

# Graham Larue

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## SUMMARY

I am a computational biologist/bioinformatician specializing in comparative genomics and molecular evolution. I am finishing a PhD in Quantitative and Systems Biology from UC Merced (anticipated Spring 2022) with 8+ years of Python experience, and have published first-author bioinformatics research in prominent scientific journals including *Nucleic Acids Research* and *Current Biology*. I also have more than 10 years of experience in the service industry. Going forward, I am interested in building tools for/answering biological questions in the areas of genomics and next-generation sequencing technologies.

## EDUCATION

- 2016 – 2022 **Ph.D. (anticipated)**  
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 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:** Novel machine-learning based intron sequence classification algorithm (intronIC), *de novo* transcriptome assembly, NGS-based eukaryotic gene annotation, custom gene orthology and intron homology identification, 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.* o. <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