

Daniel M. Portik

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<http://github.com/dportik>

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SUMMARY

Skilled bioinformatician with substantial genomics experience, strong research record, ability to analyze complex data, and desire to work in a collaborative team environment.

CORE QUALIFICATIONS

- Strong ability to work in cross-functional teams with members from diverse backgrounds.
- Eight years of NGS bioinformatics pipeline construction and data analysis in Python.
- Extensive hands-on experience with NGS molecular lab work.
- Demonstrated scientific writing ability (40+ [publications](#)), production of clear and comprehensive software documentation, and strong interpersonal communication skills.
- Excellent problem-solving skills and ability to work with diverse and novel datasets.

TECHNICAL SKILLS

Programming: Python, R, SQL, Jupyter Notebooks, Snakemake

Statistics: Parametric and non-parametric statistics, linear regression, likelihood, PCA

Sequencing: Illumina and HiFi sequencing & processing (RNAseq, ddRADseq, targeted sequence capture, shotgun genomics)

Genomics Software: Assembly (CANU, Flye, hifasm, Spades, Velvet), sequence alignment (Clustal, MAFFT, Muscle, MACSE, trimaL), similarity filtering/mapping (BLAST+, BWA, CD-HIT, minimap2), and genomics tools (bedtools, mosdepth, Samtools, Seqtk, vcftools)

Molecular Lab Work: DNA & RNA extraction, PCR, primer design, gel electrophoresis, Sanger Sequencing, DNA quantification (BioAnalyzer, Qubit, Nanodrop), sonication

NGS Lab Work: RNA & DNA library prep, RNA-Seq (transcriptome sequencing), ddRADseq, assay/probe design, multiplexed sequence capture, Illumina sequencing

EXPERIENCE AND RELEVANT PROJECTS OVERVIEW

Senior Bioinformatics Scientist, Pacific Biosciences (PacBio) Sep 2021 – Present

- Expanded scope of HiFi applications to include methylation, pharmacogenomics, and genome assembly projects in addition to long-read shotgun metagenomics.

Bioinformatics Scientist II, Pacific Biosciences (PacBio) June 2020 – Sep 2021

- Develop bioinformatics tools and resources for PacBio HiFi applications, with primary emphasis on long-read shotgun metagenomics.
- Perform proof-of-concept projects and data analysis for industry partners and research labs. Topics include metagenomics, genome assembly, and pharmacogenomics.
- Deliver information through webinars, publications, and research conferences.
- Coding repository: <https://github.com/PacificBiosciences/pb-metagenomics-tools>

Postdoctoral Researcher, California Academy of Sciences Sep 2019 – May 2020

- Developed [Stacks pipeline](#), a Python workflow to automate ddRADseq data processing, including read trimming, locus assembly, custom data filtering, and formatting. Wrote [documentation](#) including background overview of all steps and explanation of code usage.

- Provide consultation and custom solutions for collaborators working on NGS projects.

Postdoctoral Researcher, University of Arizona

Sep 2017 – Sep 2019

- Developed [SuperCrunch](#), a modular Python bioinformatics toolkit. Allows database searching, homology filtering, sequence alignment, and formatting of GenBank data using algorithms built with BioPython, SQL and genetic tools. Wrote extensive user [documentation](#), presented code and tutorials at conference workshops; providing ongoing technical support.
- Performed lab work and data processing for NGS target sequence capture (DNA library prep, sequence capture reactions, Illumina sequencing, bioinformatics pipelines).

Postdoctoral Researcher, University of Texas at Arlington

Jan 2016 – Sep 2017

- Developed [dadi pipeline](#), a custom Python workflow designed to optimize maximum likelihood searches to fit population demographic models to genomic SNP data.
- Project manager. Trained collaborators in genomic data analysis, maintained communication to evaluate project progression, assisted in troubleshooting, and co-authored publications.

PhD Student, University of California, Berkeley

Aug 2009 – Dec 2015

- Designed, tested, and implemented new transcriptome-based sequence capture method to enrich orthologous exons in genomic libraries, specifically for non-model systems. Assisted in development of bioinformatics tools for data assembly and evaluation of capture efficiency.

EDUCATION

Ph.D. Integrative Biology: University of California, Berkeley

December 2015

M.S. Evolutionary Biology: Villanova University

August 2009

B.S. Biology: John Carroll University

May 2007

SELECTED PUBLICATIONS AND PRE-PRINTS

- Bickhart, D.M., Kolmogorov, M., Tseng, E., **Portik, D.M.**, Korobeynikov, A., Tolstoganov, I., Uritskiy, G., Liachko, I., Sullivan, S.T., Shin, S.B., Zorea, A., Andreu, V.P., Panke-Buisse, K., Medema, M.H., Mizrahi, I., Pevzner, P.A., and T.P.L. Smith. **2022**. Generation of lineage-resolved complete metagenome-assembled genomes by precision phasing. *Nature Biotechnology*, <https://doi.org/10.1038/s41587-021-01130-z>
- Feng, X., Cheng, H., **Portik, D.**, and H. Li. **2021**. Metagenome assembly of high-fidelity long reads with hifiasm-meta. *arXiv*, in review at *Nature Methods*. [arXiv:2110.08457](https://arxiv.org/abs/2110.08457)
- Gerhig, J.L., **Portik, D.M.**, Driscoll, M.D., Jackson, E., Chakraborty, S., Gratalo, D., Ashby, M., and R. Valladares. **2021**. Finding the right fit: a comprehensive evaluation of short-read and long-read sequencing approaches to maximize the utility of clinical microbiome data. *bioRxiv*, in review at *Microbial Genetics*. <https://doi.org/10.1101/2021.08.31.458285>
- Portik, D.M.**, and J.W. Wiens. **2021**. Do alignment methods matter for phylogenomic (UCE) analyses? *Systematic Biology*, 70: 440–462.
- Portik, D.M.**, and J.W. Wiens. **2020**. SuperCRUNCH: a toolkit for creating and manipulating supermatrices and other large phylogenetic datasets. *Methods in Ecology and Evolution*, 11: 763–772.
- Hutter, C.R., Cobb, K.A., **Portik, D.M.**, Travers, S., and R.M. Brown. 2019. FrogCap: a modular sequence capture probe set for phylogenomics and population genetics for all frogs, assessed across multiple phylogenetic scales. *bioRxiv*, <https://doi.org/10.1101/825307>.
- Portik, D.M.**, Bell, R.C., Blackburn, D.C., Bauer, A.M., Barratt, C.D., Branch, W.R., Burger, M., Channing, A., Colston, T.J., Conradie, W., Dehling, J.M., Drewes, R.C., Ernst, R., Greenbaum, E., Gvoždík, V., Harvey, J., Hillers, A., Hirschfeld, M., Jongsma, G.F.M., Kielgast, J., Kouete, M.T., Lawson, L., Leaché, A.D., Loader, S.P., Lötters, S., van der Meijden, A., Menegon, M., Müller, S., Nagy, Z.T., Ofori-Boateng, C., Ohler, A., Papenfuss, T.J., Röbber, D., Sinsch, U., Rödel, M.-O., Veith, M., Vindum, J., Zassi-Boulou, A.-G., and J.A. McGuire. 2019. Sexual dichromatism drives diversification within a major radiation of African amphibians. *Systematic Biology* 68: 859–875.
- Portik, D.M.**, Smith, L.L., and K. Bi. 2016. An evaluation of transcriptome-based exon capture for frog phylogenomics across multiple scales of divergence (Class: Amphibia). *Molecular Ecology Resources* 16: 1069–1083.