at Evolution 2021 meeting, recognizing creative and high-quality dissertation research.
- 2019 **DAAD Short-Term Research Grant**, Provided travel support to work with Sebastian Höhna in Munich, October 2019.
- 2019 **Walker Family Endowed Fellowship in Biology**, Award offered to UW Biology graduate students for research or travel expenses.
- 2016 **NSF-GRFP Fellow**
- 2016 **ARCS Foundation Fellow**
- 2015 **University Medal**, The University Medal is the highest campus honor, awarded to a single graduating senior in recognition of superior scholarship and achievement.
- 2014 **Barry Goldwater Scholarship**, Awarded to undergraduates (nominated by their institution) demonstrating academic merit and potential for a career in research.

Software

treess	R package for Bayesian phylogenetic MCMC diagnostics. Link .	(Principal developer)
BEAST	Field-standard software for Bayesian phylodynamic analysis. Link .	(Contributor)
RevBayes	General purpose package for Bayesian phylogenetic analysis. Link .	(Contributor)
CRABS	R package for birth-death model identifiability. Link .	(Co-developer)
BIOL 481	Material for two R-based dry labs for UW BIOL 481. Link .	(Principal developer)

Teaching experience

- 2018 BIOL 481: While TAing for this class (Experimental Evolution and Ecology), I helped to develop a set of computational (dry) labs for the course. I devised lab protocols and wrote R code necessary for students to investigate population cycling and the mechanism of mutation.
- 2017 BIOL 180: TA for UW Biology’s first course in the intro series. Wrote recommendations for several students.

- 2014 ISHP Fall Seminar: I and a team of other undergraduates planned and ran a mandatory seminar for the 115 freshmen in the Integrated Studies Honors Program (ISHP). The seminar provided an interdisciplinary look at ways students engage with society and nature. I and another student were charged with one class period, for which we brought in a guest speaker, engaged students with scientific literature, and led a discussion about the cognitive benefits of nature.
- 2014 ISHP Colloquium: I co-led a weekly discussion for the fall seminar in which my partner and I attempt to have the students engage with the material in engaging ways, such as informal debates. Our end goal was for students to engage with the material on a philosophical level.
- 2013 ISHP Spring Seminar: I and four other students led a seminar on ethics for 80 sophomores in the ISHP. The course included lectures and whole class discussions.

Professional service

Reviewer

- BMC Evolutionary Biology
- Methods in Ecology and Evolution
- Molecular Biology and Evolution
- Molecular Ecology Resources
- Systematic Biology
- Virus Evolution

Departmental Service

- 2020-2021 Member, UW Biology Graduate Programming Committee
- 2019-2020 Member, UW Biology Graduate Programming Committee