Graham Larue

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SUMMARY

I am a bioinformatician/computational biologist with expertise in molecular evolution and comparative genomics. I have more than 8 years of Python experience, extensive familiarity with Bash/Linux, and have published first-author bioinformatics research and software in prominent scientific journals including *Nucleic Acids Research* and *Current Biology*. In addition to my scientific background, I have more than ten years of experience in the service industry. Going forward, I am interested in building tools for—and addressing questions in—the areas of molecular evolution, genomics and next-generation sequencing technologies and their applications.

EDUCATION

2016 – 2022	**Ph.D.** - Quantitative and Systems Biology *University of California Merced*
2013 – 2015	**M.S.** - Cell and Molecular Biology *San Francisco State University*
2002 – 2008	**B.S.** - Biology *University of California Santa Cruz*

WORK EXPERIENCE

University of California Merced | AUG. 2016 - AUG. 2022
Graduate student

Bioinformatics and molecular evolution doctoral research in Dr. Scott Roy's group, focused on the evolutionary dynamics of minor spliceosomal introns across diverse eukaryotic genomes. Throughout my PhD I developed software to: classify genomic sequences using machine learning techniques, identify orthologous gene clusters using graph-based algorithms, extract and catalog annotated genomic feature sequences, and download and organize thousands of genome and annotation files from online databases. Additionally, I built pipelines of existing software to update eukaryotic genome annotations using NGS data, and acted as system administrator for an academic Linux server for 7+ years.

DOE Joint Genome Institute | JUN. 2019 – SEP. 2019
Summer Graduate Intern

Big data comparative genomic analysis of intron lengths in fungi.

University of California Berkeley | JUL. 2011 – JUL. 2013
Staff Research Associate I - Depts. of Neurobiology & Electrical Engineering

Electrophysiological investigation of mammalian retinal architecture in the labs of Professor Frank Werblin (Nerobiology) and Dr. Long-Sheng Fan (EE).

Santa Cruz Biotechnology | JAN. 2009 – NOV. 2010
Research Assistant

Microarray screening and sample prep. in hybridoma monoclonal antibody production group.

PROGRAMMING LANGUAGES

BASIC	R, Julia, Perl, SQL, C++
ADVANCED	Python, Bash

TECHNICAL EXPERIENCE

Bioinformatics: Designed and built: novel ML-based intron sequence classification algorithm (intronIC), custom ortholog and intron homology identification pipelines, command-line JGI data retrieval utility (jgi-query). Experience with: *de novo* transcriptome assembly, NGS-based eukaryotic gene annotation, phylogenetic tree construction, PAML, BLAST, DIAMOND, HISAT, bowtie, StringTie, STAR, AUGUSTUS, Trinity, PASA, Kallisto, Salmon, samtools, bedtools, fastq-dump

Computing: Linux system administration, GNU coreutils, grep, sed, awk, Slurm

Data visualization: Matplotlib, Seaborn

Wet lab: ELISA, microarray, confocal and two-photon microscopy, multi-electrode array, retinal tissue culture and dissection, patch-clamp, rodent husbandry and euthanasia, sterile technique.

SELECTED PUBLICATIONS

Larue, G.E., Eliáš, M., Roy, S.W., 2021. "Expansion and transformation of the minor spliceosomal system in the slime mold *Physarum polycephalum*." *Curr. Biol.* 31, 3125-3131.e4. https://doi.org/10.1016/j.cub.2021.04.050

Moyer, D.C.*, **Larue, G.E.***, Hershberger, C.E., Roy, S.W., Padgett, R.A., 2020. "Comprehensive database and evolutionary dynamics of U12-type introns." *Nucleic Acids Res.* https://doi.org/10.1093/nar/gkaa464. (*co-first author)

Hudson, A.J., McWatters, D.C., Bowser, B.A., Moore, A.N., **Larue, G.E.**, Roy, S.W., Russell, A.G., 2019. "Patterns of conservation of spliceosomal intron structures and spliceosome divergence in representatives of the diplomonad and parabasalid lineages." *BMC Evol. Biol.* 19, 162. https://doi.org/10.1186/s12862-019-1488-y.

Slabodnick, M.M., Ruby, J.G., Reiff, S.B., Swart, E.C., Gosai, S., Prabakaran, S., Witkowska, E., **Larue, G.E.**, Fisher, S., Freeman, R.M., Gunawardena, J., Chu, W., Stover, N.A., Gregory, B.D., Nowacki, M., Derisi, J., Roy, S.W., Marshall, W.F., Sood, P., 2017. "The Macronuclear Genome of *Stentor coeruleus* Reveals Tiny Introns in a Giant Cell." *Curr. Biol.* 27, 569–575. https://doi.org/10.1016/j.cub.2016.12.057.

PERSONAL REFERENCES

References available on request