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PROFESSIONAL PREPARATION

- University of Southampton, United Kingdom, Molecular Biology, Ph.D. 2010
- King's College London, United Kingdom, Biological Sciences, B.Sc. 2005

APPOINTMENTS

2019 –	Assistant Professor, Department of Marine Sciences, University of Georgia (joint appointment with the UGA Institute of Bioinformatics)
2016 – 2019	Assistant Professor, Department of Nematology, University of California, Riverside
2015 – 2016	Project Scientist, Center for Genomics and Systems Biology, New York University (Lab of Jane Carlton)
2014 – 2015	Birmingham Fellow**,** School of Biosciences, University of Birmingham, UK
2012 – 2014	Postdoctoral researcher, University of California, Davis; UCD Genome Center & Associate with the Center for Population Biology (Advisor: Jonathan Eisen)
2010 – 2011	Postdoctoral researcher, Hubbard Center for Genome Studies, University of New Hampshire (Advisor: W. Kelley Thomas)

RESEACH GRANTS AWARDED

- Principal Investigator, "*Developing free-living marine nematodes as a new model system for the study of aquatic symbioses"*, awarded by the Gordon and Betty Moore Foundation ($350,000; Sept 2020 – Feb 2023)
- Senior Personnel, "*Health Disparities Research at UC Riverside*", National Institutes of Health U54 award (PI: David Lo at UC Riverside, $3,226,921; Aug 2019 – Feb 2024)
- Principal Investigator, "*Assessing the health and productivity of Southern California estuaries using high-throughput sequencing of benthic meiofauna"*, awarded by California Sea Grant ($69,990; Mar 2019 – Feb 2021)
- Principal Investigator, "*End-User driven Jupyter Notebooks for common –Omics workflows"*, awarded by the Gordon and Betty Moore Foundation ($40,000; Nov 2018 – Oct 2019)
- Principal Investigator, "*Phinch: An interactive, exploratory data visualization framework for environmental –Omic datasets*", awarded by the Alfred P. Sloan Foundation ($499,480; July 2017 – Dec 2022)
- Co-PI and Steering Committee Member, "*Understanding the ecological relevance of eDNA in freshwater lotic ecosystems – eDNA: LOFRESH*", awarded by the UK Natural Environment Research Council (PI: Simon Creer at Bangor University, £239,865; Dec 2015 – Mar 2020)
- Principal Investigator, JGI Community Science Program New Investigator Proposal, "Metabolic characterization and carbon cycling potential of nematode-associated bacteria/archaea" (in-kind support for shotgun metagenomic sequencing of 92 samples; Jan 2019 – Dec 2019)
- Co-PI, *"Genomic Responses to the Deepwater Horizon event and development of high-throughput biological assays for oil spills",* awarded by the Gulf of Mexico Research Initiative (PI: Kelley Thomas at Univ. New Hampshire, $367,361; Jan 2016 – Dec 2019)
- Principal Investigator, *"Collaborative Research: RCN EukHiTS: Eukaryotic biodiversity research using high-throughput sequencing",* DBI-1262480 awarded by the National Science Foundation ($296,485; Sept 2013 – Aug 2019)
- Principal Investigator, "*Comparing the Diversity of Nematodes and other Microbial Metazoa across Different Habitats in the Shipley-Skinner Reserve*", awarded by the Shipley Skinner Endowment through the UCR Center for Conservation Biology ($7,490; July 2017 – June 2018)
- Principal Investigator, PressForward Partnership award for development of the Deep-Sea Biology Society website ($10,000; Sept 2015 – Dec 2016)

- Co-PI, *"Assessing benthic meiofaunal community structure in the Alaskan Arctic: A high-throughput DNA sequencing approach",* awarded by the North Pacific Research Board (PI: Sarah Hardy at Univ. Alaska Fairbanks, $40,906; July 2013 – August 2016)
- Principal Investigator, *"A Research-Driven Data Visualization Framework for High-Throughput Environmental Sequence Data"*, awarded by the Alfred P. Sloan Foundation ($247,189; July 2013 – Aug 2014)
- Principal Investigator, *"SMBE Satellite Meeting on Eukaryotic –Omics"* ($27,741 awarded by the Society for Molecular Biology and Evolution; meeting held April 29-May 2, 2013 at UC Davis)
- Co-PI, NESCent Catalysis Meeting on *"High-Throughput Biodiversity Assessment using Eukaryotic Metagenetics"* awarded through the National Evolutionary Synthesis Center (NESCent), Durham, NC. (PI: Kelley Thomas at Univ. New Hampshire, 24 participants funded to attend meeting in January 2011)

AWARDS & HONORS

- Recipient of a 2014 Birmingham Fellowship in Bioinformatics
- "Professors for the Future" Fellowship (2013-14 cohort at UC Davis)

ACADEMIC SERVICE

- Advisory Board, *Environmental DNA,* Wiley open access journal (2018—present)
- Associate Editor, *mSystems*, an American Society for Microbiology journal (2015—present)
- Associate Editor, *Molecular Ecology* and *Molecular Ecology Resources* (2014—present)
- Vice President for Communication (elected Executive Board position), Deep-Sea Biology Society (2014—2018)
- External Review Board, NASA JPL Mars 2020 "Spore to Viable Organism" project (April 2017)
- Deep Carbon Observatory, External Midterm Review Committee (reporting to the President of the Alfred P. Sloan Foundation; October 2014)
- Remote panel service, NIH National Institute of Allergy and Infectious Diseases (2019)
- Ad hoc reviewer, Alfred P. Sloan Foundation (2014—present)
- Ad hoc reviewer and panel service, National Science Foundation (2012—present)
- DOE JGI reviewer for community sequencing proposals (2013—present)
- Ad hoc reviewer, international science agencies (2011—present; Austrian Science Fund, FWO Research Belgium, Hong Kong Research Grants Council, UK Biotechnology and Biological Sciences Research Council)
- Journal Review Work**:** *Aquatic Microbial Ecology, Bioinformatics, BMC Bioinformatics, BMC Biology, BMC Ecology, BMC Evolutionary Biology, Diversity, Environmental Microbiology, Environmental Science and Pollution Research, Experimental Marine Biology, F1000 Research, Freshwater Biology, Frontiers in Earth Science, Frontiers in Zoology, Geobiology, Journal of Biogeography, Journal of Eukaryotic Microbiology, Molecular Ecology, Molecular Ecology Resources, Nature Ecology & Evolution, PeerJ, PLoS Biology, PLoS ONE, PNAS, Proceedings of the Royal Society B, Scientific Reports, The ISME Journal*

PUBLICATIONS – Submitted or in preparation

- **Bik HM**, Pitch Interactive (2014) Phinch: An interactive, exploratory data visualization framework for –Omic datasets, *bioRxiv*, doi: http://dx.doi.org/10.1101/009944 (preprint);

PUBLICATIONS – Peer-reviewed research articles

1. Mincks SL, Pereira TJ, Sharma J, Blanchard A, **Bik HM.** *(in press)* Composition of marine nematode communities across broad longitudinal and bathymetric gradients in the Northeast Chukchi and Beaufort Seas, *Polar Biology*, DOI: 10.1007/s00300-020-02777-1
2. Pereira TJ, De Santiago A, Schuelke T, Hardy SM, **Bik HM** (2020) The impact of intragenomic rRNA variation on metabarcoding-derived diversity estimates: A case study from marine nematodes, *Environmental DNA*, 2(4): 519-534.

3. Qing X$^{\#}$**, Bik HM$^{\#}$**, Yergaliyev TM, Gu J, Fonderie P, Brown-Miyara S, Szitenberg A, Bert W. (2019) Widespread prevalence but contrasting patterns of intragenomic rRNA polymorphisms in nematodes: implications for phylogeny, species delimitation, and life history inference, *Molecular Ecology Resources*, 20(1):318-332. ($^{\#}$ joint first author)
4. Nascimento FJA, Dahl M, Deyanova D, Lyimo LD, **Bik HM**, Schuelke T, Pereira TJ, Björk M, Creer S, Gullström M. (2019) Above-below surface interactions mediate effects of seagrass disturbance on meiobenthic diversity, nematode and polychaete trophic structure, *Communications Biology*, 2: 362.
5. **Bik HM**, Alexiev A, Aulakh S, Bharadwaj L, Flanagan J, Haggerty M, Hird S, Jospin G, Lang JM, Sauder L, Neufeld J, Shaver A, Sethi A, Eisen JA, Coil D (2019) Microbial community succession and nutrient cycling responses following perturbations of experimental saltwater aquaria, *mSphere*, 4 (1): e00043-19.
6. Nascimento FJA, Lallias D, **Bik HM**, Creer S (2018) Sample size effects on the assessment of eukaryotic diversity and community structure in aquatic sediments using high-throughput sequencing, *Scientific Reports,* 8: 11737.
7. Schuelke T, Pereira TJ, Hardy SM, **Bik HM** (2018) Nematode-associated microbial taxa do not correlate with host phylogeny, geographic region or feeding morphology in marine sediment habitats, *Molecular Ecology*, 27(8): 1930-1951. ***(Invited submission for "Host-Associated Microbiome" Special Issue)***
8. Seymour M, Durance I, Cosby BJ, Ransom-Jones E, Deiner K, Ormerod SJ, Colbourne JK, Wilgar G, Carvalho GR, de Bruyn M, Edwards F, Emmett BA, **Bik HM**, Creer S (2018) Acidity promotes degradation of multi-species environmental DNA in lotic mesocosms, *Communications Biology,* 1(1):4. **(editors' picks for one-year anniversary collection)**
9. Brannock PM, Sharma J, **Bik HM**, Thomas WK, Halanych KM (2017) Spatial and temporal variation of intertidal nematodes in the Northern Gulf of Mexico after the Deepwater Horizon oil spill, *Marine Environmental Research*,130:200-212.
10. **Bik HM**, Maritz JM, Luong A, Shin H, Dominguez-Bello MG, Carlton JM (2016) Microbial community patterns associated with Automated Teller Machine (ATM) keypads in New York City, *mSphere,*1(6):e00226-16.
11. Derycke S, De Meester N, Rigaux A, Creer S, **Bik H**, Thomas WK, Moens T (2016) Coexisting cryptic species of the *Litoditis marina* complex (Nematoda) show differential resource use and have distinct microbiomes with high intraspecific variability, *Molecular Ecology,* 25(9):2093-2110.
12. Adams R$^{\#}$, Bateman AC$^{\#}$, **Bik HM$^{\#}$**, Meadow JF$^{\#}$ (2015) Microbiota of the indoor environment: a meta-analysis, *Microbiome,* 3:49. ($^{\#}$ all authors contributed equally)
13. Chariton A, Ho K, Proestou D, **Bik H**, Simpson S, Portis L, Cantwell M, Baguley J, Burgess R, Pelletier M, Perron M, Gunsch C (2014) A molecular-based approach for examining responses of microcosm-contained eukaryotes to contaminant-spiked estuarine sediments, *Environmental Toxicology and Chemistry*, 33(2): 359-369.
14. Darling A, Jospin G, Lowe E, Matsen FA, **Bik HM,** Eisen JA (2014) PhyloSift: phylogenetic analysis of genomes and metagenomes, *PeerJ,* 2:e243.
15. **Bik HM**, Fournier D, Bergeron RD, Sung W, Thomas WK (2013) Intra-Genomic Variation in the Ribosomal Repeats of Nematodes, *PLoS ONE,* 8(10): e78230
16. Stoltzfus A, Lapp H, Matasci N, Deus H, Sidlauskas B, Zmasek CM, Vaidya G, Pontelli E, Cranston K, Vos R, Webb CO, Harmon LJ, Pirrung M, O'Meara B, Pennell MW, Mirarab S, Rosenberg MS, Balhoff JP, **Bik HM**, Heath T, Midford P, Brown JW, McTavish EJ, Sukumaran J, Westneat M, Alfaro ME, Steele A (2013) Phylotastic! Making Tree-of-Life Knowledge Accessible, Re-usable and Convenient, *BMC Bioinformatics*, 14(1):158.
17. Ho KT, Chariton AA, Portis LM, Proestou D, Cantwell MG, Baguley JG, Burgess RM, Simpson S, Pelletier MC, Perron MM, Gunsch CK, **Bik HM**, Katz D, Kamikawa A (2013) Use

of a novel sediment exposure to determine the effects of triclosan on estuarine benthic communities, *Environmental Toxicology and Chemistry*, 32(2):384–92.

18. **Bik HM**, Halanych KM, Sharma J, Thomas WK (2012) Dramatic shifts in benthic microbial eukaryote communities following the Deepwater Horizon oil spill, *PLoS ONE*, 7(6):e38550.
19. **Bik HM**, Sung W, De Ley P, Baldwin JG, Sharma J, Rocha-Olivares A, Thomas WK (2012) Metagenetic community analysis of microbial eukaryotes illuminates biogeographic patterns in deep-sea and shallow water sediments, *Molecular Ecology,* 21(5):1048-1059. **(*"From the Cover" paper*)**
20. Bhadury P[#], **Bik H**[#], Lambshead PJD, Austen MC, Smerdon GR, Rogers AD (2011) Molecular diversity of fungal phylotypes co-amplified alongside nematodes from coastal and deep-sea marine environments, *PLOS One,* 6 (10):e26445. ([#] joint first author)
21. **Bik HM**, Lunt DH, Thomas WK, Lambshead PJD (2010) Low endemism, continued deep-shallow interchanges, and evidence for cosmopolitan distributions in free-living marine nematodes (order Enoplida), *BMC Evolutionary Biology,* 10:389.
22. **Bik HM**, Thomas WKT, Lambshead PJD, Lunt DH (2010) Moving towards a complete molecular framework of the Nematoda: A focus on the Enoplida and early-branching clades, *BMC Evolutionary Biology*, 10:353.
23. **Bik HM**, Hawkins LE, Hughes JA, Lambshead PJD (2009) Rapid decline of PCR amplification from genomic extracts of DESS-preserved, slide-mounted nematodes, *Nematology*, 11(6):827-34.

PUBLICATIONS – Peer-reviewed reviews and perspectives

24. Ingels J, Aronson R, Smith C, Baco A, **Bik H**, Blake J, Brandt A, Cape M, DeMaster D, Dolan E, Domack E, Fire S, Geisz H, Gigliotti M, Griffiths H, Halanych K, Havermans C, Huettmann F, Ishman S, Kranz S, Leventer A, Mahon A, McClintock J, McCormick M, Mitchell B, Murray A, Peck L, Rogers A, Shoplock. B, Smith K, Steffel B, Stukel M, Sweetman A, Taylor M, Thurber A, Truffer M, Van de Putte A, Vanreusel A, Zamora-Duran M. (2021) Antarctic Ecosystem Responses following Ice Shelf Collapse and Iceberg Calving: Science Review and Future Research, *WIREs Climate Change*, 12(1): e682.
25. Wilkins LGE, Leray M, O'Dea A, Yuen B, Peixoto RS, Pereira TJ, **Bik HM**, Coil DA, Duffy JE, Herre EA, Lessios HA, Lucey NM, Mejia LC, Rasher DB, Sharp KH, Sogin EM, Thacker RW, Vega Thurber R, Wcislo WT, Wilbanks EG, Eisen JA. (2019) Host-associated microbiomes drive structure and function of marine ecosystems, *PLoS Biology*, 17(11): e3000533
26. **Bik, HM** (2019) Microbial Metazoa Are Microbes Too, *mSystems*, 4: e00109-19. ***(invited perspective)***
27. Zinger L, Bonin A, Alsos I, Bálint M, **Bik H**, Boyer F, Chariton A, Creer S, Coissac E, Deagle B, De Barba M, Dickie I, Dumbrell A, Ficetola GF, Fierer N, Fumagalli L, Gilbert T, Jarman S, Jumpponen A, Kauserud H, Orlando L, Pansu J, Pawlowski J, Tedersoo L, Thomsen P, Willerslev E, Taberlet P (2019) DNA metabarcoding—Need for robust experimental designs to draw sound ecological conclusions, *Molecular Ecology*, 28(8): 1857-1862.
28. Katz DS, Allen G, Barba LA, Berg DR, **Bik H**, Boettiger C, Borgman CL, Brown CT, Buck S, Burd R, de Waard A, Eve MP, Granger BE, Greenberg J, Howe A, Howe B, Khanna M, Killeen TL, Mayernik M, McKiernan E, Mentzel C, Merchant N, Niemeyer KE, Noren L, Nusser SM, Reed DA, Seidel E, Smith M, Spies JR, Turk M, Van Horn JD, Walsh J (2018) The principles of tomorrow's university, *F1000Research*, 7: 1926.
29. Deiner K, **Bik HM**, Mächler E, Seymour M, Lacoursière-Roussel A, Altermatt F, Creer S, Bista I, Lodge DM, de Vere N, Pfrender ME, Bernatchez L (2017) Environmental DNA metabarcoding: transforming how we survey animal and plant communities, *Molecular Ecology*, 26(21): 5872-5895. ***(invited review)***
30. **Bik HM** (2017) Let's Rise Up to Unite Taxonomy and Technology, *PLoS Biology*, 15(8): e2002231. ***(invited perspective)***

31. Creer S, Deiner K, Frey S, Porazinska D, Taberlet P, Thomas WKT, Potter C, **Bik HM** (2016) The ecologist's field guide to sequence-based identification of biodiversity, *Methods in Ecology and Evolution*, 7(9): 1008-1018. ***(invited review)***
32. **Bik HM**, Dove ADM, Goldstein MC, Helm RR, MacPherson R, Martini K, Warneke A, McClain C (2015) Ten Simple Rules for Effective Online Outreach, *PLoS Computational Biology* 11(4): e1003906.
33. NESCent Working Group on the Evolutionary Biology of the Built Environment, Martin LJ, Adams RI, Bateman A, **Bik HM**, Hawks J, Hird SM, Hughes D, Kembel SW, Kinney K, Kolokotronis SO, Levy G, McClain C, Meadow JF, Medina RF, Mhuireach G, Moreau CS, Munshi-South J, Nichols LM, Palmer C, Popova L, Schal C, Täubel M, Trautwein M, Ugalde JA, Dunn RR (2015) Evolution of the Indoor Biome, *Trends in Ecology and Evolution*, 30(4): 223–232.
34. **Bik HM** (2014) Deciphering diversity and ecological function from marine metagenomes, *The Biological Bulletin,* 227:107-116. ***(invited review)***
35. **Bik HM,** Coil D, Eisen JA (2014) microBEnet: Lessons learned from building an interdisciplinary scientific community in the online sphere, *PLoS Biology,* 12(6): e1001884.
36. Morgan MJ, Bass D, Birky CW, **Bik H**, Blaxter M, Crisp MD, Derycke S, Fitch D, Fontaneto D, Hardy CM, King AJ, Kiontke KC, Moens T, Pawlowski JW, Porazinska D, Tang CQ, Thomas WK, Yeates DK, Creer S (2014) A critique of Rossberg et al.: noise obscures the genetic signal of meiobiotal ecospecies in ecogenomic datasets, *Proceedings of the Royal Society B*, 281(1783): 20133076.
37. Burleigh JG, Alphonse K, Alverson AJ, **Bik HM**, Blank CE, Cirranello AL, Cui H, Daly M, Dietterich TG, Gasparich G, Irvine J, Julius M, Kaufman S, Law E, Liu J, Moore LR, O'Leary MA, Passarotti M, Ranade S, Simmons NB, Stevenson DW, Thacker RW, Theriot EC, Todorovic S, Velazco PM, Walls RL, Wolfe JM, Yu A (2013) Next Generation Phenomics for the Tree of Life, *PLOS Currents Tree of Life,* doi:10.1371/currents.tol.085c713acafc8711b2ff7010a4b03733
38. **Bik HM**, Goldstein MC (2013) An Introduction to Social Media for Scientists, *PLoS Biology*, 11(4): e1001535.
39. **Bik HM,** Thomas WK (2012) Metagenomics will highlight and drive links to taxonomic data: reply to Murray, *Trends in Ecology and Evolution*, 27(12): 652-653.
40. **Bik HM**, Porazinska DL, Creer S, Caporaso JG, Knight R, Thomas WK (2012) Sequencing our way towards understanding global eukaryotic biodiversity, *Trends in Ecology and Evolution,* 27(4):233-243.
41. **Bik HM** (2010) Small worms, big ideas: Evolutionary inferences from nematode DNA, *Journal of Biogeography*. 37(1):1-2.
42. **Bik HM** (2009) Unraveling post-glacial colonization through molecular techniques: new insight from estuarine invertebrates, *Journal of Biogeography,* 36:16-17.

PUBLICATIONS – Book chapters

- Ingels J, Amon D, Bernardino A, Bhadury P, **Bik H**, Clark MR, Dahlgren T, Jones DOB, McClain C, Nunnally C, Snelgrove P, Yasuhara M. (*in press*) Chapter 7.O: Abyssal Plains. In: *United Nations, Second World Ocean Assessment*
- **Bik HM,** Thomas WK (2016) Biodiversity and the (data) Beast. In: Hughes J., Cotton, J., and Olson, P. (eds.) *Next Generation Systematics: Studying Evolution and Diversity in the Era of Ubiquitous Genomics,* Cambridge University Press, UK.
- Thaler AD, Zelnio KA, Freitag A, MacPherson R, Shiffman D, **Bik H**, Goldstein MC, McClain C (2012) Digital Environmentalism: Tools and strategies for the evolving online ecosystem. In: D. Gallagher (ed.) *Environmental Leadership: A Reference Handbook,* SAGE Publications, London.

PUBLICATIONS – Meeting Reports

- Arora R, Li X, Hurwitz B, Fay D, Panda DK, Valeev E, Wang S, Moore S, Chandrasekaran S, Cao T, **Bik H**, Curry M, Islam T (2020) Future Directions of the Cyberinfrastructure for Sustained Scientific Innovation (CSSI) Program, arXiv, DOI: arXiv:2010.15584, https://arxiv.org/abs/2010.15584
- Bates ST, Ahrendt S, **Bik HM**, Bruns TD, Caporaso JG, Cole J, Dwan M, Fierer N, Gu D, Houston S, Knight R, Leff J, Lewis C, Maestre JP, McDonald D, Nilsson RH, Porras-Alfaro A, Robert V, Schoch C, Scott J, Taylor DL, Wegener Parfrey L, Stajich JE (2013) Meeting Report: Fungal ITS Workshop (October 2012), *Standards in Genomic Sciences*, 8(1): doi:10.4056/sigs.3737409
- Robbins RJ, Amaral-Zettler L, **Bik H**, Blum S, Edwards J, Field D, Garrity G, Gilbert JA, Kottmann R, Krishtalka L, Lapp H, Lawrence C, Morrison N, Tuama EO, Parr C, San Gil I, Schindel D, Schriml L, Vieglas D, Wooley J (2012) RCN4GSC Workshop Report: Managing data at the interface of biodiversity and (meta)genomics, March 2011, *Standards in Genomic Sciences*, 7(1): doi:10.4056/sigs.3156511

OTHER SCIENTIFIC PRODUCTS

- Phinch (http://phinch.org) – an interactive, exploratory data visualization framework for high-throughput sequence data; open source code available on Github
- Github, open source software repositories – https://github.com/BikLab (UCR Lab) https://github.com/hollybik (personal)
- Bik HM et al. (2012) Data from: Dramatic shifts in benthic microbial eukaryote communities following the Deepwater Horizon oil spill. Dryad Digital Repository. doi:10.5061/dryad.4sd51d4b (environmental 18S rRNA amplicon dataset)
- Bik HM et al. (2011) Data from: Metagenetic community analysis of microbial eukaryotes illuminates biogeographic patterns in deep-sea and shallow water sediments. Dryad Digital Repository. doi:10.5061/dryad.vd094 (environmental 18S rRNA amplicon dataset)

INVITED TALKS (selected)

2019	Invited speaker, 7th Annual Southern California Microbiome Symposium, UC Irvine
2019	Invited Talk, Gordon Research Conference on Marine Molecular Ecology, Hong Kong *(withdrawn due to medical leave of absence)*
2019	Plenary speaker, 8th International Barcode of Life Conference, Trondheim, Norway *(withdrawn due to medical leave of absence)*
2019	Invited seminar, Scripps Oceanographic Institute, University of California—San Diego
2019	Invited seminar, Department of Ecology and Evolutionary Biology, University of California—Los Angeles
2019	Invited seminar, Department of Biology, California State University Northridge
2019	Plenary speaker, Advances in Genome Biology and Technology (AGBT) General Meeting, Marco Island FL
2019	Invited seminar, Department of Entomology, University of California—Riverside
2018	Invited seminar, Institute of Bioinformatics, University of Georgia
2018	Invited speaker, NYU “Brave New World” metagenomics symposium, New York City
2018	Invited speaker, International Congress of Plant Pathology, Boston, MA
2018	Invited speaker, UCSD Probabilistic Microbial Modeling Symposium
2018	Invited seminar, Department of Ecology and Evolutionary Biology, University of California—Davis
2018	Invited seminar, Invited seminar, Harvey Mudd College, Claremont, CA
2018	Invited seminar, Department of Biology, California State University San Bernardino
2017	Invited speaker and session chair, CSHL Genome Informatics Conference
2017	Invited seminar, Quantitative and Systems Biology, University of California–Merced
2017	Invited speaker, Society of Nematology 2017 Annual Meeting, Williamsburg, VA

2017 Invited seminar, Department of Bioinformatics and Genomics, University of North Carolina Charlotte
2016 Invited seminar, Department of Marine & Environmental Biology, University of Southern California
2016 Invited speaker, Ecological Society of America Annual Meeting, Ft. Lauderdale, FL
2016 Invited panel speaker, FORCE2016 conference, Portland, Oregon
2016 Invited seminar (*declined*), School of Natural Resources and the Environment, University of Arizona (faculty job candidate)
2016 Invited seminar, Department of Biological Sciences, University of Rhode Island (faculty job candidate)
2016 Invited seminar, School of Life Sciences, Arizona State University (faculty job candidate)
2016 Invited seminar, Marine Science Institute, University of Texas at Austin (faculty job candidate)
2016 Invited seminar, Department of Biology, Boston University (faculty job candidate)
2016 Invited seminar, Department of Plant Pathology and Environmental Microbiology, Penn State University (faculty job candidate)
2016 Invited seminar, Department of Ecology & Evolutionary Biology, Tulane University (faculty job candidate)
2016 Invited seminar, Division of Biology and Biological Engineering, California Institute of Technology (faculty job candidate)
2016 Invited seminar, Department of Nematology, UC Riverside (faculty job candidate)
2015 Invited speaker, Infectious Disease Genomics Conference, Wellcome Genome Campus, Hinxton, UK
2015 Invited speaker, Frontiers in Phylogenetics Symposium, Smithsonian NMNH, Washington DC
2015 Invited speaker, Gordon Research Conference on Ecological and Evolutionary Genomics, Biddeford, ME
2015 Keynote speaker, Bioinformatics Open Source Conference, Dublin, Ireland
2015 Invited seminar, Department of Engineering, University of Glasgow, Scotland
2015 Invited speaker, NGS Bioinformatics User Group, James Hutton Institute, Scotland
2014 Invited speaker, World Conference on Marine Biodiversity, Qingdao, China
2014 Invited speaker, Oxford Genome Science Meeting, Oxford, UK
2014 Invited speaker, Joint Aquatic Sciences Meeting, Portland, OR
2014 Invited seminar, Monterey Bay Aquarium Research Institute, Moss Landing, CA
2014 Invited seminar, IBEST seminar series, University of Idaho
2014 Invited seminar, Department of Integrative Biology, Oregon State University
2013 Session Chair, Gordon Research Conference on Ecological and Evolutionary Genomics, Biddeford, ME
2013 Invited speaker, SMBE annual meeting, Chicago, IL
2013 Keynote speaker, iEvoBio Conference, Snowbird, UT
2013 Invited speaker, Int'l Assoc. for Great Lakes Research meeting, Lafayette, IN
2013 Invited speaker, 2nd Microbiology of the Built Environment meeting, Boulder, CO
2013 Invited seminar, Institute of Ecology & Evolution, University of Oregon
2012 Invited speaker and Session Chair, Evolution of *C. elegans* and other Nematodes meeting, Cold Spring Harbor, NY
2012 Invited speaker, Assoc. of Biomolecular Research Facilities meeting, Orlando, FL
2011 Invited seminar, Univ. of South Florida/US Geological Survey, St. Petersburg, FL
2011 Invited speaker, Society of Nematology Annual Meeting, Corvallis, OR
2011 Invited speaker, iEvoBio conference, Norman, OK
2010 Invited seminar, US Environmental Protection Agency, Cincinnati, OH

TEACHING EXPERIENCE

- UGA Course Instruction: MARS 3450 Marine Biology (~50 person upper division undergraduate course)
- UC Riverside Course Instruction: MCBL 211 Microbial Ecology, Biol 020 The Dynamic Genome, BIOL 159 Biology of Nematodes
- Software Carpentry Instructor Certification: Formal certification in bioinformatics training and pedagogical techniques as applied to computational course content, completed June 2018.
- Graduate Student Supervision**:** Patricia Holt-Torres (Primary Advisor, UC Riverside), Mirayana Marcelino Barros (Primary Advisor, UC Riverside), Hannah Kissinger (Primary Advisor, UC Riverside), Alexis Walker (MSc, University of Alaska Fairbanks), Hollie Marshall (MSc, University of Birmingham)
- Undergraduate and K12 Student Mentoring: Alejandro De Santiago Perez (2017-present, UC Riverside), Christian Udealor (2018-present, UC Riverside), Amy Hodges and Vanessa Guzman (2017 SALSA Summer Research Interns, UC Riverside), Jordan Ramsdell (work-study undergraduate project at UNH), Evan Dube (High School student, summer project at UNH), Alison Federer (undergraduate meeting mentor at SMBE Kyoto 2011), Tamar Dickerson and Kayla Hinson (ASLO Multicultural Program, undergraduate meeting mentor at 2012 Ocean Sciences Meeting), bioinformatics advisor for undergraduate research projects at UC Davis (2012-2014).
- Instructor and course organizer**:** "Benthic Invertebrate Taxonomy, Metagenomics, and Bioinformatics" (BITMaB) Workshops at Texas A&M University (2017, 2018) – courses focused on interdisciplinary training in morphological taxonomy (microscopy) and bioinformatics workflows of microbial metazoan taxa. Course participants included undergraduates and researchers of all career stages (graduate students to full professors).
- Instructor and course organizer: "Bioinformatics & Biodiversity" undergraduate workshops at Auburn University (2011) and the University of New Hampshire (2014, 2015) – courses focused on the intersection of taxonomy and high-throughput sequencing methods, in the context of the Deepwater Horizon oil spill.
- Seminar on College Teaching: Semester-long course on pedagogy and practical teaching techniques, completed at UC Davis in 2014.
- Workshop Instructor, "Using Social Media to promote your research", UC Davis GradPathways Workshops, (2012-2014)

LEADERSHIP ACTIVITIES

- Primary Chair, "From microbes to mammals: Using environmental DNA sequencing to advance marine biomonitoring and management" oral and poster session at the 2020 Ocean Sciences Meeting (San Diego, CA – February 16-21, 2020)
- Lead Organizer, NSF RCN EukHiTS Ideas Lab on "Research Frontiers and Grand Challenges in Microbial Eukaryote -Omics" (San Diego, CA – August 21-23, 2019)
- Lead Organizer, "Speeding Up Science" workshops for developing reproducible bioinformatics workflows and data visualizations (two workshops at UC Davis – May 2019 and October 2019)
- Primary Chair, "Molecular Ecology Approaches and Cyberinfrastructure for Marine Microbial 'Omics" oral and poster session at the 2018 Ocean Sciences Meeting (Portland, OR – February 11-16, 2018)
- Co-Chair, "Benthic Meiofauna Structure, Pattern, and Function in Ocean Basins" poster session at the 2018 Ocean Sciences Meeting (Portland, OR – February 11-16, 2018)
- Lead Organizer, Phinch Data Visualization End User Workshop (University of California, Riverside – November 8-9, 2017)
- Lead Organizer, Invited workshop at the 2017 British Ecological Society Annual Meeting, "Who is there and how do we know? Navigating the Complexities of Taxonomy assignments during eDNA Metabarcoding Studies." (Ghent, Belgium – December 11-14, 2017)

- Lead Organizer, Symposium at the Joint 2014 British/French Ecological Society Annual Meeting, “Accelerating ecology and biodiversity research via ecometagenomics: species, communities and environmental DNA” (Lille, France – December 9-12, 2014)
- Lead Organizer, “Ecometagenomics” Special Session and full-day workshop, Ecological Society of America 2014 Annual Meeting (Sacramento, CA, August 10-15, 2014)
- Lead Organizer, UC Davis Genome Assembly Masterclass (Davis, CA, Dec 16-20, 2013)
- Organizing Committee, Evolution of *Caenorhabditis* and Other Nematodes 2014 Meeting (Hinxton, UK – June 14-17, 2014)
- Organizing Committee, iEvoBio 2013 (Snowbird, UT – June 25-26, 2013)
- Co-Convener (“Phylogenomics and Microbial Species Concepts” Session at the American Society for Microbiology Annual Meeting (Denver, CO – May 18-21, 2013)
- Lead Organizer and Co-PI, SMBE Satellite Meeting on Eukaryotic -Omics and QIIME software workshop (Davis, CA – April 29-May 4, 2013)
- Council Member, UC Davis Postdoc Association (2012-2014)
- Lead Organizer, NESCent Catalysis Meeting, “High-throughput biodiversity assessment using Eukaryotic Metagenetics” (Durham, NC – January 24-26, 2011)
- Lead Organizer, “UNH Metageniuses” data analysis discussion group (2010-2011, University of New Hampshire)
- Organizing Committee, Natural History Museum Annual Postgraduate Conferences, London Evolutionary Research Network Annual Conferences, NHM Phylogenetics and Genomics Workshop, and London (2007-2009)
- Council Member and Representative, The Natural History Museum London Students’ Association, London Evolutionary Research Network (2007-2009)

WORKSHOPS AND WORKING GROUPS

- Invited Participant and Speaker, Marine Microbes and Symbiosis Workshop (December 2-8, 2019, Smithsonian Tropical Research Institute, Panama)
- Invited Participant, 2019 NSF Workshop on the Future Directions for the Cyberinfrastructure for Sustained Scientific Innovation (CSSI) Program (October 29-30, Austin, TX)
- Steering Committee and Workshop Participant, NSF DEB-1839205 “Collaborative Research: Revolutionizing Systematics - Revitalizing Monographs (Oct 2018 – July 2020; PIs Marymegan Daly, Ohio State University; Felipe Zapata, University of California Los Angeles)
- Advisory Board, NSF ABI-1458484 "An Ontology-Based System for Querying Life in a Post-Taxonomic Age" (May 2015-April 2018; PIs Nico Cellinese, University of Florida; Hilmar Lapp, Duke University)
- Invited Participant, "Never Home Alone" microbial ecology working group (North Carolina State University, Raleigh, NC - November 15-17, 2018)
- Invited Participant, US Research Software Sustainability Institute, Second Workshop (October 23-24, 2018 – Chicago, IL)
- Invited Participant, 4D Workshop: Deep-time Data Driven Discovery and the Evolution of Earth (June 4-6, 2018 – Carnegie Institute, Washington DC)
- Invited Participant, Teaching and Developing QIIME 2 workshop (May 9-11, 2018 – University of California San Diego)
- Invited Participant, “Antarctic Ecosystem Research following Ice Shelf Collapse and Iceberg Calving Events” Workshop (November 18-19, 2018 – Florida State University Marine Laboratory)
- Invited Participant, Binder Workshop (October 18-19, 2017 – University of California, Davis)
- Invited Participant, “Imagining Tomorrow's University” Workshop (March 8-9, 2017 – Chicago, IL)
- Invited Participant, Deep Carbon Observatory Modeling and Visualization Workshop (May 11-13, 2015 – Smithsonian NMNH, Washington DC)
- Invited Participant, NEON Advanced Analysis of Genomic Data in Microbial Ecology Research Workshop (July 14-16, 2014 – NEON headquarters, Boulder, CO)

- Invited Participant, Evolution of the Indoor Biome (June 11-13, 2013 – NESCent, Durham, NC) and Indoor Evolution Meta-analysis working group (ongoing)
- Data Provider, NSF AVAToL Project “Next-generation Phenomics for the Tree of Life” (3-year project, 2012-2014; http://avatol.org)
- Invited Participant, Phylotastic Hackathon (June 4-8, 2012 - NESCent, Durham, NC)
- Invited Participant, NSF Ideas Lab for Advancing and Visualizing the Tree of Life, (August 22-26, 2011 – Lake Placid, NY)
- Invited Participant, Genomic Standards Consortium, Biodiversity Working Group (March 21-22, 2011 – San Diego, CA; activities are ongoing)
- Invited Participant, Ecogenomics, environmental barcoding and biomonitoring workshop, hosted at Biodiversity Institute of Ontario (August 12-13, 2010 – Guelph, Canada)
- Invited Participant, Natural Resource Damage Assessment (NRDA) in Arctic Waters, sponsored by UNH Coastal Response Research Center and Alaska’s Oil Spill Response Institute (April 20-22, 2010 – Anchorage, AK)

SCIENTIFIC & PROFESSIONAL TRAINING

- CREDITS Team Science Retreat, UCLA Lake Arrowhead Conference Center (Sept 2018)
- Software Carpentry Instructor Training (UC Davis, June 2018)
- Mozilla “Open Leaders” Training, Round 5 (10 week mentored training program administered by the Mozilla Foundation, globally competitive application process)
- NYU Advanced Science Communication Workshop - Arthur L. Carter Journalism Institute, Instructed by Steven Hall (4 weeks, 12 contact hours; April/May 2016)
- NYU Science Communication Workshop - Arthur L. Carter Journalism Institute, Instructed by Steven Hall (4 weeks, 12 contact hours; March 2016)
- Software Carpentry Workshop (NERC Advanced Training Short Course) – University of Leeds, United Kingdom (2015)
- UC Davis Genome Assembly Masterclass – Davis, CA (2013)
- Advancing Towards Professorship in Biology, Ecology, and Earth Systems Sciences – Oregon State University, Corvallis, OR (2012)
- NIGMS Workshop for Postdocs Transitioning to Independent Positions – NIH campus, Bethesda, MD (2012)
- Perl programming for Bioinformatics, 3-week intensive course – University of New Hampshire (2011)
- ARB/SILVA training workshop – Bremen, Germany, (2010)
- Deep-sea DNA Barcoding Workshop sponsored by Census for the Diversity of Marine Life (CeDAMar) – Seneckenberg Research Institute, Wilhelmshaven, Germany (2008)
- Benthic Marine Invertebrate Workshop sponsored by the Royal Society of the UK – University of the Western Cape, Cape Town, South Africa (2007)
- Deep-sea Nematode Taxonomy Workshop sponsored by MarBEF – University of Ghent, Belgium (2007)

CONFERENCE PRESENTATIONS (selected)

- Lake Arrowhead Microbial 2018 meeting (LAMG18), Lake Arrowhead, CA, September 16-20, 2018 – “Phinch: An interactive, exploratory data visualization framework (Poster)
- 15th Deep Sea Biology Symposium, Monterey, CA, September 9-14, 2018 – “The (meta)genome of a single worm: unexpected ecological and evolutionary insights from nematode –Omics” (Contributed Talk)
- Society of Systematic Biologists Standalone meeting 2018, Columbus, OH, June 1-4, 2018 – “What are the barriers to revisionary / monographic work?” panel discussion (Invited Panelist)
- 6th International Symposium on Chemosynthesis-Based Ecosystems (CBE6), Woods Hole, MA, August 27-September 3, 2017 – “Nematode-associated microbial taxa in chemosynthetic and background habitats” (Contributed Talk)

- 2016 Moore-Sloan Data Science Summit, NYU Kimmel Center, October 26, 2016 - "Phinch: An interactive, exploratory data visualization framework for -Omic datasets" (Lightning Talk)
- Lake Arrowhead Microbial 2016 meeting (LAMG16), Lake Arrowhead, CA, September 18-22, 2016 – "Biodiversity and biogeography of microbial eukaryote communities in arctic sediments" (Poster)
- International Society for Microbial Ecology 2016 Conference (ISME16), Montreal, Canada, August 21-26, 2016 – "Biodiversity and biogeography of microbial eukaryote communities in arctic sediments" (Poster)
- EMBO Meeting on Exploring the Genomic Complexity and Diversity of Eukaryotes, Sant Feliu de Guixols, Spain, October 17-22, 2015 – "Biodiversity, Biogeography, & Evolution
- of Microbial Metazoa" (Contributed Talk)
- 14th Deep-Sea Biology Symposium, Aveiro, Portugal, August 31-September 4, 2015 – "Environmental sequencing approaches for microbial eukaryotes in deep-sea sediments" (Contributed Talk)
- Deep Carbon Observatory March 2015 International Science Meeting, Munich, Germany, March 26-28, 2015 "Phinch: An interactive, exploratory data visualization framework for environmental sequence data" (Invited Poster)
- International Environmental Omics Synthesis Conference (iEOS 2014), Liverpool, UK, September 15-17, 2014 – "Phinch: An interactive, exploratory data visualization framework for environmental sequence data" (Contributed Talk)
- SMBE 2014 Annual Meeting, San Juan, Puerto Rico, June 8-12, 2014 – "Phinch: An interactive, exploratory data visualization framework for metagenomic datasets" (Contributed Talk)
- VIZBI 2014, Heidelberg, Germany, March 5-7, 2014 – "Phinch: An interactive, exploratory data visualization framework for metagenomic datasets" (Poster and Software Demo)
- Evolution 2013, Snowbird, UT, June 21-25, 2013 – "Phylosift: phylogenetic analysis of genomes and metagenomes" (Contributed Talk)
- American Society for Microbiology Annual Meeting, Denver, CO, May 18-21 2013 – "Phylosift: phylogenetic analysis of genomes and metagenomes" (Poster)
- SMBE 2012 Annual Meeting, Dublin, Ireland, June 23-26, 2012 – "Phylosift: phylogenetic taxonomy assignments from environmental metagenome data" (Poster)
- Ocean Sciences 2012 Meeting, Salt Lake City, UT, February 20-24, 2012 – "Rapid biodiversity assessment of microbial eukaryotes using High-Throughput Sequencing: A case study from the BP oil spill" (Poster)
- World Conference on Marine Biodiversity, Aberdeen, Scotland, Sept 26-30, 2011 – "Rapid biodiversity assessment of marine meiofauna using high-throughput sequencing: A case study from the BP oil spill" (Contributed Talk)
- SMBE 2011 Annual Meeting, Kyoto, Japan, July 26-30, 2011 – "Rapid biodiversity assessment of microbial eukaryotes using high-throughput sequencing: A case study from the BP oil spill" (Contributed Talk)
- Deepwater Horizon Oil Spill Principal Investigator (PI) Conference sponsored by the NSTC Joint Sub-Committee on Ocean Science and Technology, St. Petersburg, FL, October 5-6, 2010 – "RAPID: Taxonomic and metagenetic test of species distributions for marine meiofauna in the Gulf of Mexico" (Poster)
- 12th International Deep-sea Biology Symposium, Reykjavik, Iceland, June 7-11, 2010 – "Metagenetic analysis of biodiversity patterns in deep-sea benthic meiofaunal communities" (Contributed Talk)
- SMBE 2009 Annual Meeting, Iowa City, IA, June 3-7, 2009 – "Resolving phylogenetic relationships within the basal clade Enoplida (Phylum Nematoda): an integrative approach combining molecular and morphological data" (Contributed Talk)

OUTREACH & BROADER IMPACTS (selected)

- Contributing Scientist and Associate Editor, “Deep-sea News” Blog (2010 to present) – Utilizing social media (Blogs, Twitter) to disseminate my research and highlight important publications in marine biology and genomics.
- The Taproot Podcast Interview (January 2020) – “Staying Afloat – Time Management in a Sea of Obligations”
- BOOM: Biomechanics on our Minds Podcast Interview (July 2019) – talking about fashion in science and how to navigate scientific conferences
- UC Merced RadioBio Podcast Interview (October 2017) – interview about my research by a group of graduate students operating a university podcast.
- Radio Interview for the WGBH Innovation Hub (December 2016) – “How ATMs spread Money and Microbes” interview about ATM microbiome manuscript I led as first author.
- Invited speaker, NYC Open Science Meetup (April 2016) – “Marine Biology Meets Open Science”
- Invited participant, SciFoo2015 (June 2015) – invitation-only interdisciplinary “unconference” held at Google headquarters in Mountain View, CA
- Radio segment on the "Academic Minute" (July 2014) – I gave an “elevator pitch” of my research on this two-minute segment produced by WAMC Northeast Public Radio
- “Girls Who Code” guest speaker (August 2013) – an 8-week summer immersion program in computer science, web design, and mobile apps for high school girls. Sponsored by Intel and held at UC Davis.
- US National Commission on the BP Deepwater Horizon Oil Spill and Offshore Drilling: Report to the President (2011), NSF RAPID project highlighted
- “Open Lab: Best Science Writing on the Web” (2010), my online blog posts were selected for inclusion in this edited print anthology
- “Nature Live” Events, The Natural History Museum, London, UK (2007-2010) – Half-hour “behind the scenes” events run for the general public.
- A-Level Biology days, The Natural History Museum, London, UK (2008-2010) – Hour-long session bringing high-school students into contact with active researchers.
- “Researchers in Residence” Program, St James’ Senior Girls School, London, UK (2008-2009) – National UK program placing early-career researchers into secondary schools.