Graham Larue

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SUMMARY

I am a computational biologist/bioinformatician with a background in comparative genomics and molecular evolution, finishing a PhD in Quantitative and Systems Biology from UC Merced (anticipated summer 2022). I have 8+ years of Python experience, 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 answering question in—the areas of 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

*anticipated summer 2022

WORK EXPERIENCE

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

Bioinformatics/molecular evolution doctoral research in Dr. Scott Roy's group, where I wrote software to classify genomic sequences using machine learning techniques, identify orthologous gene clusters using a graph-based algorithm, extract 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 a Linux system administrator for a shared lab 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 data retrieval utility (jgi-query). Experience with: *de novo* transcriptome assembly, NGS-based eukaryotic gene annotation, 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.

REFERENCES

References available on request