

Internship

Work on data analyses for kelp and urchin datasets

<u>California Conservation Genomics Project</u>: project PI Rachael Bay

Current team: Serena Caplins (Postdoc), Vanessa Guerra (Postdoc), Rachael Bay (Associate Professor), Maddie Armstrong (PhD student), Josh Melendez (MS student CSULA)

+ 3 undergraduate students!

Part-time for 8 weeks = \$15/hour for 160 hours (\$2500).

Start Mid June – End of August

Participate in data analyses, figure generation, and statistical analyses, read scientific papers, and software documentation

Weekly team meetings

Internship Application:

Due May 4th





Interns will be selected based on a one-page essay response to the following questions:



What skills/experiences do you hope to gain in this internship?



What skills that you've developed through course work or work experience, do you hope to bring to this internship?



What's the best team you've ever been a part of and why? (Describe what makes a good team)



Application form posted on Canvas!

What is Marine Genomics?

Using genomic data to answer questions about the evolutionary biology of marine organisms.

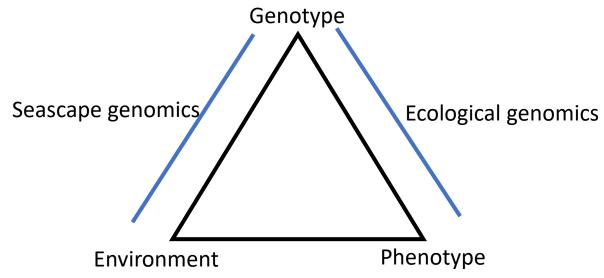




Figure modified from: https://link.springer.com/article/10.1007/s11295-013-0596-x

MOLECULAR ECOLOGY

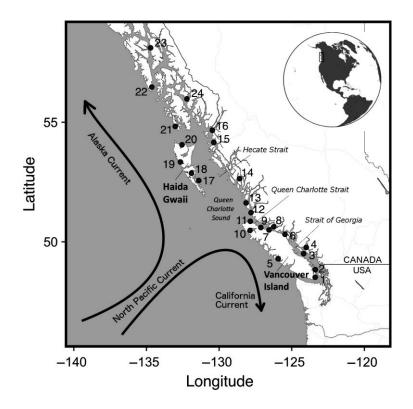
ORIGINAL ARTICLE | 🙃 Full Access

Asymmetric oceanographic processes mediate connectivity and population genetic structure, as revealed by RADseq, in a highly dispersive marine invertebrate (*Parastichopus californicus*)

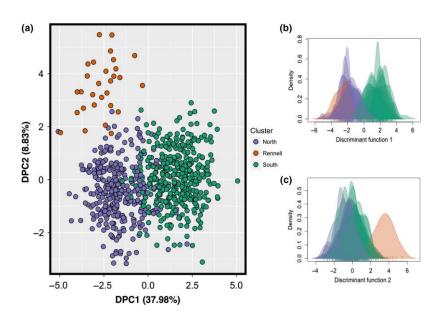
Amanda Xuereb Laura Benestan, Éric Normandeau, Rémi M. Daigle, Janelle M. R. Curtis, Louis Bernatchez, Marie-Josée Fortin

First published: 14 April 2018 | https://doi.org/10.1111/mec.14589 | Citations: 35

UC-eLinks







CrossMan

ORIGINAL ARTICLE

A Genome-Wide Association Study Identifies the Genomic Region Associated with Shell Color in Yesso Scallop, Patinopecten yessoensis

Liang Zhao 1 · Yangping Li 1 · Yajuan Li 1 · Jiachen Yu 1 · Huan Liao 1 · Shuyue Wang 1 · Jia Lv 1 · Jun Liang 2 · Xiaoting Huang 1 · Zhenmin Bao 1,3

Mar Biotechnol (2017) 19:301-309

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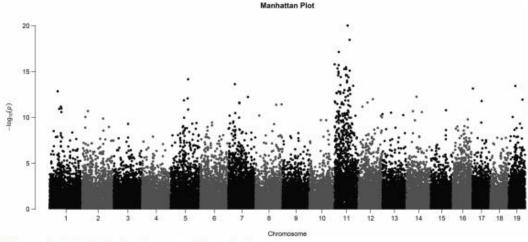


Fig. 2 Manhattan plot of -log10 (P value) for genome-wide association study



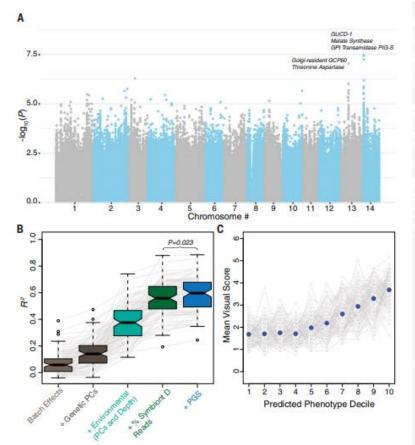
Fig. 1 Reddish-orange shell variant (a) and brown shell variant (b) of Yesso scallop, Patinopecten yessoensis

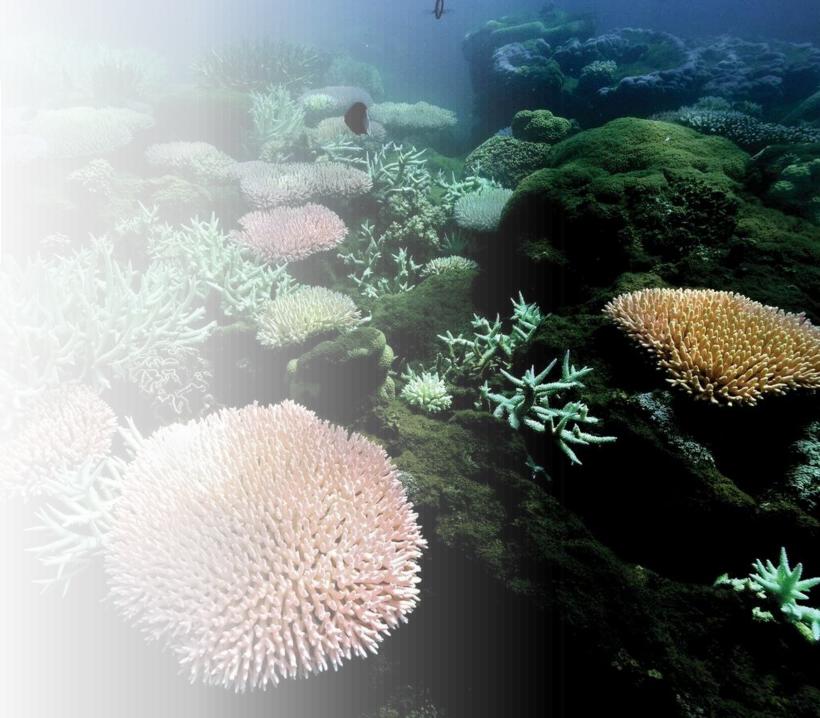
RESEARCH ARTICLE SUMMARY

CORAL GENOMICS

Population genetics of the coral *Acropora millepora*: Toward genomic prediction of bleaching

Zachary L. Fuller*, Veronique J. L. Mocellin, Luke A. Morris, Neal Cantin, Jihanne Shepherd, Luke Sarre, Julie Peng, Yi Liao, Joseph Pickrell, Peter Andolfatto, Mikhail Matz†, Line K. Bay*†, Molly Przeworski*†





How do we do marine genomics?

Design experiment

Lab experiment Field collection scheme

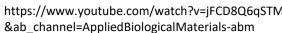


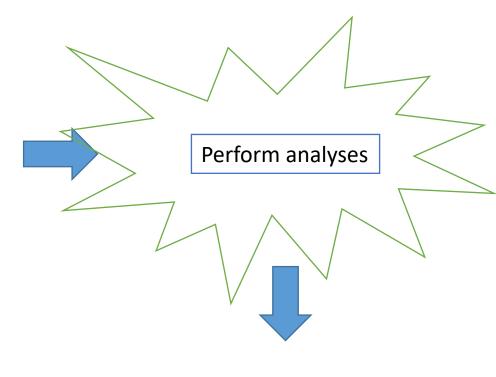


Extract DNA/RNA









Present results at conference Publish paper

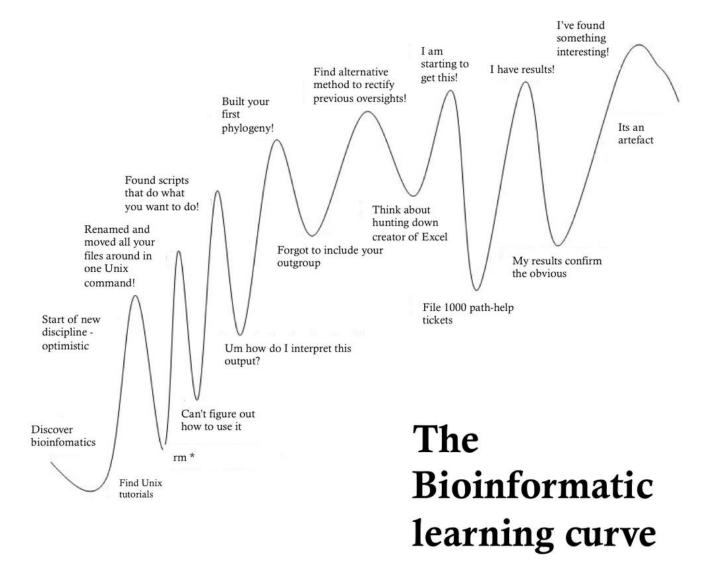
We use bioinformatics to understand these questions

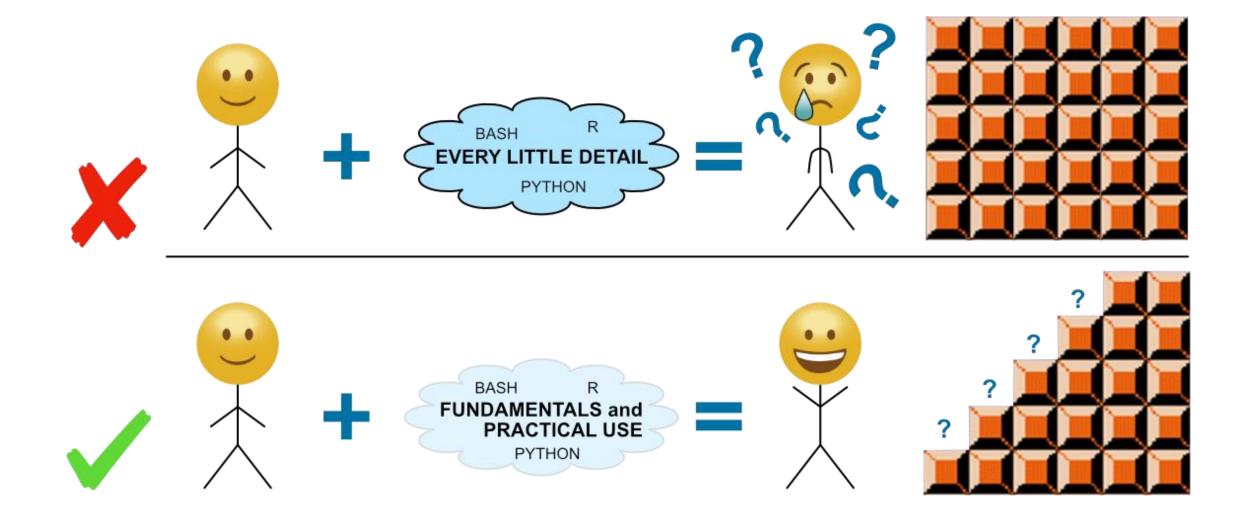
We'll cover two main areas

- The shell or Bash/UNIX
- R

Many of these analyses are very computationally intensive

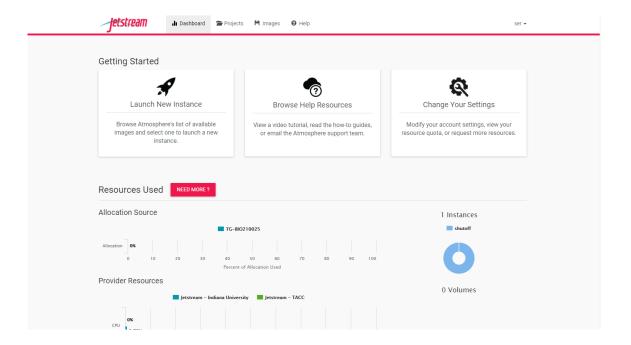
We will use a cloud computing resource called Jetstream





Jetstream via xsede





Why learn bioinformatics?

Gain many transferable skills!

- Data science
- Personalized medicine
- NGO agency scientist

Undergraduate degree

- Grad school
 - Postdoc
 - Professor
 - Research scientist in industry



About Careers News Science

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Spot the pattern, treat the cancer.

At Freenome, we're connecting people with next-generation blood tests for early cancer detection powered by our multiomics platform.

