**Robert S. Harbert, Ph.D.**

**Curriculum Vitae**

Stonehill College, Easton, MA

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1. **WORK AND EDUCATION**  
     
   **EMPLOYMENT HISTORY**   
   Stonehill College, Easton, MA. Assistant Professor of Biology. August 2016 to present.  
     
   American Museum of Natural History, New York, NY, Gerstner Scholar in Bioinformatics and Computational Biology. July 2016-June 2018.  
     
   **OTHER APPOINTMENTS**  
     
   American Museum of Natural History, New York, NY. Visiting Scientist at the Sackler Institute for Comparative Genomics. 2018-present  
     
   **EDUCATION**   
     
   **Ph.D**., Plant Biology, Cornell University, Ithaca, NY. 2016. Dissertation: “The intersection of climate and niche: Likelihood estimation of modern and past climate using plant biodiversity”, Advisor: Dr. Kevin C. Nixon  
     
   **B.S.** Biology, Roanoke College, Salem, VA. 2011. Advisor: Dr. Leonard Pysh.
2. **SCHOLARSHIP**  
     
   **PEER REVIEWED PUBLICATIONS**  
     
   **Harbert, R.,** Cunningham, S.W. and Tessler, M., 2020. Spatial modeling could not differentiate early SARS-CoV-2 cases from the distribution of humans on the basis of climate in the United States. *PeerJ*, *8*, p.e10140.  
     
   Moore, G., Tessler, M., Cunningham, S.W., Betancourt, J. and **R. Harbert.** 2020. Paleo‐metagenomics of North American fossil packrat middens: Past biodiversity revealed by ancient DNA. *Ecology and Evolution*, 10(5), pp.2530-2544. https://doi.org/10.1002/ece3.6082   
     
   **Harbert, R.S.,** and A. Baryiames. 2019. cRacle: R Tools for Estimating Climate from Vegetation. *Applications in Plant Sciences*, e11322. <https://doi.org/10.1002/aps3.11322>**Harbert, R.S.,** and K.C. Nixon. 2018. Dynamic Quaternary vegetation as a proxy for 50,000 years of climate change in Western North America. *Open Quaternary*, https://doi.org/10.5334/oq.46   
     
   **Harbert, R.S.** 2018. Algorithms and database strategy for the reconstruction of plant communities from ancient and environmental DNA. *Applications in Plant Sciences*, e1034   
     
   Martinez, C., T.Y.S. Choo, D. Allevato, K. Nixon, W. Crepet, **R. Harbert**, C. Daghlian. 2016. Rariglanda jerseyensis a new ericalean fossil flower from the Late Cretaceous of New Jersey. *Botany* 94: 747–758 dx.doi.org/10.1139/cjb-2016-0062   
     
   **Harbert, R.S.,** and K.C. Nixon. 2015. Climate reconstruction analysis using coexistence likelihood estimation (CRACLE): A method for the estimation of climate using vegetation. *American Journal of Botany*, doi:10.3732/ajb.1400500   
     
   **Harbert, R.S.,** A.H.D. Brown, and J. Doyle. 2014. Climate Niche Modeling in the Perennial Glycine (Leguminosae) Allopolyploid Complex. *American Journal of Botany* 101(4):710-721.   
     
   Pysh, L., N. Alexander, L. Swatzyna, and **R. Harbert**. 2012. Four alleles of AtCESA3 form an allelic series with respect to root phenotype in Arabidopsis thaliana. *Physiologia Plantarum* 144:369-381.  
     
   **PREPRINTS AND PROTOCOLS**  
     
   Callahan, J., **R. Harbert**. 2020. Aquatic eDNA sampling and plant community metabarcoding with portable Nanopore Flongle sequencing (v0.0.3). *protocols.io,* dx.doi.org/10.17504/protocols.io.bc4wiyxe  
     
   **PROFESSIONAL PRESENTATIONS AND POSTERS**   
     
   O’Shea, Patrick and **R.S. Harbert**. 2019. Using convex hulls to identify outliers in population distribution models. *Student Conference on Conservation Science-New York. American Museum of Natural History.*   
     
   **Harbert, R.S.** 2017. Efficient data mining of global primary biodiversity data using SQL database mirrors. *Biodiversity Informatics & Herbarium Digitization Session 1. Botanical Society of America.* Fort Worth, TX. <http://www.botanyconference.org/engine/search/index.php>? func=detail&aid=286   
     
   **Harbert, R.S.**, and K.C. Nixon. 2017. 50,000 Years of climate inferred using plant macrofossils from packrat (*Neotoma* spp.) middens in western North America. *Cookson/Moseley Award Presentations. Botanical Society of America.* Fort Worth, TX. <http://www.botanyconference.org/engine/> search/index.php?func=detail&aid=399   
     
   **Harbert, R.S.**, and K.C. Nixon. 2016. Applications of a novel model (CRACLE) for the estimation of >30,000 years of paleoclimate using packrat (Neotoma spp.) midden plant macrofossils from the American Southwest. *33Rd Northeast-Midcontinent Paleobotanical Colloquium*, Cornell University, Ithaca, NY May 13-15, 2016.   
     
   **Harbert, R.S.**, and J.Doyle. Climate niche, invasiveness, and allopolyploidy: The case of perennial *Glycine* (Leguminosae). Presentation, *Botany 2013*, New Orleans, LA  
     
   **Harbert, R.S.** Growth and Nutrient Accumulation Responses to Phosphorus Deficiency in Cellulose Synthase Mutants of Arabidopsis thaliana. Poster presentation, *2011 Meeting of the American Society of Plant Biologists,* Minneapolis, MN   
     
   **Harbert, R.S.** Root architecture responses to phosphorus in cellulose synthase mutants of *Arabidopsis thaliana*. Poster presentation, *2010 Meeting of the American Society of Plant Biologists,* Montreal, ON, Canada   
      
     
   **IN PROGRESS WORK**  
     
   **Harbert, R.S.,** J.J. Callahan, V. Rapela, C. Ponder, E. Pederson, A. Laguerre, T. Frazier, C. Powell, M. Raposa, W. Gilmore, and A. Williams. Monitoring plant biodiversity in aquatic eDNA with low-cost Nanopore Flongle sequencing. Target: *Applications in Plant Sciences*(Submit SP2021)  
     
   **SCIENTIFIC SOFTWARE**  
     
   eDNA BLAST -- <https://github.com/developing-bioinformatics/eDNA_BLAST> -- Core analysis tools for processing eDNA sequence data.  
     
   cRacle – <https://github.com/rsh249/cRacle.git> -- R Library for the estimation of climate from vegetation  
     
   USGS packrat midden database archive -- <https://github.com/rsh249/usgs_packrat_midden_db> -- code for opening access to a USGS curated database of packrat midden plant macrofossils.  
     
   rasterExtras – <https://github.com/rsh249/rasterExtras.git> -- R Library for parallel computation on raster files  
     
   ISOETES1 – <https://github.com/rsh249/ISOETES1.git> -- Pipeline for comparison of metagenomic methods for short-read DNA sequence data.  
     
   NeotomaSeq – <https://github.com/rsh249/NeotomaSeq.git> -- Pipeline for metagenomic analysis of ancient DNA from packrat middens.  
     
   raster\_PET – <https://github.com/rsh249/raster_PET.git> -- R code for calculating Evapotranspiration from global climate data.  
     
   **INVITED DEPARTMENT SEMINARS**   
     
   March 2018, UMass Dartmouth  
   August 2017, New York Botanic Gardens
3. **TEACHING**  
     
   **COURSES**  
   BIO101 – Biological Principles I (Lecture/Lab)  
   BIO102 – Biological Principles II (Lecture/Lab)  
   BIO303 – Environmental Botany  
   BIO316 – R Programming for Biologists  
   BIO331 – Introduction to Bioinformatics   
   BIO332 – Applied Bioinformatics   
   DAN602 – Statistics for Data Analytics  
   DAN606 -- Big Data Management  
     
   **OPEN EDUCATIONAL MATERIALS**  
     
   Developing Bioinformatics community -- <https://github.com/developing-bioinformatics> (continuing)  
     
   Introduction to Bioinformatics: <https://bio331.devbioinformatics.org> (2021)  
     
   Applied Bioinformatics: <https://bio332.devbioinformatics.org> (2020)  
     
   R Programming for Biologists: <https://r4bio.devbioinformatics.org> (2020)  
     
   AMNH -- RGGS short course in Spatial Bioinformatics: <https://rsh249.github.io/spatial_bioinformatics/> (2018)  
     
   AMNH -- SICG Workshop – Python Programming for Bioinformatics: <https://rsh249.github.io/python_workshop> (2018)  
     
   **MENTORING**

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| **Year** | **Program** | **Student Name** | **Project** |
| 2020 | BIO496 (Fall) | Natasha Moniz | Independent Research (1 credit) |
| 2020 | BIO496 (Fall) | Andrew Williams | Independent Research (1 credit) |
| 2020 | BIO496 (Fall) | Yaniv Kovalski | Independent Research -- Developing a cRacle web application (3 credits) |
| 2020 | BIO496 (Fall) | Cameron DeChristopher | Independent Research -- R training (3 credits) |
| 2020 | BIO496 (Fall) | Nicholas Steege | Independent Research – Ancient DNA bioinformatics (3 credits) |
| 2020 | Internship | Nicholas Steege | Internship at BGI in Boston, MA |
| 2020 | BIO496 (Fall) | Wafae El Arar | Independent Research (2 credits) |
| 2020 | BIO496 (Spring) | Camryn Thompson | Independent Research (1 credit) |
| 2020 | BIO496 (Spring) | Anh Woang | Independent Research -- *Elodea* chloroplast movement experiments (1 credit) |
| 2020 | BIO496 (Spring) | Wafae El Arar | Independent Research -- eDNA lab training (2 credits) |
| 2020 | BIO496 (Spring) | Andrew Williams | Independent Research (1 credit) |
| 2020 | BIO496 (Spring) | Caroline Pitten | Independent Research (2 credits) |
| 2019 | BIO490 (Fall) | Nicholas Botelho | “Paleo-niche modeling of *Larrea tridentata*" (1 credit) |
| 2019 | BIO496 (Fall) | Jordan Callahan | Independent Research (3 credit) |
| 2019 | BIO496 (Fall) | Caroline Pitten | Independent Research (1 credit) |
| 2019 | BIO496 (Fall) | Andrew Williams | Independent Research (1 credit) |
| 2019 | SURE\*\* | Jordan Callahan | “Monitoring Biodiversity from Aquatic eDNA with Nanopore Sequencing” |
| 2019 | SURE\*\* | Patrick O’Shea | “Machine Learning for Spatial Biodiversity Modeling” |
| 2019 | Thesis Reader | Nick Perry | “De-speciation in Madagascar songbird” |
| 2019 | BIO496 (Spring) | Caroline Pitten | Independent Research (1 credit) |
| 2019 | BIO496 (Spring) | Patrick O’Shea | Independent Research (1 credit) |
| 2019 | BIO496 (Spring) | Andrew Williams | Independent Research (1 credit) |
| 2019 | BIO496 (Spring) | Jordan Callahan | Independent Research (1 credit) |
| 2019 | BIO496 (Spring) | Alex Baryiames | ‘cRacle R library development’ (3 credits) |
| 2018 | AMNH REU\* | Grace Moore | “Paleogenomics of Ancient DNA from *Neotoma* packrat midden plant macrofossils” |
| \*NSF funded Research Experience for Undergraduates (REU) at the American Museum of Natural History, New York, NY. \*\*Summer Undergraduate Research Experience (SURE) at Stonehill College | | | |

1. **SERVICE AND ENGAGEMENT ACTIVITIES**   
     
   **COLLEGE SERVICE**  
     
   Technology Advisory Committee (TAC) member (2019-2021)  
     
   Faculty Learning Community for Machine Learning in collaboration with Tim Balint (CS) is launching in SP2021 and will focus on bringing together faculty with computational interests in teaching and scholarship.  
     
   Assisted collaboration with the Massachusetts Green High-Performance Computing Center (MGHPCC) to bring high-performance computing opportunities to Stonehill faculty for teaching and research.  
     
   **DEPARTMENT SERVICE**  
   Biology Department Seminar Co-Coordinator (2019-2021)  
     
     
   **EXTERNAL SERVICE**   
   *Editorial Board, Open Quaternary*. 2018 -- Present.   
   *PlantingScience* —Mentor - 2016-2018   
   *Student Conference on Conservation Science* - New York – 2017 & 2019. Mentorship of students (graduate and undergraduate), poster judging, and discussion hosting.   
   Reviewer for *PLoS One, Genes, Journal of Systematics, Journal of Biogeography, Applications in Plant* Sciences.  
     
   **PROFESSIONAL SOCIETIES**  
   Botanical Society of America (2013-present)
2. **ACADEMIC AWARDS AND FUNDING**   
     
   **OPEN APPLICATIONS**  
   American Philosophical Society, Franklin Grant Program. ($5000)  
     
   **FUNDED**  
   Stonehill College CTL, Curriculum Fellowship, 2020  
   Stonehill College CTL, Curriculum Development Grant, 2018. $1000  
   NVIDIA Product Grant, 2019. Awarded: NVIDIA Titan V GPU (MSRP:$2999)  
   Gerstner Postdoctoral Fellowship, AMNH, 2016-2018. $155,000   
   Student Research Travel Grant. Cornell University, 2013. $2000.   
   Student Travel Award from the Ecological Section, Botanical Society of America, 2013. $500   
   Summer Undergraduate Research Fellowship, 2010. American Society of Plant Biologists. $2500   
     
   **AWARDS**  
   Outstanding Teaching Assistant Award, 2014-2015, College of Agriculture and Life Sciences (CALS), Cornell University, Ithaca, NY 14850.   
   Phi Beta Kappa Honors Society, 2011