Chandra Earl

904-699-8280 | sunray1@ufl.edu
https://github.com/sunray1
Florida Museum of Natural History
3215 Hull Rd. Gainesville, Florida 32608

Skills

Programming Languages/Tools: Fluent: Python, R, SQL; Proficient: HTML, Unix(bash), Markdown, Git; Familiar: JavaScript, CSS, Mathematica, TensorFlow (Machine Learning)

Mathematics: Calculus (I, II, III), Differential Equations, Linear Algebra, Statistical Analyses

Genetics: NextGen Sequencing Analyses (Assembly, Annotation, Gene Expression), DNA Extraction

Education

Doctor of Philosophy (Ph.D.) in Genetics and Genomics — *Expected June 2020*
University of Florida, *Gainesville, FL*
In progress, GPA: 3.76

Bachelor of Science (B.S) in Biology — *2015*
University of Florida*, Gainesville, FL*
Emphasis in Biotechnology; Bioinformatics minor, GPA: 3.14

High School Diploma — *2011*
Bartram Trail High School, *Jacksonville, FL*
Advance Placement Program; graduated magna cum laude, GPA: 4.2

Career History & Accomplishments

Bioinformatics Research Assistantship, *University of Florida; Florida Museum of Natural History; Dr. Rob Guralnick* — *2018 - current*
- Four-year, co-advised appointment for a Ph.D. (Second half)
- Using informatics approaches to describe the biodiversity and endemism of North American butterfly species
- Produced a phylogeny of NA butterfly species using data collected from a variety of sources
- Comparing metrices with those found in plants to draw conclusions about plant/host interactions

Smithsonian Summer Internship, *Smithsonian Institution; Dr. Rebecca Dikow; Dr. Paul Frandsen* — *Summer 2018*
- Two-month appointment in Washington, D.C.
- Developed deep machine learning techniques to classify bumblebee images
- Familiarized with Mathematica and TensorFlow
- Trained neural networks to recognize images

Bioinformatics Research Assistantship, *University of Florida; Florida Museum of Natural History; Dr. Akito Kawahara* — *2016-2018*
- Four-year, co-advised appointment for a Ph.D. (first half)
- Affiliated with ButterflyNet – a GoLife grant designed to produce a set of online tools and databases for comparative studies of butterflies
- Assisted students with bioinformatics and phylogenetic programs in the lab
- Worked on a butterfly phylogeny using available sequence data in conjunction with ButterflyNet
- Developed new pipelines and analyses related to synthesizing ButterflyNet products (GeneDumper)

2015-2016

Graduate Research Assistantship, *University of Florida; Genetics and Genomics Ph.D. Program*

- One-year appointment
- Rotated through several labs and learned diverse bioinformatics techniques
- Dr. Lei Zhou; Searched for proto-oncoprotein MDM2 lineage in Arthropods using PSSM models
- Dr. David Reed; Integrated ecological niche modelling and coalescent modelling for species delimitation
- Dr. Ana Conesa; Investigated differences in GO enrichment due to isoform levels using a novel R script

2014-2015

Undergraduate Bioinformatics Assistant, *University of Florida; Dr. Akito Kawahara*

- Transcriptome assembly and annotation of butterflies
- Performed targeted enrichment analyses
- Introduced to bioinformatic modules and tools
- Developed novel pipelines designed for contamination discovery and cleanup in Illumina sequence reads and Anchored Hybrid Enrichment analysis

2012-2014

Undergraduate Laboratory Researcher, *University of Florida; Dr. Bryan Kolaczkowski*

- Researched binding kinetics of immune receptors in cells
- Educated in DNA manipulation methods, such as digests, ligation, primer building, sequence reading etc.
- Educated in protein purification through cell culturing, chromatography, molecular binding assays and gel runs
- Introduced to bioinformatic skills such as phylogeny building and ancestral state reconstruction
- Learned basic Linux bash coding and program usage
- Knowledgeable in basic laboratory safety measures

Publications and Programs

- Co-Author: de Souza Cortez MB, Guralnick RP, Barve V, **Earl C**, Soltis D, Soltis P. **The Hyperdiverse *campos rupestres* Revealed through Macroevolutionary Patterns of Plant Lineages.** *In preparation*.
- Author: **Earl C**, White A, Frandsen P, Guralnick, RP, Kawahara AY, Dikow R. **Using Machine Learning to Distinguish Between and Discover Patterns of Biodiversity in Insects**, *In preparation.*
- Developer: **Earl C**, Stucky B, Guralnick R, Kawahara AY. **GeneDumper**, https://github.com/sunray1/GeneDumper, *In preparation.*
- Lead Developer: **Earl C**, Gaynor S, Whelpley J. **SSB2020 Conference Website**; https://systbiol.github.io/ssb2020/. 2019.
- Co-Author: Toussaint EFA, Breinholt JW, **Earl C**, Warren AD, Brower AVZ, Yago M, Dexter KM, Espeland M, Pierce NE, Lohman DJ, Kawahara AY. **Anchored Phylogenomics Illuminates the Skipper Butterfly Tree of Life**. *BMC Evolutionary Biology*, 2018. doi: 10.1186/s12862-018-1216-z.
- Co-Author: Breinholt JW, **Earl C**, Lemmon AR, Lemmon EM, Xiao L, Kawahara AY. **Resolving Relationships among the Megadiverse Butterflies and Moths with a Novel Pipeline for Anchored Phylogenomics**, *Systematic Biology*, 2018. doi: 10.1093/sysbio/syx048.
- Author: **Earl C**, Guralnick, RP, Kawahara AY. **Digest: Imperfect Convergence in Butterfly Wing Patterns**, *Evolution*, 2017. doi: 10.1111/evo.13215.
- Co-author: Korithoski B, Kolacakowski O, Mukherjee K, Kola R, **Earl C**, Kolaczkowski B. **Evolution of a Novel Antiviral Immune-Signaling Interaction by Partial-Gene Duplication**, *PloS One*, 2015. doi: 10.1371/journal.pone.0137276.
- Co-Developer: Breinholt JW**, Earl C**. **DeconC**: **a python pipeline used to find and remove contamination in transcriptomes**; 2014.

Presentations

- Oral presentation; Biodiversity RCN, May 2019
- Oral presentation; Genetics and Genomics Seminar, February 2019
- Oral presentation; Entomology 2018, November 2018
- Poster presentation; Biological Data Science Meeting, November 2018
- Oral presentation; McGuire Seminar, August 2018
- Poster presentation; Smithsonian Staff Picnic, June 2018
- Oral presentation; 8th Dresden Meeting on Insect Phylogeny, September 2017
- Oral presentation; Undergraduate Research Seminar; June 2013
- Poster presentation; Microbiology and Cell Science Undergraduate Research Symposium; April 2013

Workshops and Conferences

- SSB2020 Standalone Meeting; Gainesville, FL; January 2020
- USDA-ARS / Machine Learning Training; Gainesville, FL; August 2019
- Biodiversity Research Coordination Network meeting; Gainesville, FL; May 2019
- Carpentries Instructor Training; Gainesville FL; March 2019
- HexaSoTol Status Meeting; Chicago, IL; August 2018
- NIH Data Science Hackathon; Bethesda, MD; July 2018
- Harvard Personal Genome Project Hackathon; Boston, MA; July 2018
- Data Carpentries Workshop; Washington, DC; June 2018
- Software Carpentries Workshop, Gainesville, FL; August 2016
- Workshop on Molecular Evolution, MBL; Woods Hole, MA; July 2016
- UF ICBR Introduction to Mammalian Cell Culture Techniques workshop; Gainesville, FL November 2015
- Phenotype Prediction using Genomic Data Workshop; Gainesville, FL; August 2013
- NCBI’s Discovery Workshop; Bethesda, MD; July 2013

Grants and Awards

- Smithsonian Internship Grant ($5720); June 2018
- 4R Scholarship ($1000); July 2017
- Graduate Student Counsel Travel Grant ($300); July 2016

Public Outreach

- PBS American Spring Live!, April 2019
- Oral presentation; Girls Who Code: DC, July 2018