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*. In addition to my scientific background, I also have more than 10 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)** 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 (Nerobiology) 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.* 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