Brandon M. Lind, Ph.D.

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PROFESSIONAL EXPERIENCE

Adjunct Faculty, Research Fellow – Ecological and Conservation Genomics — April 2024 – Present
Department of Ecology & Evolutionary Biology, Institute for Systems Genomics
University of Connecticut, Connecticut, USA
Research Supervisor: Dr. Jill Wegrzyn

Executive Committee — June 2024 – Present
National Science Foundation: "The Evolving Meta-Ecosystems (EVOME) Biology Integration Institute"
Department of Ecology & Evolutionary Biology
University of Connecticut, Connecticut, USA

Research Fellow – Artificial Intelligence, Adaptation to Complex Environments — January 2022 – March 2024
Department of Marine & Environmental Sciences
Northeastern University, Massachusetts, USA
Research Supervisor: Dr. Katie Lotterhos

Research Fellow – Ecological Genomics of Climate Adaptation in Conifers — June 2018 – December 2021
Centre for Forest Conservation Genetics, Department of Forest and Conservation Sciences
University of British Columbia, British Columbia, Canada
Research Supervisors: Drs. Sally Aitken, Sam Yeaman

EDUCATION

Virginia Commonwealth University — Richmond, Virginia
Ph.D. Integrative Life Sciences — May 2018
Advisor: Dr. Andrew Eckert
Dissertation title: Understanding Natural and Anthropogenic Drivers of Tree Evolutionary Dynamics

Iowa State University — Ames, Iowa
Graduate coursework in ecology, genetics, and plant physiology — August 2010-May 2011

University of Northern Iowa — Cedar Falls, Iowa
Bachelor's in chemistry — May 2010
Bachelor's in biology — May 2010

ACADEMIC FELLOWSHIPS, GRANTS, & AWARDS

- ORG.one: Blueprints of conservation: Sequencing, assembly, and annotation of the reference genomes for the imperiled longleaf pine and red-cockaded woodpecker. Collaboration with the U.S. Fish & Wildlife Service, U.S. Forest Service, the University of Florida, and the Archbold Biological Station. $15,000. — 2025
- NSF DBI: The Evolving Meta-Ecosystems Biology Integration Institute. *Contributed substantially to the conceptual framework of research and currently serve on the Executive Committee.* $2,465,534. — 2024
- Nominated – IUFRO Excellence in Forest Molecular Biology and Genomics — 2022
- Smith Fellowship (unfunded): Conserving an American icon: Integrating multi-omic data to identify chestnut blight resistance factors to save the American chestnut. Requested budget : $32,520 — 2020
- USDA NIFA (unfunded): Integrating Multi-Omic Data to Identify Chestnut Blight Resistance Factors Requested budget: $164,484 — 2020
- VCU Graduate School Dissertation Fellowship - academic year $25,000 — 2017-2018
- VCU College of Humanities and Sciences Outstanding Ph.D. student — 2016-2017
- Integrative Life Science Travel Award $1,000 USD — 2016

- New Phytologist Trust Student Travel Award $500 USD 2015
- Integrative Life Science Travel Award $1,000 USD 2015
- NSF GRFP (unfunded, ranked as Excellent): Genomic diversity of sugar and jeffrey pine under factorial fire & thinning: Forecasting the future of forests, industry, & the white pine-blister rust pathosystem 2013
- VCU Graduate School Research Fellowship - 12 month $25,000 2013-2014
- VCU Graduate School Research Fellowship - 12 month $25,000 2012-2013
- NSF REU: Spatially Maximized Arrays of DNA Nanofibers. Resulted in publication in ACS Nano. Iowa State University 2010

MANUSCRIPTS IN PREPARATION AVAILABLE UPON REQUEST

link to public code on p. 6; * shared first authorship; † undergraduate author

21. **BM Lind**, M Lu, P Singh, D Vidakovic, SN Aitken, S Yeaman. Development and validation of a split 50k Axiom array for lodgepole pine and Douglas-fir.
20. **BM Lind***, L Rettenbacher*†, R Candido-Ribeiro, S Aitken. Barking up the same tree: Lineages of North American Douglas-fir transplanted in Europe target genomic variation underlying local adaptation for native North American populations.
19. R Candido-Ribeiro, **BM Lind**, M Lu, P Singh, DO Vidakovic, P Smets, C Chourmouzis, TR Booker, S Yeaman, SN Aitken. Polygenic architecture of climate-adaptive traits in a widespread conifer.
18. BA Roskilly, MR Henry, **BM Lind**, SN Aitken. Phenotypic and genomic signals of weak local adaptation and limited adaptive potential to drought in a deciduous conifer.

PUBLICATIONS

17. (2025) **BM Lind***, I Cobo-Simón*, M Myles*, G Barrett, E Grau, R Ramnath, V Savitsky, JL Wegrzyn. CartograPlant: Bridging genomic, phenotypic, and environmental data to advance plant resilience and eco-evolutionary insight. In review at *GENETICS*. Available on ecoevoRxiv: https://doi.org/10.32942/X2Q06D
16. (2025)# **BM Lind**, KE Lotterhos. A comparison between genomic forecasts based on genotypes versus allele frequencies. Accepted to *The American Naturalist*.
15. (2025)# M Lu, N Feau, **BM Lind**, P Singh, D Vidakovic, R Hamelin, SN Aitken, S Yeaman. Genetic architecture underlying response to the fungal pathogen *Dothistroma septosporum* in *Pinus contorta*, *Pinus banksiana*, and their hybrids. *Evolutionary Applications*. https://doi.org/10.1111/eva.70078
14. **COVER** (2024)# **BM Lind**, KE Lotterhos. The accuracy of predicting maladaptation to new environments with genomic data. *Molecular Ecology Resources*, 00, e14008. DOI: https://doi.org/10.1111/1755- 0998.14008
13. (2024)# **BM Lind**, R Candido-Ribeiro, P Singh, M Lu, D Vidakovic, T Booker, M Whitlock, N Isabel, S Yeaman, SN Aitken. How useful is genomic data for predicting maladaptation to future climate? *Global Change Biology* 30 (4), e17227. https://doi.org/10.1111/gcb.17227
12. (2024)# P Singh, B St Clair, **BM Lind**, R Cronn, NP Wilhelmi, M Lu, D Vidakovic, R Hamelin, D Shaw, SN Aitken, S Yeaman Genomic architecture of resistance and tolerance to Swiss needle cast and *Rhabdocline* needle cast diseases in Douglas-fir. *New Phytologist*. https://doi.org/10.1111/nph.19797
11. (2024) J Whiting, TR Booker, **BM Lind**, Genomics Consortium, S Yeaman. The genetic architecture of repeated local adaptation to climate in distantly related plants. *Nature Ecology & Evolution* 1-15. https://doi.org/10.1038/s41559-024-02514-5
10. (2022) R Jasper, TK McDonald, P Singh, M Lu, C Rougeux, **BM Lind**, S Yeaman. Evaluating the accuracy of variant calling methods using the frequency of parent-offspring genotype mismatch. *Molecular Ecology Resources* (22) 2254-2533. https://doi.org/10.1111/1755-0998.13628
09. (2022)# **BM Lind***, M Lu*, D Vidakovic, P Singh, T Booker, SN Aitken, S Yeaman. Haploid, diploid, and pooled exome capture recapitulate features of biology and paralogy in two non-model tree species. *Molecular Ecology Resources* (00) 1-14. https://doi.org/10.1111/1755-0998.13474
08. (2021) IR MacLachlan, TK McDonald, **BM Lind**, LH Rieseberg, S Yeaman, SN Aitken. Genome-wide shifts in climate-related variation underpin responses to selective breeding in a widespread conifer. *Proceedings of the National Academy of Science* 18(10) e2016900118. https://doi.org/10.1073/pnas.2016900118

07. (2020) CR Mahoney, IR MacLachlan, **BM Lind**, JB Yoder, T Wang, SN Aitken. Evaluating genomic data for management of local adaptation in a changing climate: A lodgepole pine case study. *Evolutionary Applications* 00:1-16. https://doi.org/10.1111/eva.12871
06. (2019) CJ Friedline, TM Faske, **BM Lind**, EM Hobson†, P Dylan†, R Dyer, D Johnson, L Thompson, K Grayson, AJ Eckert. Evolutionary genomics of gypsy moth populations sampled along a latitudinal gradient. *Molecular Ecology* 28:2206-2223. https://doi.org/10.1111/mec.15069
05. (2019)# **BM Lind**, MP North, PE Maloney, AJ Eckert. Effect of fire and thinning on fine-scale genetic structure and gene flow in fire-suppressed populations of sugar pine (Pinus lambertiana Douglas). *Forest Ecology and Management* 447:115-129. https://doi.org/10.1101/448522
04. **INVITED** (2018)# **BM Lind**, M Mennon, CE Bolte, TM Faske, AJ Eckert. The genomics of local adaptation in trees: Are we out of the woods yet? *Tree Genetics & Genomes* 14: 29. https://doi.org/10.1007/s11295-017-1224-y
03. (2017)# **BM Lind**, CJ Friedline, JL Wegrzyn, PE Maloney, DR Vogler, DB Neale, AJ Eckert. Water availability drives signatures of local adaptation in whitebark pine (*Pinus albicaulis*) across fine spatial scales of the Lake Tahoe Basin, USA. *Molecular Ecology* 26: 3168-3185. http://dx.doi.org/10.1111/mec.14106
02. (2016) AJ Eckert, DE Harwood, **BM Lind**, EM Hobson†, A Mix, PE Maloney, CJ Friedline. The genetic architecture of local adaptation II: The QTL landscape of water-use efficiency for foxtail pine (*Pinus balfouriana* Grev. & Balf.). https://doi.org/10.1101/038240
01. (2015) CJ Friedline, **BM Lind**, EM Hobson†, DE Harwood, A Mix, PE Maloney, AJ. The genetic architecture of local adaptation I: The genomic landscape of foxtail pine (*Pinus balfouriana* Grev. & Balf.) as revealed from a high-density linkage map. *Tree Genetics & Genomes* 11:1-15. http://dx.doi.org/10.1007/s11295-015-0866-x

PRESENTATIONS

Keynote Speaker

23. (Sept 2023) **BM Lind** The limits of predicting maladaptation to future climates with genomic data. EvolTree European Network conference. Transilvania University of Braşov. Braşov, Romania.

Invited

22. (Apr 2025) **BM Lind** Genetic blueprints for conservation: Insights from forest trees. Department seminar, Department of Ecology & Evolutionary Biology, University of Connecticut.
21. (Feb 2025) **BM Lind** Genomic insights into plant evolution: linking organismal resilience to molecular mechanisms underlying adaptation. Department seminar, Department of Plant and Microbial Biology, North Carolina State University.
20. (Jan 2024) **BM Lind** How useful is genetic data for species management? Lessons from Forest Trees. Department seminar, Nicholas School of the Environment, Duke University.
19. (Dec 2022) **BM Lind** Leveraging ecological genomics to inform species management. Department seminar, Department of Marine & Environmental Sciences, Northeastern University.
18. (Sept 2021) **BM Lind**, R Candido-Ribeiro, P Singh, M Lu, D Vidakovic, T Booker, M Whitlock, N Isabel, S Yeaman, SN Aitken. How off are genetic offset predictions? Lessons from common gardens and three conifer taxa. EVOLTREE conference. Virtual.
17. (Jan 2020) **BM Lind**; P Singh, S Yeaman, SN Aitken. Convergence of Polygenic Climate Adaptation in Conifers. Tree Genetics Workshop, Plant & Animal Genome conference. San Diego, California.
16. (Jan 2019) **BM Lind**; M Lu, D Vidakovic, S Yeaman, SN Aitken. An efficient method to genotype species with large and complex genomes. Tree Genetics Workshop, Plant & Animal Genome conference. San Diego, California.
15. (Oct 2016) **BM Lind**; CJ Friedline, JL Wegrzyn, PE Maloney, DR Vogler, CE Jensen, AD Mix, DB Neale, and AJ Eckert. Local adaptation of three white pine species across fine spatial scales of the Lake Tahoe Basin, USA: Implications to sustainable management and conservation of conifer species. Natural Areas conference. Davis, California.

Contributed

14. (June 2025) **BM Lind** Unravelling genomic diversity within and between arctic willow species. Forest Genetics Conference. State College, Pennsylvania.

13. (Jan 2025) **BM Lind** CartograPlant: A web-based platform for FAIR-compliant meta-analysis of georeferenced forest tree populations. Plant and Animal Genome Conference. San Diego, California.
12. (Nov 2024) **BM Lind** Branching Out: Evaluating the use of genomics to predict responses of plant populations to climate change. Plant Resilience and Conservation Symposium, Botanical Society of America. Virtual.
11. (July 2024) **BM Lind**, KE Lotterhos. Prospects and limitations of predicting maladaptation to changing environments. Evolution Conference. Toronto, Canada.
10. (June 2024) **BM Lind**, L Rettenbacher, SN Aitken. Quantitative and population genetics of North American and European lineages of coastal Douglas-fir. North American Forest Genetics Association Conference. Oaxaca, Mexico.
09. (June 2024) **BM Lind**, M Myles, I Harding, J Gamer, R Wolther, JL Wegrzyn, I Cobo-Simon, R Ramanth, E Grau, V Savitsky, G Barrett, N Herndon, M Staton. CartograPlant: Integration of FAIR data stewardship, analytics, and georeferenced plant populations for a changing world. North American Forest Genetics Association Conference. Oaxaca, Mexico. Poster.
08. (May 2021) **BM Lind**, S Yeaman, SN Aitken. Patterns and climate drivers of adaptive variation in Douglas-fir. Western Forest Genetics Association conference. Virtual.
07. (June 2019) **BM Lind**, M Lu, D Obreht Vidakovic, S Yeaman, SN Aitken. Combining exome capture and pool-seq: Lessons from three conifer species. Evolution conference. Providence, RI.
06. (June 2017) **BM Lind**, M North, AJ Eckert. Time to tree-think the genetics effects of forest management: Assessing patterns and processes beyond heterozygosity indices. Evolution conference. Portland, OR.
05. (Feb 2017) **BM Lind**; M Menon, C Bolte, T Faske, AJ Eckert. The genomics of local adaptation in trees: Are we out of the woods yet? ILS Showcase. Richmond, Virginia.
04. (June 2016) **BM Lind**; CJ Friedline, JL Wegrzyn, PE Maloney, DR Vogler, DB Neale, and AJ Eckert. When local means local: polygenic signatures of local adaptation within whitebark pine (*Pinus albicaulis* Engelm.) across the Lake Tahoe Basin, USA. Evolution conference. Austin, Tx.
03. (June 2015) **BM Lind**; PE Maloney, DR Vogler, DB Neale, and AJ Eckert. Genetic architecture of fitness-related traits in whitebark pine (*Pinus albicaulis* Englm.). 35th New Phytologist Symposium - The Genomes of Forest Trees: New Frontiers in Forest Biology. Harvard University. Boston, MA. Poster.
02. (Nov 2014) Friedline CJ; **BM Lind**, EM Hobson, DE Harwood, AD Mix, PE Maloney, and AJ Eckert. Local adaptation and linkage maps - a first step towards the genomic architecture of fitness-related phenotypes in natural populations. VCU Integrative Life Science Ph.D. Showcase. Richmond, VA. Poster.
01. (June 2014) **BM Lind**; EM Hobson, MP North, AJ Eckert. Proposal: Genetic effects of factorial fire and thinning in fire-suppressed populations of Jeffrey and sugar pine. Evolution conference. Raleigh, NC. Poster.

TEACHING

Instructor of Record

2025	Biodiversity and Conservation Genomics training program (summer through spring 2026)	Storrs, CT
2025	Statistical Population Genomics (spring)	Storrs, CT
2024	Biodiversity and Conservation Genomics training program (summer through spring 2025)	Storrs, CT
2024	Conservation Genomics seminar (fall)	Storrs, CT

Lecture Series

2023	Logistics for Project Informatics: From File Systems to Project API	Nahant, MA
2023	Version control, git, and GitHub	Nahant, MA
2023	Primer in Geographic Information Systems	Nahant, MA
2022	Bioinformagics: Tips, tricks, and best practices for productive and reproducible research	Nahant, MA

Guest Lecturer

2022	Reproducibility and Publication Bias (in: Intro to environmental, social, and biological data)	Nahant, MA
2018	Hardy-Weinberg equilibrium (in: Evolution)	Richmond, VA
2017	Hardy-Weinberg equilibrium (in: Evolution)	Richmond, VA
2016	Null hypotheses in evolutionary biology (in: Evolution)	Richmond, VA
2015	Population differentiation/genetics, F_{ST} (in: Evolution)	Richmond, VA

Teaching Assistant

2014-2017 Introduction to Biology Laboratory Richmond, VA

- When I began teaching the laboratory sections for this course, there were no teaching materials to link hypothesis testing and their midterm or final experiments
- To address this, developed a drag-and-drop statistical analysis in R so that students could incorporate hypothesis testing (support for null or alternative hypothesis) into their experimental results and discussions
- The drag-and-drop analysis was customizable with custom error messages so that it would prompt students for sample sizes and measurement type to check their data for errors and to ensure the correct statistical test was run consistently across lab sections, without the need for entry-level students to use R and instead how to drag and drop the script file into R and hit enter, which would automatically find and run analysis on their data file

CONTRIBUTIONS TO COMMUNITY, BELONGING, AND MENTORSHIP

Mentorship (ongoing)

† undergraduate

Student mentees

- (2025) *NSF REU Mentor* – Sarah Antebi† – Toolik Field Station, Alaska, The Evolving Meta-Ecosystems (EVOME) Biology Integration Institute
- (2024-present) *UConn Biology and Conservation Genomics year-long training program* - Andrew Deierlein†, Sia Gbondo†, Adam Glendening†, Samira Obbu†, Alan Roger†, Anastasia Serating†, Nicholas Hancox†, Peyton Durant†, Avery DeSilva†, Tyler Cocchiola†, Deirdre McCrohan†, Jenna Kent†
- (2024) *Research and Mentoring for Post-Baccalaureates in Biological Sciences (RaMP)* - Airianna McGuire
- (2018-2024) Rafa Candido-Ribeiro, Beth Roskilly, Madeline Eppley, Sarit Truskey, Camille Rumberger, Kiran Bajaj†, Elisabeth Leung†, Nicole Mongillo†, Clara Winguth†
- (2012-2018) Britta Austin†; Shelby Bennett†; Ayana Ferrer†; Casey Harless†; Erin Hobson†; Angela Simpson†; Rachel Stevenson†; Alexandrea Stylianou†; Tammy Tran†; Hugo Vargas Cruz†

VCU Graduate Student Mentorship Program (2013 – 2016)

- Paired with and mentored three undergraduate students planning on applying to graduate school within a formal mentoring program at Virginia Commonwealth University. Paired for one academic year. All three of my mentees have been accepted to graduate school ranging from medical school to academic research in a Ph.D. program.

Workshops and Seminars (attendee)

2024 – *Wabanaki Climate Change Adaptation: Indigenous science, research partnership, and justice*. Northeastern University.

2023 – Genetics Society of America / pgED Webinar Series : *Genetics, History, and the American Eugenics Movement*.

2022 – Society for the Study of Evolution (Evolution Meeting online): *Evolution's Rainbow: An evening of talks on sex, gender, & sexuality in nature*.

Assisted in creating land acknowledgment statement for Nahant campus of Northeastern University (2023)

UBC Forestry Diversity Crew member (2020 – 2021)

VCU Rice Rivers Center outreach weekend (2012)

- Assisted in and helped organize educational weekend at Virginia Commonwealth University nature center for the Virginia School for the Deaf and Blind

PHILANTHROPY AND OUTREACH

Skype a Scientist (2017 – 2022, 2024)

- I have been matched with various elementary, middle, and high school classrooms across the United States to help communicate science. These meetings are structured so that students can ask questions about my research as well as about science careers in general.

St. Jude Children's Research Hospital's "Up 'til Dawn", University of Northern Iowa (2006-2008)

Founder / Director UNI Chapter – Cedar Falls, IA

- Contacted St. Jude regional office and began collaboration for new Up 'til Dawn chapter
- Arranged campus wide informational meetings to recruit, review, and select members of the executive board
- Organized, planned and ran weekly meetings for the executive board as well as organization's budget
- Raised >$23,000 the inaugural year, and >$100,000 over the chapter's lifetime

Other Philanthropy (2004-2008)

(Co)Founder – Cedar Falls, IA

- Relay for Life Benefit Concert – 'Rock-4-a-Cure' on Main Street, $1,600 annual average
- American Diabetes Association Dodge Ball Tournament, $500 annual average
- Valentine's Day registration tables for the Iowa Donor Network – 'Truly Give Away Your Heart'
- Organized and volunteered at annual volunteer efforts for Big Brothers Big Sisters, Highway Cleanup, Habitat for Humanity, Special Olympics as well as the flood relief efforts in Black Hawk County, Iowa

SERVICE

Data Editor – *The American Naturalist* (2021 – 2023)

- Responsible for assessing code and data archives for manuscripts accepted to *The American Naturalist*

Journal Peer Review (ongoing)

- Molecular Ecology; Heredity; New Phytologist; Plant Ecology & Diversity; Conservation Genetics; Evolutionary Applications; Global Change Biology; G3 Genes | Genetics | Genomes; Forest Ecology & Management; Ecology & Evolution; BMC Ecology & Evolution; Diversity & Distributions; The American Naturalist; Journal of Ecology

Grant Review (2025)

- Dutch Research Council (Nederlandse Organisatie voor Wetenschappelijk Onderzoek) Veni Research proposal

Society member

- American Genetic Association
- Society for the Study of Evolution
- Natural Areas Association
- Society of Molecular Biology & Evolution

Poster Judge – BIOL 318 University of British Columbia (April 2018)

Virginia Junior Academy of Science judge (2013 – 2014)

PUBLIC CODING AND GENETIC RESOURCES

Analysis code from previous and current research:

13. Lind BM. (2024c) GitHub.com/brandonlind/geno_af_gradientforests. Preprint release (Version 1.0.0). Zenodo. https://doi.org/10.5281/zenodo.13899117 (see Publication 16)
12. Lind BM. (2024b) GitHub.com/ModelValidationProgram/MVP-offsets: Revision release (Version 1.0.1). Zenodo. https://zenodo.org/doi/10.5281/zenodo.10611682 (see Publication 14)

11. Lind BM. (2024a) GitHub.com/brandonlind/offset_validation: Publication release (Version 1.1.0). Zenodo. https://doi.org/10.5281/zenodo.7641225 (see Publication 13)
10. Lind BM. (2023a). GitHub.com/brandonlind/jack_pine_natural_populations: Offset Revision 1 (v1.0.0). Zenodo. https://doi.org/10.5281/zenodo.8018892 (see Publication 13)
09. Lind BM. (2023b). GitHub.com/brandonlind/douglas_fir_natural_populations: Offset Revision 1 (v1.0.0). Zenodo. https://doi.org/10.5281/zenodo.8018894 (see Publication 13)
08. Lind BM. (2021a) GitHub.com/CoAdapTree/gatk_pipeline: Publication release (Version 1.0.0). Zenodo. http://doi.org/10.5281/zenodo.5083321 (see Publication 09)
07. Lind BM. (2021b) GitHub.com/CoAdaptree/varscan_pipeline: Publication release (Version 1.0.0). Zenodo. http://doi.org/10.5281/zenodo.5083302 (see Publication 09)
06. Lind BM. (2021c) GitHub.com/CoAdaptree/testdata_validation: Publication release (Version 1.0.0). Zenodo. http://doi.org/10.5281/zenodo.5083292 (see Publication 09)
05. Lind BM. (2021d) GitHub.com/CoAdaptree/cmh_test: Preprint release (Version 1.0.0). Zenodo. http://doi.org/10.5281/zenodo.5083798 (see Publications 12, 15)
04. Lind BM. (2019) GitHub.com/brandonlind/teakettle (see Publication 05)
03. Lind BM. (2018) GitHub.com/brandonlind/out_of_the_woods (see Publication 04)
02. Lind BM (2017) GitHub.com/brandonlind/whitebark_pine (see Publication 03)

Foxtail pine genetic linkage map:
01. Tree Genes Comparative Map Database, Accession Number: TG151 (see Publication 01)

TECHNICAL EXPERIENCE

Teakettle Experimental Forest Sierra National Forest, CA
Field Technician June 2011 – August 2011

- Working unsupervised, measured ecological attributes for a project examining trade-offs of management practices' impact on forest dynamics via the inclusion and exclusion of Rx fire as well as thinning treatments
- Collected and individual-level data (DBH, species, decay/disease class)
- Surveyed forest spatial inventory using offset GPS (laser station/Trimble)

Spatially Maximized Arrays of DNA Nanofibers, Iowa State University Ames, IA
National Science Foundation Research Experiences for Undergraduates (NSF REU) June 2010–August 2010

- Independently addressed objective to geometrically align DNA nanofibers for future use as a scaffolding for the spontaneous alignment of organized arrays of metallic nanowires for bottoms-up fabrication of electronics
- Through personally devised original methods based upon confined evaporative self-assembly, spatial area over which arrays of parallel DNA nanofibers was increased by a full order of magnitude over that of previous research in the literature, resulting in millimeter-scale nanofibers
- Formulated methods reduced cost, effort and timescale of fabrication
- Senior PI acknowledges I earned authorship for a subsequent publication in *ACS Nano*

SUPERVISOR/REFERENCE CONTACT INFORMATION

All references can be contacted.

Jill Wegrzyn, Ph.D. – Current Postdoc Advisor
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Sally Aitken, Ph.D. – Postdoc advisor 2018-2022
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