

Graham Larue



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SUMMARY

I am a computational biologist/bioinformatician specializing in comparative genomics and molecular evolution, finishing a PhD in Quantitative and Systems Biology from UC Merced (anticipated Spring 2022). I have 8+ years of Python experience, and have published first-author bioinformatics research in prominent scientific journals including *Nucleic Acids Research* and *Current Biology*. In addition to my scientific background, I also have more than ten years of experience in the service industry. Going forward, I am interested in building tools to address biological questions in the areas of genomics and next-generation sequencing technologies.

EDUCATION

- 2016 – 2022 **Ph.D. (anticipated summer 2022)**
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

AUG. 2016 - PRESENT
University of California Merced
Graduate student
Bioinformatics/molecular evolution doctoral research in Dr. Scott Roy's group, focused around sequence-based classification and comparative genomics of spliceosomal introns.

JUN. 2019 – SEP. 2019
DOE Joint Genome Institute
Summer Graduate Intern
Big data comparative genomic analysis of intron lengths in fungi.

JUL. 2011 – JUL. 2013
University of California Berkeley
Staff Research Associate I - Depts. of Neurobiology & Electrical Engineering
Electrophysiological investigation of mammalian retinal architecture in the labs of Professor Frank Werblin (Neurobiology) and Dr. Long-Sheng Fan (EE).

JAN. 2009 – NOV. 2010
Santa Cruz Biotechnology
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). Experienced using: *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