

Curriculum Vitae: Sarah E. Kingston

I leverage genomic data sets to illuminate fundamental ecological and evolutionary processes in wild populations. My broad interests include population and phylogenomics as well as adaptive responses to a dynamic environment.

Professional Preparation

University of Maryland	BEES*	PhD
The College of Charleston – the Graduate School	Marine Biology	MSc
The College of William and Mary	History	BA

*Behavior, Ecology, Evolution, and Systematics

Appointments

2017 – 2018	Visiting Assistant Professor of Biology, Bowdoin College Biology Department and Schiller Coastal Studies Center
2014 – 2016	Doherty Marine Biology Postdoctoral Scholar, Bowdoin College Biology Department and Schiller Coastal Studies Center
2012 – 2013	Postdoctoral Researcher, Smithsonian Institution (NMNH)
2011 – 2012	Graduate Research Assistantship, Smithsonian, Frontiers in Phylogenetics (NMNH)
2008 – 2011	Graduate Research Assistantship, Smithsonian, Multiple Sequence Alignment (NMNH)
2007 – 2008	Graduate Research Assistantship, Smithsonian, Early Bird project (NMNH)
2005 – 2007	Graduate Teaching Assistantship, University of Maryland
2005 – 2006	Darwin Fellowship, University of Maryland
2002 – 2005	Lab Manager and Lab Technician, NOAA Fisheries, Marine Mammal Genetics Laboratory
1999 – 2001	Graduate Teaching Assistantship, The College of Charleston

Peer-reviewed Publications

Kingston S.E., Martino P., Watling J., Melendy M., Reed, F., Carlon D. B. 2018. Linking genotype to phenotype in a changing ocean: inferring the genomic architecture of a blue mussel stress response with genome-wide association. *Journal of Evolutionary Biology*. 10.1111/jeb.13224.

Rodríguez-Clark, K.M., Davidson, B., **Kingston, S.E.**, Coyle, B.J., Huddleston, C., Duchesne, P., Braun, M.J. In Press. Evaluating a potential source of founders for *ex situ* conservation efforts: Genetic differentiation between disjunct populations of the endangered Red Siskin (*Spinus cucullatus*). *Endangered Species Research*.

Fernandez Robledo, J.A., Marquis, N.D., Countway P.D., Record, N.R, Irish, E.L. Schuldt, M., **Kingston, S.E.**, Bishop, T., Messerman, N.A., Bowden, T.J. Submitted (revision). Pathogens of marine bivalves in Maine (USA): a historical perspective. *Aquaculture*.

Reddy, S., Kimball, R.T., Pandey, A., Hosner, P.A., Braun, M.J., Hackett, S.J., Han, K-H., Harshman, J., Huddleston, C.J., **Kingston, S.E.**, Marks, B.D., Miglia, K.J., Moore, W.S., Sheldon, F.H., Witt, C.C., Yuri, T., and Braun, E.L. 2017. Why do phylogenomic data sets yield conflicting trees? Data type influences the avian tree of life more than taxon sampling. *Systematic Biology*. 66:857-869. 10.1093/sysbio/syx041.

Kingston S.E., Parchman, T.P., Gompert, Z., Buerkle, C.A., and Braun, M.J. 2017. Heterogeneity and concordance in locus-specific differentiation and introgression between

species of towhees. *Journal of Evolutionary Biology*. 30: 474-485. 10.1111/jeb/13033. *cover image*

Kingston S.E., Navarro-Sigüenza A.G., García-Trejo E.A., Vázquez H., Fagan W.F., Braun M.J. 2014. Genetic differentiation and habitat connectivity across towhee hybrid zones in Mexico. *Evolutionary Ecology*. 28(2): 277-297. 10.1007/s10682-013-9673-8.

Kingston S.E., Jernigan R.W., Fagan W.F., Braun D., Braun M.J. 2012. Genomic variation in cline shape across a hybrid zone. *Ecology and Evolution* 2(11): 2737–2748. 10.1002/ece3.375.

Kingston S.E., Adams L.D., Rosel P.E. 2009. Testing mitochondrial sequences and anonymous nuclear markers for phylogeny reconstruction in a rapidly radiating group: molecular systematics of the Delphininae (Cetacea: Odontoceti: Delphinidae). *BMC Evolutionary Biology* 9:245. 10.1186/1471-2148-9-245. *highly accessed*

Kingston S.E., Rosel P.E. 2004. Genetic differentiation among recently diverged Delphinid taxa determined using AFLP markers. *Journal of Heredity* 95:1-10. 10.1093/jhered/esh010.

Manuscripts in Development (for submission Spring 2018)

Kingston S.E., Starr, C.K., Walker, E.H. Deep ecotype-specific lineages or parallel evolution in North America? The relationship between phenotypic and genotypic divergence in *Littorina saxatilis* in the Gulf of Maine.

Luzzio, A., **Kingston, S.E.** Landscape genomics of Gulf of Maine benthic bivalve populations: linking genotype and environmental variation in *Nucula proxima* and *Arctica islandica*.

Martino, P., Carlon, D.B., **Kingston S.E.** Transcriptomic response to climate stress in the blue mussel, genus *Mytilus*.

Courses

As Faculty:

Marine Molecular Ecology and Evolution (BIOL2330/ENVS2233 in the Bowdoin Marine Science Semester)

Students apply molecular data to ecological and evolutionary questions in coastal and marine contexts. Hands-on work includes field sampling, data generation, and analysis of molecular data sets (using Next Generation Sequencing technologies). The course emphasizes robust sampling design in both ecological and population genetic contexts. Theoretical foci include evolutionary and population genetic concepts and analytical tools: tenets of Hardy-Weinberg Equilibrium, Wright-Fisher model, the coalescent, evolutionary processes and signatures in the genome, speciation, maintenance and breakdown of reproductive isolation, spatial patterns and phylogeography, selection, and linking genotype to phenotype. Students learn and apply the theoretical principles of population genetics and molecular evolution through lectures, discussions, group problem sets, bioinformatic analyses, computer-based simulations, scientific paper writing, and an independent study project. A class project involves a long-term sampling program that uses molecular tools to understand temporal and spatial change in the ocean.

The Omics Revolution: Computational Genomics and Big Data in the Field of Biology (BIOL2577 Bowdoin College)

This course features the application of computational tools to the evolving analytical landscape of genomic- and transcriptomic-scale data in the field of organismal biology. Students learn the concepts of appropriate experimental design and data collection for hypothesis testing using big data. Students gain coding skills needed to navigate the ever-changing analytical framework in bioinformatics. We analyze real data sets of DNA and RNA sequences, some collected from

marine animals in the Gulf of Maine. Practical applications emphasize the fundamentals of both frequentist and Bayesian statistical frameworks.

Evolution, guest lectures (BIOL3300 Bowdoin College)

As Graduate Teaching Assistant:

Principles of Genetics (BSCI222 University of Maryland, College Park)

Introductory Biology (College of Charleston, SC)

Animal Physiology (College of Charleston, SC)

Synergistic Activities

Pathogens of Bivalve Mollusks in Maine working group (2017 - current) Member of a collaborative research group pioneered by Bigelow Laboratory for Ocean Sciences aimed at assessing pathogens of bivalve populations in the Gulf of Maine to support and inform growth of the aquaculture industry in the state of Maine. Undergraduate summer research and honors thesis opportunities for Bowdoin students are made possible by this collaboration.

Founding Instructor, Bowdoin Marine Science Semester (2015 – current) The Bowdoin Marine Science Semester (BMSS) is an immersion experience for upper-level undergraduate students designed to emphasize field-based scientific research experiences and inquiry-based learning. The BMSS incorporates 4 courses taught one at a time in sequence: Biological Oceanography, Benthic Ecology, Writing About the Coast or History of Harpswell, and Marine Molecular Ecology and Evolution. I pilot an overarching statistical framework and R tutorial program for the BMSS students throughout the semester. While each instructor is primarily responsible for a specific course module, linkages between the modules are emphasized and instructors act as advisors for students' semester-long independent study projects. Independent study projects are student-driven from hypothesis-forming through experimental design, execution, data analysis and presentation. The BMSS includes several remote field experiences: rocky intertidal community monitoring and population genomics sampling of intertidal organisms on Kent Island in the Bay of Fundy and Hurricane Island in the Gulf of Maine; phytoplankton community sampling in estuarine and oceanic environments in the Gulf of Maine; benthic community monitoring and trophic dynamics (rocky reef) in the Gulf of California, Baja Sur.

Founding Contributor and Protocols Committee, New England Coastal Station Alliance (NeCSA) (2014 – current) Founding member of an effort among field stations in the Gulf of Maine to coordinate and contribute to long term monitoring efforts in a time where climate change is predicted to have greater impact on the Gulf of Maine than many other marine systems across the globe. This field station network received a planning grant from NSF (2015), two seed grants from Maine Sea Grant (2016, 2017), and is in the process of aiming for coordinated funds to spur monitoring efforts as well as education and outreach. I am a co-chair of the Protocols and Sensors Committee for the Alliance.

Benthic Ecology Meeting planning group (2016 meeting) Member of Organizing Committee, Scientific Committee, Web Development and Social Media, and Graphic Design for the 45th Benthic Ecology Meeting in Portland, ME, March 16-19, 2016.

Genome-enabled Research on Manakins (2012 – current) Contributor to a research group formed via an NSF-funded Catalysis Meeting focused on highly interdisciplinary genome-enabled research on manakins as a model for integrative physiological, ecological, and evolutionary research. The group successfully obtained a Research Coordination Network grant to facilitate collaboration among many researchers and institutions across the globe.

Invited Speaking:

The Story Collider (True, Personal Stories About Science - "On the Hook") – July 2014, Frontier, Brunswick, ME

NeCAN (Northeast Coastal Acidification Network) webinar series "Will Gulf of Maine populations evolve in the next century? Estimating the evolutionary response of blue mussels to multivariate climate stress" D. Carlton & S. Kingston – July 2017

Introductory Genomics Workshop "Got Omics?" – March 2018, Annual Meeting of the National Shellfisheries Association, Seattle, WA

Bowdoin College Faculty Seminar Series "Saxy Science: student-driven investigation of ecological divergence in the intertidal snail, *Littorina saxatilis*" – May 2018

Advising

16 undergraduate students (Bowdoin College)

Advised undergraduates (Bowdoin, Wheaton, Barnard) in both summer fellowship and multi-semester independent study and honors thesis settings. Under my supervision, students have utilized next generation sequencing tools to explore population genomics, trait evolution, RNA expression profiles, and evolutionary response of intertidal organisms to climate change. One student under my guidance received a \$10k grant from the Maine Outdoor Heritage Fund to link genotype, phenotype, and environmental parameters in benthic bivalve populations.

Professional Training

January 2017, June 2017, July 2018 – **New England Coastal Station Alliance (NeCSA) Intertidal Monitoring Workshop and Pilot Program**, Bowdoin College Coastal Studies Center, Orrs Island, ME and Schoodic Institute, Acadia National Park (organizer and participant, Protocols and Sensors Committee co-chair)

April 2014 – **Gulf of Maine Field Stations Workshop**, Bowdoin College, Brunswick, ME (participant) collaborated with other members of field stations in the Gulf of Maine to create a formal network for monitoring oceanic change and coordinating student-oriented research and funding opportunities

May 2013 – Annual Frontiers in Phylogenetics Spring Symposium, **Genome-scale Phylogenetics**, Smithsonian Institution, Washington, DC (organizing committee, logistical support, and participant, 2 days)

January 2013 – **Catalysis Meeting: Genome-enabled Research on Manakins**, NESCent, Durham, NC (participant, 4 days)

May 2012 – Annual Frontiers in Phylogenetics Symposium and Workshop, **Sequence Alignment and Tree Estimation**, Smithsonian Institution, Washington, DC (participant and logistical support, 3 days)

February 2012 – **RAD sequencing bioinformatics workshop** (GBS advisor, 2 weeks, 10 participants), taught library prep for GBS technique, STRI, Panama City, Panama

January 2012 – **Genomics Initiative Workshop on Sequence Capture for Next Generation Phylogenomics**, Smithsonian Institution, Washington, DC, collaboration with Brant Faircloth (LSU), (participant and logistical support, 5 days)

October 2011 – **Workshop on Comparative Genomics**, Smithsonian Institution, Washington, DC (participant and logistical support, 5 days)

April 2011 – **Next Generation Sequencing: Transformative Technology for Biodiversity Science**, Smithsonian Institution, Washington, DC (participant and logistical support, 3 days)

May 2010 – Smithsonian National Museum of Natural History **Advanced ArcGIS** course

April 2010 – Smithsonian National Museum of Natural History **Intro to ArcGIS** course

Nov 2009 – An Introduction to **WinBUGS for Ecologists** (Hierarchical Bayesian Modeling), Patuxent Wildlife Research Center

June 2009 – Smithsonian **Workshop on Molecular Evolution**

Field work

2015 - current – shallow benthic monitoring survey of rocky reefs in the Gulf of California, Isla Espiritu Santo and La Ventana

2015 - current – rocky intertidal monitoring survey in the Gulf of Maine and Bay of Fundy

2014 - current – intertidal survey of Littorine snails (*Littorina obtusata* and *L. saxatilis*) in the Gulf of Maine and Bay of Fundy

2014 - current – intertidal survey of blue mussels (*Mytilus edulis* and *M. trossulus*) in the Gulf of Maine and Bay of Fundy

2008 - 2009 – collecting effort targeting towhee hybrid populations (*Pipilo maculatus* and *P. ocai*) across the Transvolcanic Belt in Mexico

2002 - 2005 – small craft biopsy effort targeting *Tursiops truncatus* > 2 miles offshore (SC, GA)

2002 - 2004 – population health assessment-oriented live capture effort targeting estuarine and coastal *T. truncatus* (SC, NJ)

Skills

Molecular laboratory techniques including next generation sequencing, specifically reduced representation library preparation techniques: RAD tags, Genotype by Sequencing (GBS), Ultra Conserved Element (UCE) target enrichment, RNAseq

Bioinformatic pipeline tools: bowtie2, tophat2, cufflinks, bwa, samtools, stampy, STACKS, integrative genomics viewer (IGV), genome analysis toolkit (GATK), velvet, GEMMA, piMASS, MrBayes, Structure, fastStructure, Migrate-N, IMA2, RaxML, PAUP*, MAFFT, MUSCLE, SATe, GARLI, edgeR, cummerbund

UNIX shell, R, ArcGIS, WinBUGS, Circuitscape

SCUBA (NAUI open water)

Small boat handling

Social Media

instagram @scarletscience ; @bowdoinscsc

Website

<https://research.bowdoin.edu/kingston-lab/>