John L. Darcy, PhD

Curriculum Vitae (April 26, 2025)

John.L.Darcy@gmail.com github.com/darcyj Google Scholar link

Summary

Biostatistician with a publication-proven track record in statistical software development, data visualization, and automation. Specializing in multi-omic pharmacological data analysis, and microbiome data analysis. Adept at leading cross-functional teams, driving new product development, and optimizing data workflows and pipelines. Passionate in developing innovative algorithms, statistical methods, and data tools.

Research Emphases

- **SomaLogic:** Mechanism-of-action of saturated O_2 tolerance in rats. RNA-seq v.s. mass spec v.s. SomaScan characterization. QA/QC pipeline development for SomaScan assay. GSEA algorithm improvements.
- **CU Anschutz Postdoc:** Statistical methods development for high-dimensional feature data, including microbiome, metabolomic, proteomic, metagenomic, and transcriptomic data.
- **UH Manoa Postdoc:** Network analysis and island biogeography of endophytic fungi in native Hawaiian plants. Engineering and producing 3D-printed air samplers. Algorithm development for phylogeny reconstruction given un-alignable DNA sequence data.
- **CU Boulder PhD:** Mathematical modeling of human microbiome changes over time from a phylogenomic perspective. Biodiversity and biogeography of Antarctic glacier bacteria inform our understanding of human microbiome temporal dynamics. Algorithm development in fluorescence microscopy and remote sensing data.

Industry Experience

- Freelance data scientist. Fall 2024 - Present.
- Bioinformatics scientist at SomaLogic. Fall 2020 - Fall 2024.

Post-Doctoral Training

- US NIH NLM Computational Biology Post-Doctoral Fellowship at University of Colorado Anschutz Medical Campus, working with Catherine Lozupone. Fall 2018 - Fall 2020.
- Post-doctoral researcher at University of Hawai'i at Mānoa, with Anthony Amend. Fall 2017 - 2018.

Education

- PhD in Ecology and Evolutionary Biology from University of Colorado, Boulder (2017). Partly done at Duke University. Dissertation title: Biogeographic and biogeochemical drivers of microbial community assembly. Advised by Steve Schmidt (Boulder) and Diana Nemergut (Duke).
- BA in Molecular, Cellular, and Developmental Biology (2010).

First-Author Publications *(incl. equal contribution of first two authors)*

[1] **Darcy JL**. "specificity: an R package for analysis of feature specificity to environmental and higher dimensional variables, applied to microbiome species data". *Environmental Microbiome* (2022).

[2] **Darcy JL**. "A phylogenetic model for the arrival of species into microbial communities and application to studies of the human microbiome". *ISME J* (2020).

[3] **Darcy JL**. "Fungal communities living within leaves of native Hawaiian dicots are structured by landscape-scale variables as well as by host plants". *Mol Ecol* (2020).

[4] **Darcy JL**. "Island Biogeography of Cryoconite Hole Bacteria in Antarctica's Taylor Valley and Around the World". *Front Ecol Evol* (2018).

[5] **Darcy JL**. "Phosphorus, not nitrogen, limits plants and microbial primary producers following glacial retreat". *Sci Adv* (2018).

[6] **Darcy JL**. "Spatial autocorrelation of microbial communities atop a debris-covered glacier is evidence of a supraglacial chronosequence". *FEMS Microbiol Ecol* (2017).

[7] **Darcy JL**, Schmidt SK. "Nutrient limitation of microbial phototrophs on a debris-covered glacier". *Soil Biol Biochem* (2016).

[8] Schmidt SK, **Darcy JL**. "Phylogeny of ulotrichalean algae from extreme high-altitude and high-latitude ecosystems". *Polar Biol* (2015).

[9] **Darcy JL**. "Global distribution of Polaromonas phylotypes - evidence for a highly successful dispersal capacity". *PLoS ONE* (2011).

Co-Author Publications

[10] Kajihara KT. "Diversity, connectivity and negative interactions define robust microbiome networks across land, stream, and sea". *bioRxiv* (2025).

[11] Amend AS. "A ridge-to-reef ecosystem microbial census reveals environmental reservoirs for animal and plant microbiomes". *PNAS* (2022).

[12] Schmidt SK. “Microbial biogeochemistry and phosphorus limitation in cryoconite holes on glaciers across the Taylor Valley, McMurdo Dry Valleys, Antarctica”. *Biogeochem* (2022).

[13] Aran P. “Insights into an undescribed high-elevation lake (6,170 m asl) on Volcán Llullaillaco: A physical and microbiological view”. *Aquat Conserv* (2021).

[14] Hu W. “Multiple-trophic patterns of primary succession following retreat of a high-elevation glacier”. *Ecosphere* (2021).

[15] Solon A. “Gullies and Moraines Are Islands of Biodiversity in an Arid, Mountain Landscape, Asgard Range, Antarctica”. *Front Microbiol* (2021).

[16] Tipton L. “Hawaiian Fungal Amplicon Sequence Variants Reveal Otherwise Hidden Biogeography”. *Microb Ecol* (2021).

[17] Porazinska DL. “Primary succession of nematode communities following retreat of a high elevation glacier”. 2020.

[18] Schmidt SK. “ Of Microbes and Mummies: Tales of Microbial Activity and Inactivity at 6000 masl”. *Microbial Ecosystems in Central Andes Extreme Environments*. 2020. ISBN: 978-3-030-36192-1.

[19] Sommers P. “Microbial species–area relationships in Antarctic cryoconite holes depend on productivity”. 2020.

[20] Bowen T, **Darcy J**, Schmidt S. “RE: Pika’s cold adaptation a liability with climate change”. *Science* (2019).

[21] Bueno de Mesquita CP. “Evidence for phosphorus limitation in high-elevation unvegetated soils, Niwot Ridge, Colorado”. *Biogeochem* (2019).

[22] Gendron EMS. “Structure of bacterial and eukaryote communities reflect in situ controls on community assembly in a high-alpine lake”. *J Microbiol* (2019).

[23] Sommers P. “Experimental cryoconite holes as mesocosms for studying community ecology”. *Polar Biol* (2019).

[24] Sommers P. “Single-stranded DNA viruses in Antarctic cryoconite holes”. *Viruses* (2019).

[25] Sommers P. “Comparison of microbial communities in the sediments and water columns of frozen cryoconite holes in the McMurdo Dry Valleys, Antarctica”. *Front Microbiol* (2019).

[26] Tipton L, **Darcy JL**, Hynson NA. “A Developing Symbiosis: Enabling Cross-Talk Between Ecologists and Microbiome Scientists”. *Front Microbiol* (2019).

[27] Vargas-Gastélum L. “Targeted ITS1 sequencing unravels the mycodiversity of deep-sea sediments from the Gulf of Mexico”. *Environ Microbiol* (2019).

[28] Vimercati L, **Darcy JL**, Schmidt SK. “The disappearing periglacial ecosystem atop Mt. Kilimanjaro supports both cosmopolitan and endemic microbial communities”. *Sci Rep* (2019).

[29] Vimercati L. “Nieves penitentes are a new habitat for snow algae in one of the most extreme high-elevation environments on Earth”. *AAAR* (2019).

[30] Kennedy RC. “Temporal dynamics of gut microbiota in triclocarban-exposed weaned rats”. *Environ Sci Pollut R* (2018).

[31] Schmidt SK. *Life at extreme elevations on Atacama volcanoes: the closest thing to Mars on Earth?* 2018.

[32] Solon AJ. “Microbial Communities of High-Elevation Fumaroles, Penitentes, and Dry Tephra “Soils” of the Puna de Atacama Volcanic Zone”. *Microb Ecol* (2018).

[33] Sommers P. “Diversity patterns of microbial eukaryotes mirror those of bacteria in Antarctic cryoconite holes”. *FEMS Microbiol Ecol* (2018).

[34] Knelman JE. “Rapid shifts in soil nutrients and decomposition enzyme activity in early succession following forest fire”. *Forests* (2017).

[35] Schmidt SK. “Freeze–thaw revival of rotifers and algae in a desiccated, high-elevation (5500 meters) microbial mat, high Andes, Perú”. *Extremophiles* (2017).

[36] Schmidt SK. *A Naganishia in high places: functioning populations or dormant cells from the atmosphere?* 2017.

[37] Washburne AD. “Phylogenetic factorization of compositional data yields lineage-level associations in microbiome datasets”. *PeerJ* (2017).

[38] Kennedy RC. “Temporal Development of Gut Microbiota in Triclocarban Exposed Pregnant and Neonatal Rats”. *Sci Rep* (2016).

[39] Nemergut DR. “Decreases in average bacterial community rRNA operon copy number during succession”. *ISME J* (2016).

[40] Schmidt SK. “Biogeochemical Stoichiometry Reveals P and N Limitation Across the Post-glacial Landscape of Denali National Park, Alaska”. *Ecosystems* (2016).

[41] Schmidt SK, **Darcy JL**. “Phylogeny of ulotrichalean algae from extreme high-altitude and high-latitude ecosystems”. *Polar Biol* (2015).

[42] Knelman JE. “Nutrient addition dramatically accelerates microbial community succession.” *PloS one* (2014).

[43] Knelman JE. “Nutrient addition dramatically accelerates microbial community succession”. *PLoS ONE* (2014).

[44] Lynch RC. “Metagenomic evidence for metabolism of trace atmospheric gases by high-elevation desert Actinobacteria.” *Front Microbiol* (2014).

[45] Lynch RC. “Metagenomic evidence for metabolism of trace atmospheric gases by high-elevation desert actinobacteria”. *Front Microbiol* (2014).

[46] Schmidt SK. “Do bacterial and fungal communities assemble differently during primary succession?” *Mol Ecol* (2014).

[47] Naff CS, **Darcy JL**, Schmidt SK. “Phylogeny and biogeography of an uncultured clade of snow chytrids.” *Environ Microbiol* (2013).

[48] Naff CS, **Darcy JL**, Schmidt SK. “Phylogeny and biogeography of an uncultured clade of snow chytrids”. *Environ Microbiol* (2013).

[49] Nemergut DR. “Patterns and processes of microbial community assembly.” *MMBR* (2013).

[50] Rhodes M. “Alpine and arctic soil microbial communities”. *The Prokaryotes*. 2012. ISBN: 9783642301230.

[51] Schmidt SK. “A simple method for determining limiting nutrients for photosynthetic crusts”. *Plant Ecol Div* (2012).

Publication Metrics

- 51 published papers
- 3943 citations (as of 04/2025)
- h-index = 27
- i10-index = 41

Mentorship and Team Leadership

- At SomaLogic I led multiple interdisciplinary teams on various projects. For example, development of an in-house Gene-Set Enrichment Analysis (GSEA) R-package with considerations for SomaScan data’s unique properties and challenges.
- Mentored Matthew Marshall, an undergraduate student as part of CU Anschutz Summer Bioinformatics Fellowship. I mentored Matt in developing a computer program that analyzes microbial communities in a competitive-lottery framework. We met twice weekly, and I created a production schedule and advised Matt on both programming and writing. Matt is preparing software for pulic release, and has written a release note for publication.
- Led a team at UH to develop and test a 3D-printed air sampler, to be used in large-scale sampling of air microbiota on the Hawaiian Islands. Team included 2 PhD students and 3 undergraduate students. Samplers were succesfully deployed in-situ and operated without supervision in the rainforest for multiple days until collected.
- Advised Adam Solon’s honors thesis project in 2016. Adam used Illumina sequencing to compare microbial communities from multiple sites in the Chilean Atacama Desert, and this work is now published in Microbial Ecology [32]. He was awarded summa cum laude.
- Advised Cerrise Weibern honors thesis project in 2015. She sequenced genomes of 8 Janthinobacterium strains and constructed a robust phylogeny of the species. She was awarded magna cum laude.
- Advised Zack Schubert’s honors thesis project in 2014. I taught him how to implement complex simulation models in R, and together we made and compared mathematical models of water availability in soil undergoing freeze-thaw cycling. He was awarded summa cum laude.
- Mentored three undergraduate students from 2012 to 2014: Todd BT, Schrepel WA, and Choi RB. All three performed and helped design experiments. Todd BT is a co-author on several publications.
- Mentored two local middle school students, who completed a science fair project on E. coli transgenics. They won first prize in their school science fair competition, and went on to compete at state level.

Teaching

- Started “Aloha R”, a computational biology workshop for graduate students at UH (Spring 2018). Weekly meetings focused on core programming skills, since many students view R as a “copy and paste” analytical platform rather than a robust programming environment. I also emphasized code documentation and repeatability.
- Guest lecturer for Ecology of Microbial Symbiosis (Spring 2018). Taught 2 lecture classes reviewing bioinformatics approaches used by microbial symbiosis researchers.
- Guest lecturer for Microbial Ecology (Fall 2016) Taught 3 lecture classes introducing students to modern molecular and bioinformatic approaches to microbial ecology.
- Ecology Lab TA (Fall 2013) Taught ecological theory and field methods, as well as basic statistics and computer programming in R. Three-hour periods with 20 students, 2x/week.
- Microbiology lab TA (Spring 2012) Taught basic microbiological technique, and modern molecular methods. Also wrote weekly quizzes and gave recitation. Two-hour periods with 18 students, 4x/week.

Funding and Awards

- NIH NLM Computational Biology Postdoctoral Fellowship.
- 2019 Front Range Microbiome Symposium award for best presentation.
- Mycological Society of America travel award. San Juan, Puerto Rico, December 2017.
- SCAR XIIth International Biology Symposium Travel Grant. KU Leuven, December 2016.
- Remote (control) sensing: using a drone for environmental science. CU EBIO grant, April 2014.
- High-throughput climate change modeling from the gene’s perspective. Dean’s Graduate Student Research Grant Award, CU Boulder, October 2014.

Selected Presentations and Posters

- Everyone's doing GSEA wrong (Company seminar, 2024). SomaLogic seminar series. Boulder, Colorado.
- Putative mechanism-of-action for 100% oxygen tolerance in mutant rats (Company seminar, 2024). SomaLogic seminar series. Boulder, Colorado.
- Proteomic characterization of liver perfusate effectiveness (Company seminar, 2023). SomaLogic seminar series. Boulder, Colorado.
- Nepotism and Specificity In the human microbiome (Invited talk, 2020). CU Anschutz Computational Biology seminar series. Aurora, Colorado.
- What are compositional data and why do I care? (Invited talk, 2020). CU Anschutz Computational Biology seminar series. Aurora, Colorado.
- A phylogenetic model for the arrival of species into microbial communities (Invited talk, 2019). NIH NLM Computational Biology Training Conference. Indianapolis, Indiana.
- Specificity analysis of microbiome data: All the math (Chalk talk, 2019). CU Anschutz Microbiome group chalk talk.
- Monte Carlo analysis of Foliar Fungal Endophytes reveals habitat specificity to elevation, precipitation, and host plants (Seminar, 2019). Hawaii Ecosystems Conferencein Hilo, Hawaii.
- A phylogenetic model for the arrival of species into microbial communities (Poster, 2019). Front Range Microbiome Symposium in Fort Collins, Colorado.
- Cryoconite holes are microbial islands (Seminar, 2018). International Glaciological Society meeting in Kyoto, Japan.
- Island biogeography of glacial microbiota in Antarctica's Taylor Valley and around the world (Seminar, 2017). Scientific Committee on Antarctic Research Biology meeting in Leuven, Belgium.
- Using Adobe Illustrator to make scienetific figures (Seminar, 2016). CU Boulder EBIO dept. Brown-bag talk.
- Phylogenetic and biogeochemical characterization of a debris-covered glacier (Poster, 2013). ASM General Meeting 2013 in Denver CO.
- Identification and characterization of microbial communities in high-elevation snowpacks (Poster, 2013). LTER meeting 2013 in Estes Park, CO.
- Comparing spatial distributions of microorganisms using minimal genetic distance. ASM General Meeting 2012 in San Francisco, CA.

Peer-Review

Journals I've peer-reviewed for are listed on my Publons profile (slow to update).

Journal	Number of Reviews	Recency
NPJ Biofilms and Microbiomes	2	2020
Nature Communications	3	2019
Ecology and Evolution	1	2020
Data in Brief	1	2020
PeerJ	1	2019
Plant and Soil	1	2019
Molecular Ecology	4	2018
Environmental Microbiology	1	2018
Frontiers in Microbiology	1	2017
The ISME Journal	1	2018
Journal of Biogeography	1	2018

Data and Analytical Skillset

Spatial analysis [3, 4, 9]
Spatiotemporal analysis [3, 6, 39]
Comparative genomics [5, 44]
Mathematical modeling and simulation modeling [2, 3, 7]
Geographic information systems (GIS) [3, 4, 6]
Meta-analysis [2, 4, 9]
Project-level version control [5, specificity R package]
High-throughput sequencing analysis [2–4]
Temporal analysis [2, 38, 42]
Landscape ecology [3, 5, 6]
Phylogenetics [8, 47, 9]
Multivariate satistical analysis [3, 22, 6]
Spatial experimental design [4–6]
Machine learning [11, 1]
Genome and metagenome assembly/analysis [5, 44]
High-throughput sequencing pipelining [2–4]

Programming Languages

Language	Proficiency	Example
R	(expert)	github.com/darcyj/specificity
R Shiny	(expert)	https://github.com/darcyj/specificity.shiny
Shell/Bash	(advanced)	github.com/darcyj/pd_assemb
Python	(advanced)	github.com/darcyj/cardpricer
C++	(intermediate)	github.com/darcyj/specificity
LaTeX	(beginner)	github.com/darcyj/cv

General Software Knowledge

- Linux system admininstration
- Slurm
- qGIS
- Rstudio
- Mendeley
- Microsoft Office (Word, Excel, Ppt)
- Libre Office (Writer, Calc)
- Sublime Text
- MonoDevelop
- High performance computing (HPC)
- Adobe Illustrator
- Adobe Photoshop
- Zoom
- Unix command line tools

Molecular Biology and Bioinformatics Software Knlowledge

- Qiime/Qiime2
- Phyloseq
- Usearch/Vsearch
- DADA2
- BLAST
- SRA Toolkit
- SOAPdenovo
- MetaVelvet
- MaxBin
- metaSPAdes
- Samtools
- BWA
- MrBayes
- FastTree
- MUSCLE
- SEPP
- ITSxpress
- Fastx Toolkit

Laboratory Skillset

- Bacterial culture
- Microcosm experiments
- Media prep/creation
- Culture preservation
- Cloning
- PCR/qPCR/Colony PCR
- Illumina sequencing prep
- Sanger sequencing prep
- DNA/RNA purification
- Qubit/Nanodrop
- Gel electrophoresis
- Plate reader analyses
- Fluorescence microscopy
- Phase-contrast microscopy
- Staining/fixing
- Computational microscopy
- Primer development
- Various soil analyses

Fieldwork Expertise

- Sample collection in extreme conditions at high altitude (>6000 masl).
- Drone flight and data capture at high altitude (>5000 masl).
- Sampling based off of remote sensing data and planned spatial experimental designs.
- Wilderness survival after a grizzly bear destroyed my tent+bag+pad followed by 12 hours of rain.
- Extemporaneous experimental design under hypoxic conditions.
- Logistic coordination with indigenous peoples in the Peruvian Andes.
- Extended backpacking campaigns above 5000 masl.
- Experience in Antarctica's McMurdo Dry Valleys, including helicopter travel, ice climbing, and glacier traverse.
- Rainforest backpacking and sample collection in Hawaii.