

John L. Darcy, PhD

Curriculum Vitae

NIH Post-doctoral fellow, Department of Biomedical Informatics and Personalized Medicine,
University of Colorado Anschutz Medical Campus

Phone: +1 303 887 0477

Email: darcyj@colorado.edu

Website: jldarcy.tk

Google Scholar: ([click here](#))

GitHub: github.com/darcyj

RESEARCH EMPHASIS

In my research, I use mathematical models to understand how microbial communities change over time and space, and how phylogenetic relationships within microbial communities can be used to better understand microbial community assembly. My research has spanned several different study systems, including the human microbiome, mouse microbiome, native Hawaiian plants, and soil microbes living in extreme environments across the world. For my doctoral work, I studied microbial communities living on top of glaciers and also within glaciers, in order to look at the interaction between biogeography, biogeochemistry, and microbial communities. In my postdoctoral research at UH, I used machine learning approaches to “data mine” a large-scale (“big”) data set of fungi living within the leaves of native Hawaiian plants, testing patterns of biogeography, climate, and host specificity. In my current postdoctoral research at UC Anschutz, I am developing mathematical models to analyze time-series human microbiome data.

EDUCATION

PhD in Ecology and Evolutionary Biology, from the University of Colorado, Boulder (2017). Dissertation title: Biogeographic and biogeochemical drivers of microbial community assembly. Advised by Prof. Steve Schmidt.

FIRST-AUTHOR PUBLICATIONS *(incl. equal contribution of first two authors)*

- F6. **Darcy JL**, Gendron EM, Sommers P, Porazinska DL, Schmidt SK (2018) Island Biogeography of Cryoconite Hole Bacteria in Antarctica's Taylor Valley and Around the World. *Front Ecol Evol* 6: 180
- F5. **Darcy JL**, Schmidt SK, Nemergut DR, Cleveland CC, Knelman JE, Castle SC (2018) Phosphorus, not nitrogen, limits plants and microbial primary producers following glacial retreat. *Sci Adv* 4:eaaq0942
- F4. **Darcy JL**, King AJ, Gendron EM, Schmidt SK (2017) Spatial autocorrelation of microbial communities atop a debris-covered glacier is evidence of a supraglacial chronosequence. *FEMS Microbiol Ecol* 93:fix095
- F3. **Darcy JL** and Schmidt SK (2016) Nutrient limitation of microbial phototrophs on a debris-covered glacier. *Soil Biol Biochem* 95:156-163
- F2. Schmidt SK and **Darcy JL** (2015) Phylogeny of Ulotrichalean algae from extreme high-altitude and high-latitude ecosystems. *Polar Biol* 38:689-697
- F1. **Darcy JL**, Lynch RC, King AJ, Robeson MS, Schmidt SK (2011) Global distribution of *Polaromonas* phylotypes – evidence for a highly successful dispersal capacity. *PLoS One* 6:e23742

CO-AUTHOR PUBLICATIONS

- C19. Schmidt SK, Gendron EMS, Vincent K, Solon AJ, Sommers P, Schubert ZR, Vimercati L, Porazinska DL, **Darcy JL**, Sowell P (2018) Life at extreme elevations on Atacama volcanoes: the closest thing to Mars on Earth? *Antonie van Leeuwenhoek*, 1-13 *(online ahead of print)*
- C18. Kennedy RC, Fling RR, Robeson MS, Saxton AM, Schneider LG, **Darcy JL**, Bemis DA, Zhao L, Chen J (2018) Temporal dynamics of gut microbiota in triclocarban-exposed weaned rats. *Environ Sci Pollut Res*, 1-9 *(online ahead of print)*
- C17. Solon A, Vimercati L, **Darcy JL**, Aran P, Porazinska D, Dorador C, Farias ME, Schmidt SK (2017) Microbial communities of high-elevation fumaroles, penitents, and dry tephra “soils” of the Puna de Atacama volcanic zone. *Microb Ecol* <http://rdcu.be/D7Vc>.
- C16. Sommers P, **Darcy JL**, Gendron EM, Stanish LF, Bagshaw EA, Porazinska DL, Schmidt SK (2017) Diversity patterns of microbial eukaryotes mirror those of bacteria in Antarctic cryoconite. *FEMS Microbiol ecol* 93: fix095.
- C15. Knelman JE, Graham EB, Ferrenberg S, Lecouevre A, Labrado A, **Darcy JL**, Nemergut DR, Schmidt SK (2017) Rapid shifts in soil nutrients and decomposition activity in early succession following forest fire. *Forests* 9: 347.
- C14. Schmidt SK, **Darcy JL**, Sommers P, Gunawan E, Knelman JE, Yager K (2017) Freeze-thaw revival of rotifers and algae in a desiccated, high-elevation (5500 meters) microbial mat, high Andes, Peru. *Extremophiles* 21:573-580

- C13. Knelman JE, Graham EB, Ferrenberg S, Lecouvre A, Labrado A, **Darcy JL**, Nemergut DR, Schmidt SK (2017) Rapid Shifts in Soil Nutrients and Decomposition Enzyme Activity in Early Succession Following Forest Fire. *Forests* 8: 347
- C12. Schmidt SK, Vimercati L, **Darcy JL**, Aran P, Gendron EM, Solon AJ, Porazinska D, Dorador C (2017) A Naganishia in high places: functioning populations or dormant cells from the atmosphere? *Mycology* 8: 153-163
- C11. Washburne AD, Silverman JD, Leff JW, Bennet DJ, **Darcy JL**, Mukherjee S, Fierer N, David LA (2017) Phylogenetic factorization of compositional data yields lineage-level associations in microbiome datasets. *PeerJ* 5: e2969
- C10. Kennedy RC, Fling RR, Robeson MS, Saxton AM, Donnell RL, **Darcy JL**, Bemis DA, Liu J, Zhao L, Chen J (2016) Temporal Development of Gut Microbiota in Triclocarban Exposed Pregnant and Neonatal Rats. *Sci Rep* 6: 33430
- C09. Schmidt SK, Porazinska D, Concienne BL, **Darcy JL**, et al. (2016) Biogeochemical stoichiometry reveals P and N limitation across the post-glacial landscape of Denali National Park. *Ecosystems* 19:1164-1177
- C08. Nemergut DR, Knelman JE, Ferrenberg S, Bilinski T, Melbourne B, Jiang L, Violle C, **Darcy JL**, Prest T, Schmidt SK, Townsend AR (2015) Decreases in average bacterial community rRNA operon copy number during succession. *ISME J* 10: 1147-1156
- C07. Lynch RC, **Darcy JL**, Kane NC, Nemergut DR, et al. (2014) Metagenomic evidence for metabolism of trace atmospheric gases by high-elevation desert Actinobacteria. *Front Microbiol* 5:698
- C06. Knelman JE, Schmidt SK, Lynch RC, **Darcy JL**, Castle SC, Nemergut DR (2014) Nutrient Addition Dramatically Accelerates Microbial Community Succession. *PLoS ONE* 9(7): e102609
- C05. Schmidt SK, Nemergut DR, **Darcy JL**, Lynch RC (2014) Do bacterial and fungal communities assemble differently during primary succession? *Mol Ecol* 23: 254-258
- C04. Naff CS, **Darcy JL**, Schmidt SK (2013) Phylogeny and biogeography of an uncultured clade of snow chytrids. *Environ Microbiol* 15: 2672-2680
- C03. Nemergut DR, Schmidt SK, Fukami T, O'Neill SP, Billinski TM, Stanish LF, Knelman JE, **Darcy JL**, Lynch RC, Wickey P, Ferrenberg S (2013) Patterns and processes of microbial community assembly. *MMBR* 77: 342-356
- C02. Rhodes M, Knelman J, Lynch RC, **Darcy JL**, Nemergut DR, Schmidt SK (2013) Alpine and Arctic Soil Microbial Communities. In *The Prokaryotes* pp. 43-55
- C01. Schmidt SK, Nemergut DR, Todd BT, Lynch RC, **Darcy JL**, Cleveland CC, King AJ (2012) A simple method for determining limiting nutrients for photosynthetic crusts. *Plant Ecol Div* 5: 513-519

PAPERS IN PREP OR IN REV

- P1. **Darcy JL**, Washburne AD, Robeson MS, Prest T, Schmidt SK (2018) A phylogenetic model for the arrival of species into microbial communities. (*in prep for ISMEj*)
- P2. **Darcy JL**, Swift S, Cobian G, Zahn G, Amend AS (2018) Fungal communities within native Hawaiian plant leaves are structured by evapotranspiration, elevation, and host plants at the landscape scale. (*in rev, Biogeography*)

PUBLICATION METRICS

- 25 peer-reviewed publications
- 667 total citations (as of November 2018)
- h-index: 10
- i10 index: 11

COMPUTATIONAL, BIOINFORMATIC, AND STATISTICAL SKILLS

All papers I published during my PhD had a strong bioinformatic component. I routinely process high-throughput amplicon DNA sequencing data using software like QIIME, Vsearch, and BLAST. However, the bulk of my research is done with code I've written in R, Python, Bash shell, and C#. I am well versed in:

- Linux system use and administration, incl. various networking protocols (ssh/scp, rsync, etc)
- Building mathematical/simulation models for complex data such as compositional data and distance matrices (F4, F3, C18, C10, P1, P2, current postdoctoral research focus)
- Multivariate analysis of higher dimensional data (F5, F3, C11, P2)
- Spatial statistics (F6, F4, F1, C09, C04, P1, P2)
- Time-series analysis of complex data types (F4, C18, C10, C08, P1)
- Metagenome and metatranscriptome analysis (F5, F1, C07)
- Machine-learning (P2, current postdoctoral research focus)
- Phylogenetic analysis (F2, F1, C12, C11, C07, C04, C01, P1)
- Geographic information systems (GIS; F5, F4, P2)

PUBLISHED SOFTWARE (only includes software I'm proud of. Available at github.com/darcyj)

fastq-from-ITSx. The program ITSx extracts the ITS region from DNA sequence data, but only works for fasta files. I wrote this program to make ITSx compatible with fastq files, so that quality scores are extracted too.

de_zoomify.r. Images hosted on the Internet are often split into tiles, to enable faster loading. The UH Herbarium had many specimen images in this tiled format, and had lost the original full images. I wrote **de_zoomify** to re-constitute those tiled images. An example of one such image is included in the repository.

GarbageTree. Makes garbage trees out of garbage data. Makes “phylogenetic” trees out of unalignable sequence data using kmer frequencies.

split_libraries_dumb.r. A script that can de-multiplex paired-end sequence data with no filtering. Written before this functionality was added to QIIME2.

fractalgen.r. Visualizes simple geometric fractals in R.

simplify_contigs.r. A program to assemble contigs together after genome or metagenome assembly and subsequent binning. Removes redundant contigs as well.

PROGRAMMING LANGUAGES

- R (expert)
- C# (advanced)
- Bash shell (advanced)
- Python (intermediate)
- HTML+CSS (beginner – see my website for example: jldarcy.tk/)
- C (beginner)

LABORATORY SKILLS

Most laboratory work I did during my PhD was preparation for high-throughput (Illumina) sequencing. This included PCRs, gel electrophoresis, using various DNA extraction kits, use of PCR robots, and other routine molecular biological work. I am also skilled at bacterial, fungal, and algal, and bryophyte isolation, as well as various types of microscopy (light, phase, chlorophyll autofluorescence, epifluorescence).

FUNDING AND AWARDS

- NIH Computational Biology Postdoctoral Fellowship (present position).
- International Geological Society travel grant. Kyoto, Japan, December 2017. ¥100,000.
- Mycological Society of America travel award. San Juan, Puerto Rico, December 2017. \$2,500.
- SCAR XIIth International Biology Symposium Travel Grant. KU Leuven, December 2016. \$2,500.
- Remote (control) sensing: using a drone for environmental science. CU EBIO grant, April 2014. \$992.
- High-throughput climate change modeling from the gene's perspective. Dean's Graduate Student Research Grant Award, CU Boulder, October 2014. \$5,000.

MENTORSHIP AND LEADERSHIP

- Lead 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 undergrads.
- Advised Solon A's honors thesis project in 2016. Student used Illumina sequencing to compare microbial communities from multiple sites in the Chilean Atacama Desert, and this work is now published in *Microbial Ecology* (C17). Student was awarded summa cum laude.
- Advised Weibern C's honors thesis project in 2015. Student sequenced genomes of 8 *Janthinobacterium* strains and constructed a robust phylogeny of the species. Student was awarded magna cum laude.
- Advised Schubert ZR's honors thesis project in 2014. Student made and compared mathematical models of water availability in soil undergoing freeze-thaw cycling. Student 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 EXPERIENCE

- Started “Aloha R”, a workshop I run 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.

PRESENTATIONS AND POSTERS

- 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 scientific 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.

FIELDWORK EXPERTISE

- Sample collection in extreme conditions at high altitude (>6000 masl).
- Wilderness survival after a grizzly bear destroyed my tent+bag+pad followed by 12 hours of rain.
- Drone flight and data capture at high altitude (>5000 masl).
- 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 and glacier traverse.

OTHER EXPERIENCE

- High performance computing server administrator (2013-2016)
- Hazardous waste lab coordinator (2011-2015)
- Website admin for amo.colorado.edu (2011-2015)
- Laboratory technician at University of Colorado, Boulder (2010-2011)
- SEO and database manager, Inkonomy.com (2007-2008)