Daniel M. Portik

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http://github.com/dportik

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SUMMARY

Skilled bioinformatician with substantial NGS experience, strong research record, attention to detail, 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.
- Six years of NGS bioinformatics pipeline construction and data analysis in Python.
- Extensive hands-on experience with NGS molecular lab work.
- Demonstrated scientific writing ability (30+ 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
Statistics: Parametric and non-parametric statistics, linear regression, likelihood, PCA
Sequencing: Illumina library prep & data processing (RNAseq, ddRADseq, sequence capture)
Genomics Software: ABYSS, BLAST+, Bowtie, CD-HIT, GATK, PAML, Picard, Samtools, STACKS, Trinity, Velvet, sequence alignment (Clustal, MAFFT, Muscle, MACSE, trimaL)
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

Postdoctoral Researcher, California Academy of Sciences   Sep 2019 – Jun 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*   *of 36 total

Portik, D.M., and J.J. Wiens. 2020. SuperCRUNCH: A toolkit for creating, filtering, and manipulating large molecular phylogenetic data sets and supermatrices, *Methods in Ecology and Evolution,* Early View.

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., Rößler, 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.

Barratt, C.D., Bwong, B.A., Jehle, R., Liedtke, H.C., Nagel, P., Onstein, R.E., **Portik, D.M.**, Streicher, J.W., and S.P. Loader. 2018. Vanishing refuge: testing the forest refuge hypothesis in coastal East Africa using genomewide sequence data for seven amphibians. *Molecular Ecology* 27: 4289–4308.

Portik, D.M., Leaché, A.D., Rivera, D., Blackburn, D.C., Rödel, M.-O., Barej, M.F., Hirschfeld, M., Burger, M., and M.K. Fujita. 2017. Evaluating mechanisms of diversification in a Guineo-Congolian forest frog using demographic model selection. *Molecular Ecology* 26: 5245–5263.

Schield, D.R., Adams, R.H., Card, D.C., Perry, B.W., Pasquesi, G.M., Jezkova, T., **Portik, D.M.**, Andrew, A.L., Spencer, C.L., Sanchez, E.E., Fujita, M.K., Mackessy, S.P., and T.A. Castoe. 2017. Genomic patterns of divergence and admixture in a widely-distributed rattlesnake provide insight into speciation with gene flow. *Ecology and Evolution* 7: 3951–3966.

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.