

The background image shows a dramatic sunset or sunrise over a rugged coastline. A large, powerful wave is breaking in the foreground, its white spray contrasting with the dark, textured water. In the distance, a small lighthouse is visible on a rocky outcrop. The sky is filled with heavy, dark clouds, with patches of bright orange and yellow light from the setting sun.

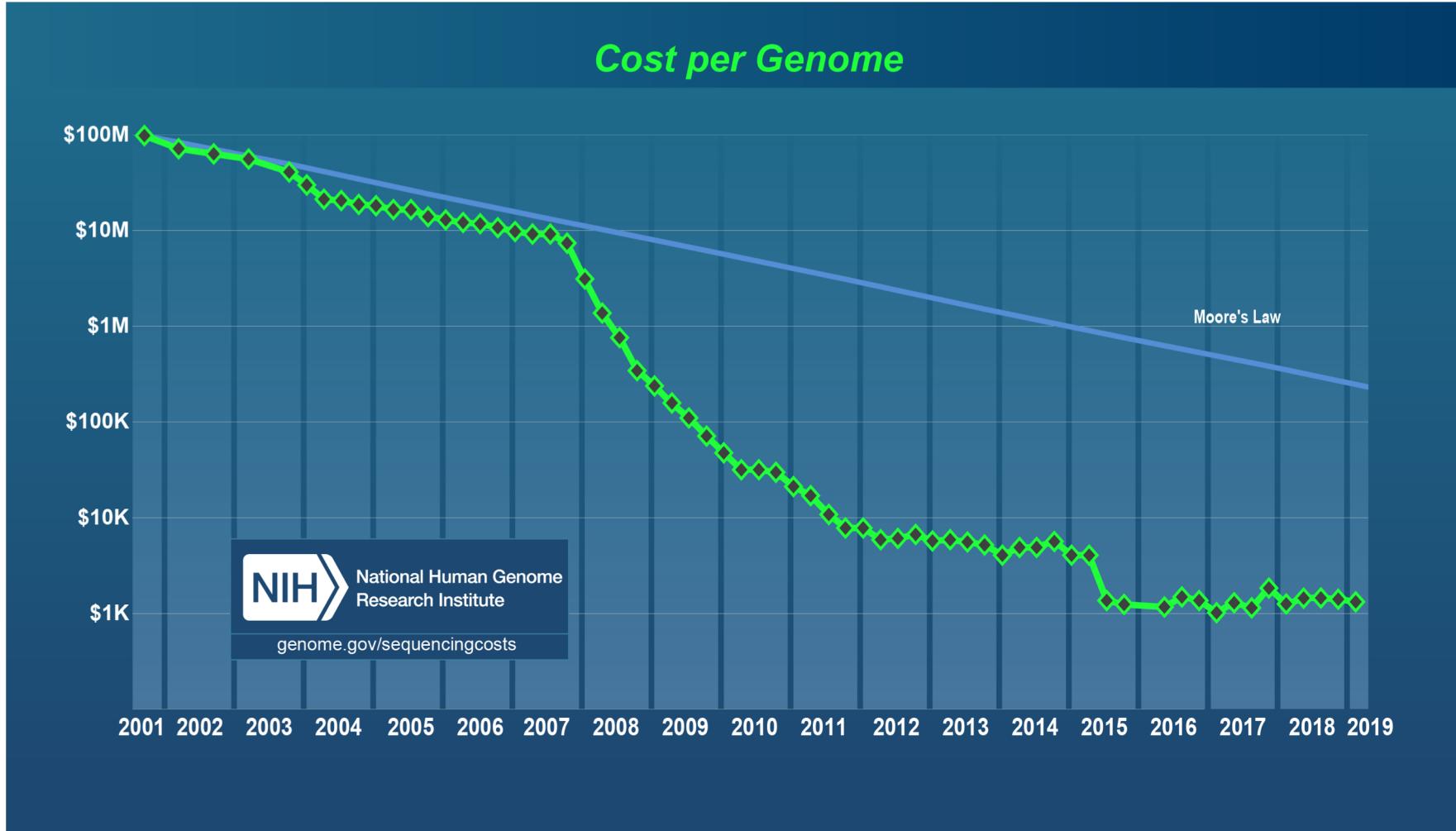
Welcome!

Marine Genomics

What is Marine Genomics?

Using genomic data to answer questions
about the evolutionary processes acting on
marine organisms

Genomic data is becoming more and more accessible (== cheaper)



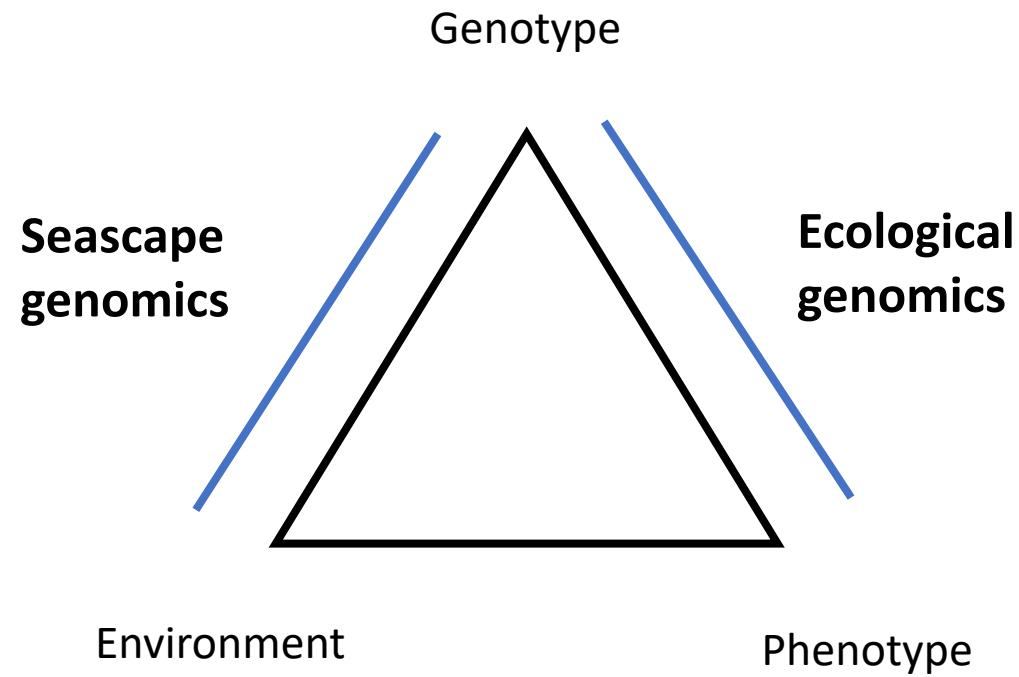
Evolutionary questions in Marine Biology

What limits range size? How does genetic diversity differ across the species' range?

What influences patterns of gene flow & migration? How does gene flow & migration impact selection or local adaptation?

What are the primary selective factors shaping phenotypic variation?

What is Marine Genomics?

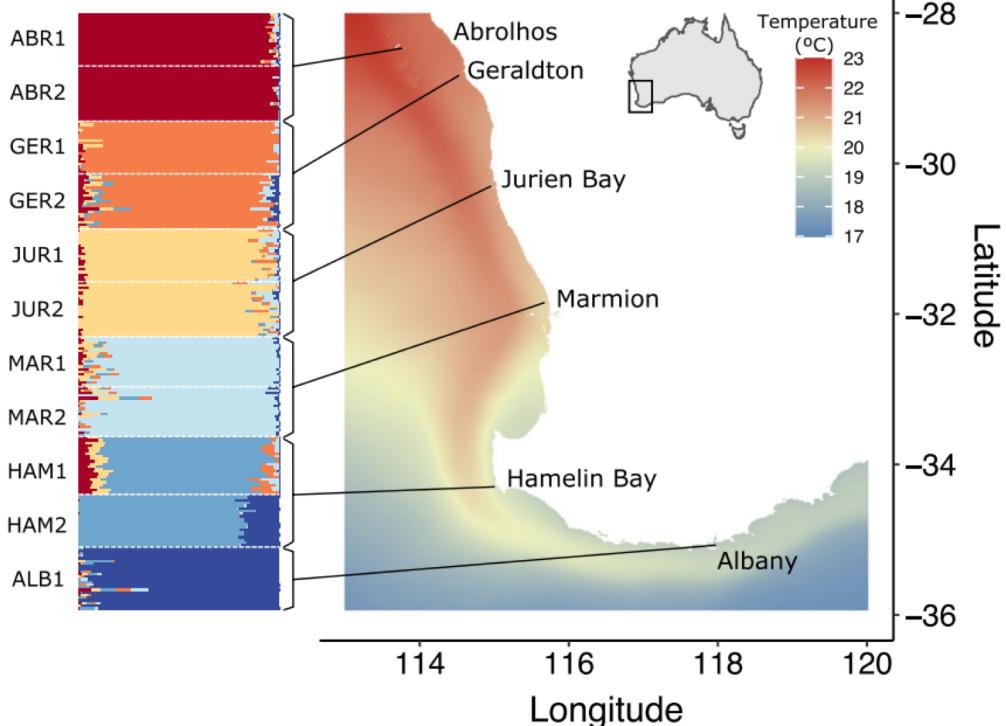


Genotype-Environment mismatch of kelp forests under climate change

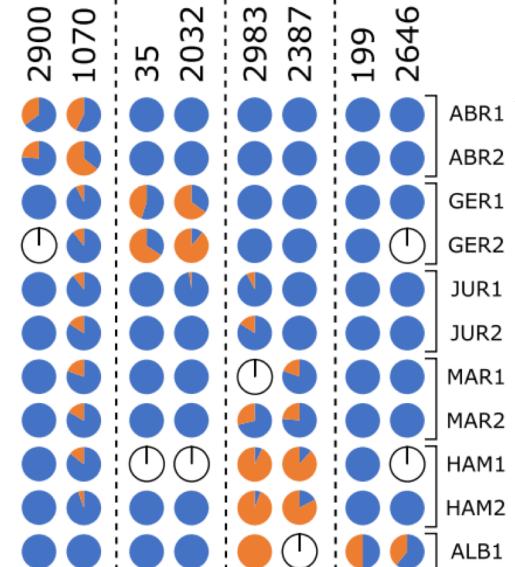
Sofie Vranken^{1,2} | Thomas Wernberg^{1,2,3} | Armin Scheben^{2,4} |
Anita Alice Severn-Ellis² | Jacqueline Batley² | Philipp Emanuel Bayer² |
David Edwards² | David Wheeler⁵ | Melinda Ann Coleman^{2,6,7}

3734 | WILEY MOLECULAR ECOLOGY

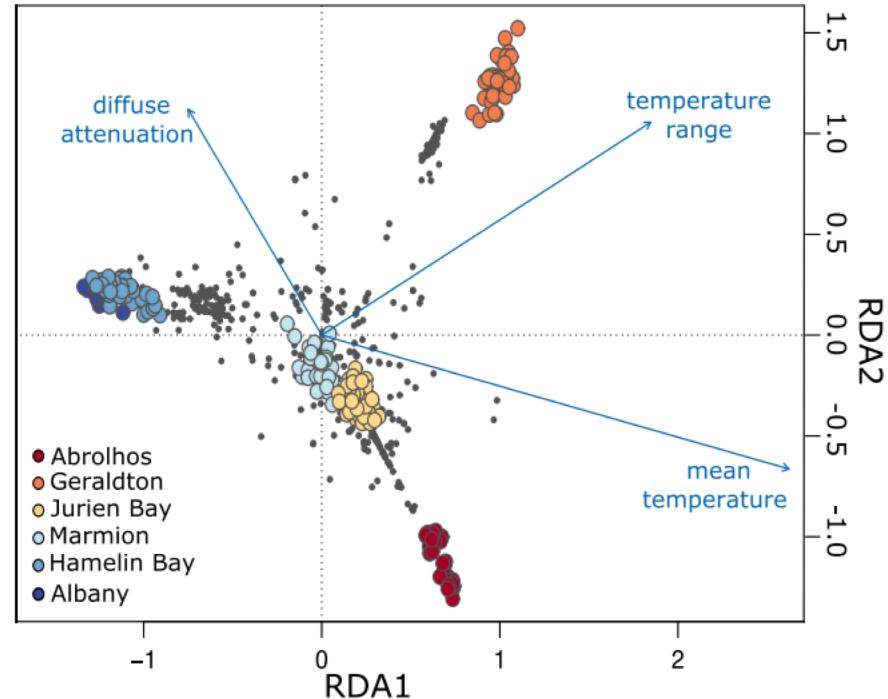
(a)



Example loci under selection



(b)



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

Liang Zhao¹ · Yangping Li¹ · Yajuan Li¹ · Jiachen Yu¹ · Huan Liao¹ · Shuyue Wang¹ ·
Jia Lv¹ · Jun Liang² · Xiaoting Huang¹ · Zhenmin Bao^{1,3}

Mar Biotechnol (2017) 19:301–309

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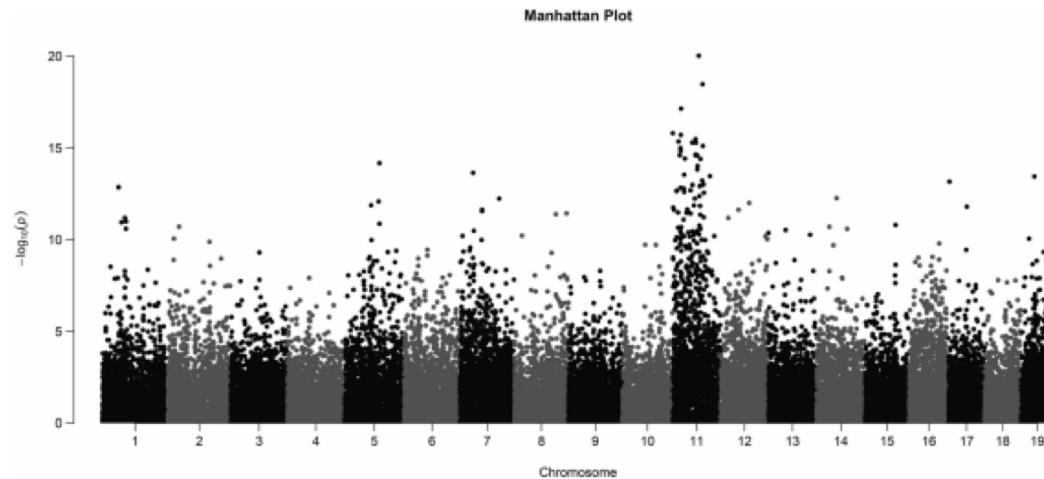


Fig. 2 Manhattan plot of $-\log_{10}(P$ value) for genome-wide association study

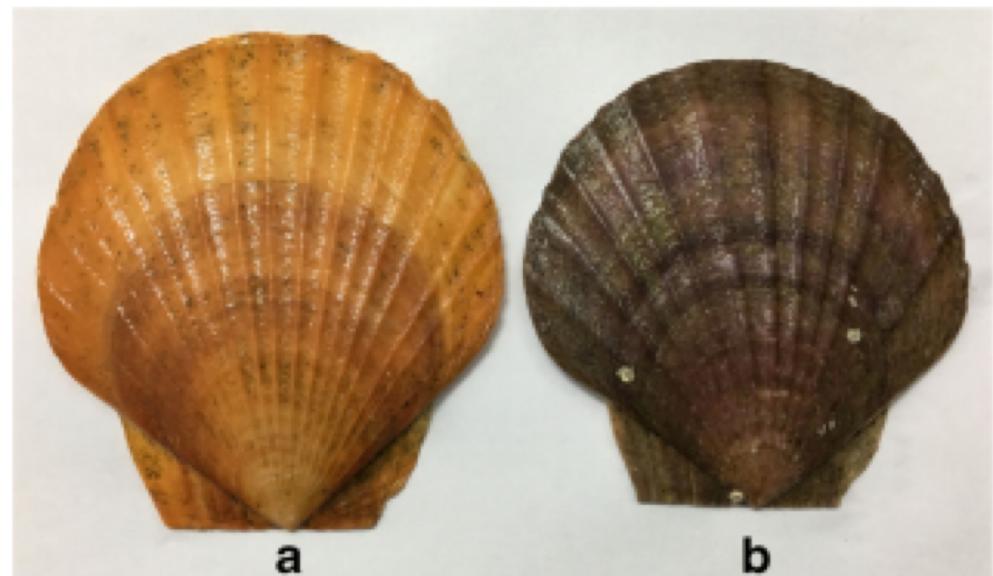


Fig. 1 Reddish-orange shell variant (a) and brown shell variant (b) of Yesso scallop, *Patinopecten yessoensis*

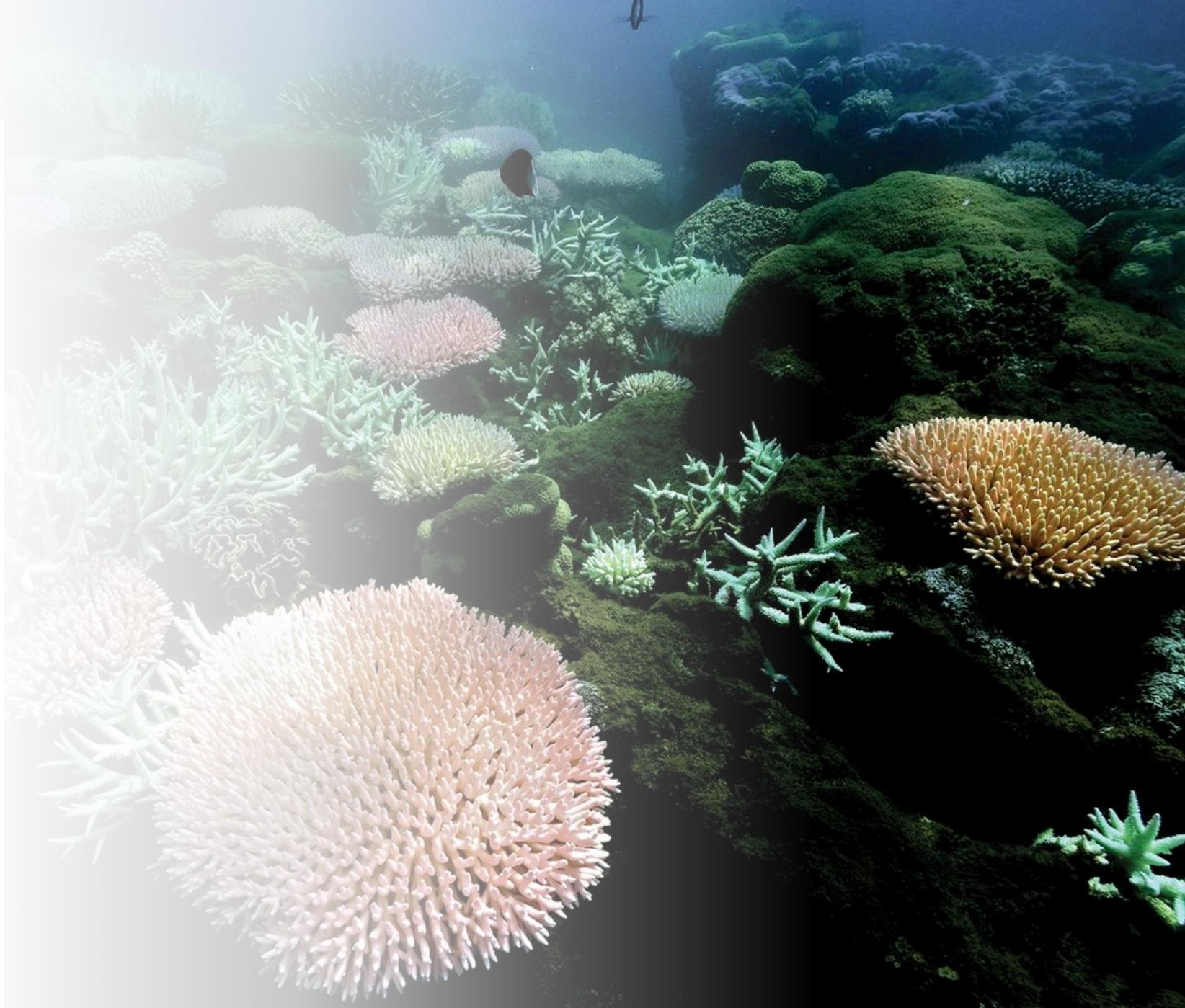
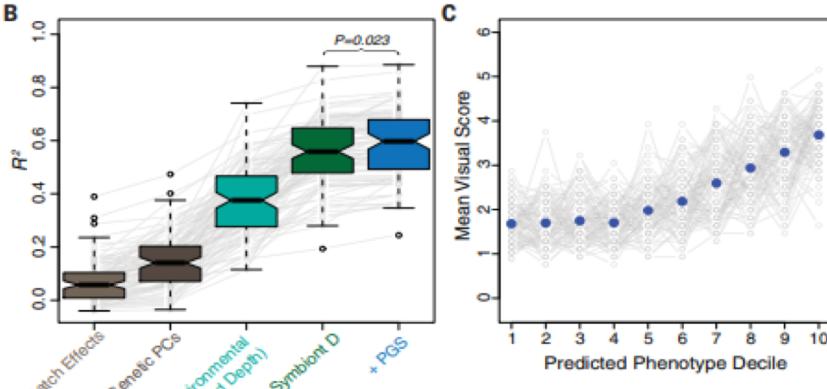
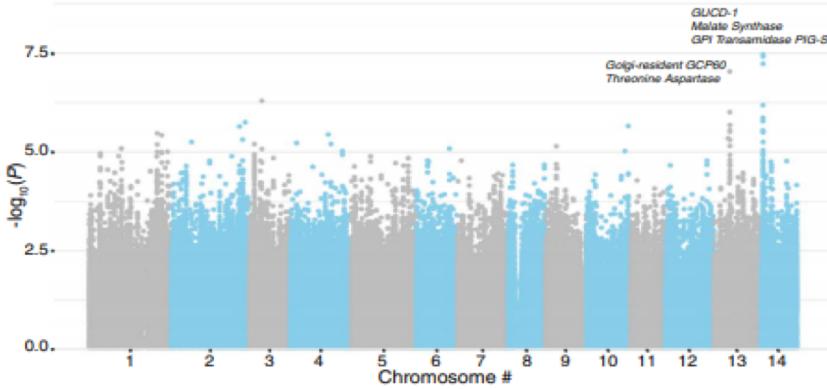
RESEARCH ARTICLE SUMMARY

CORAL GENOMICS

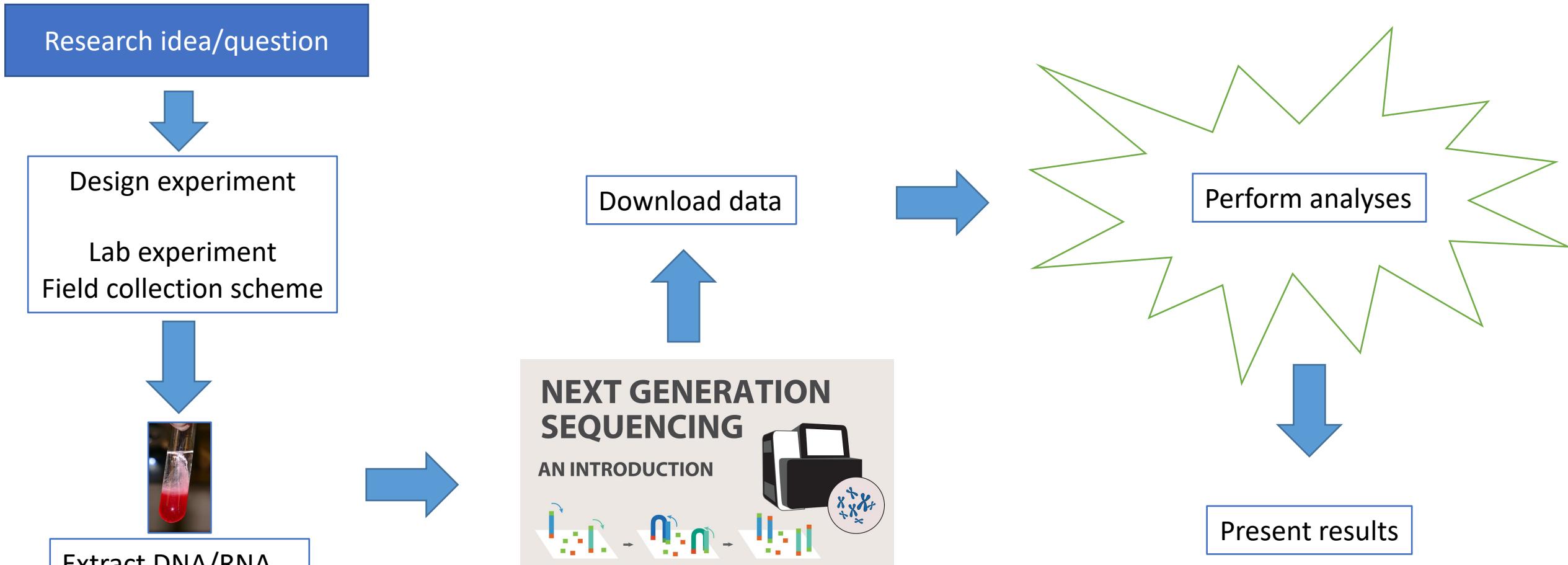
Population genetics of the coral *Acropora millepora*: Toward genomic prediction of bleaching

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

A



How do we do marine genomics?



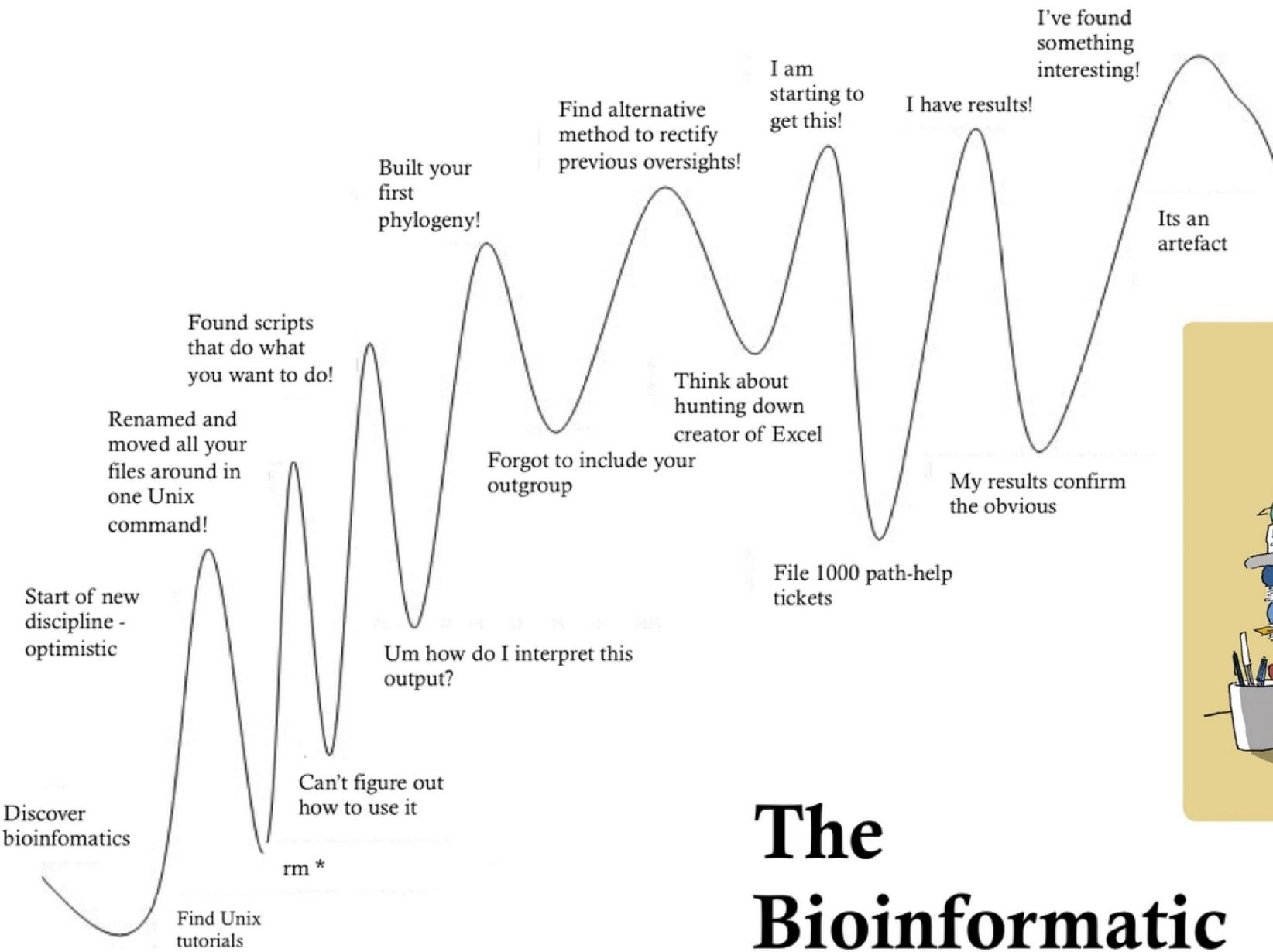
We use bioinformatics to answer these questions

We'll cover two main areas:

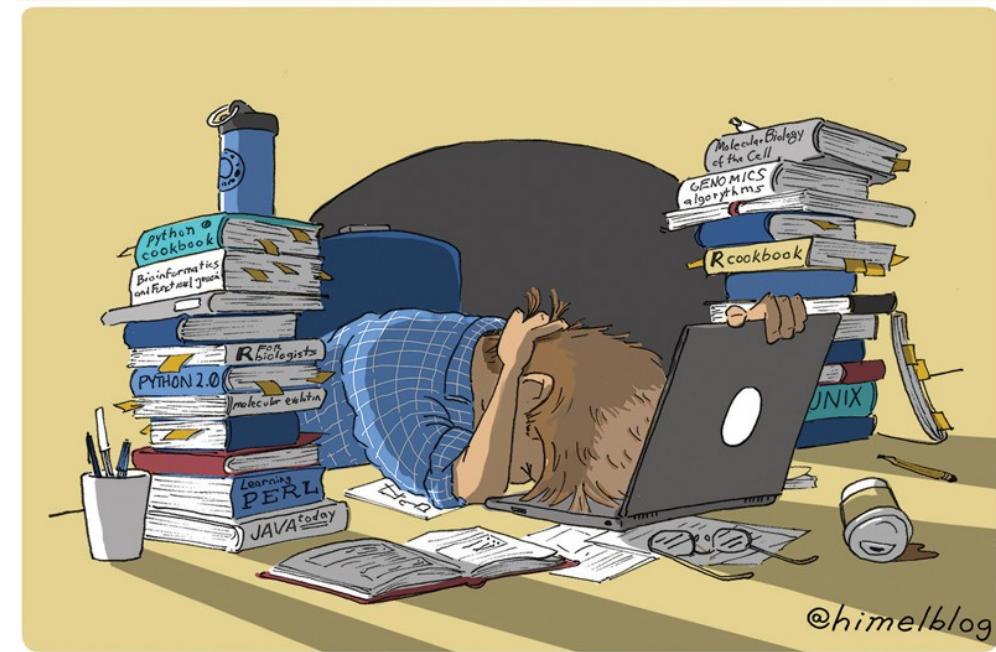
- The shell or Bash/UNIX
- R

Many of these analyses are very computationally intensive

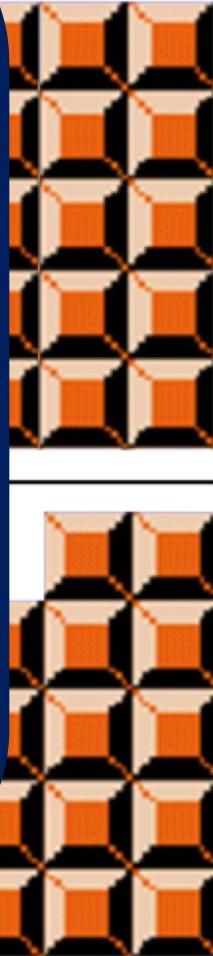
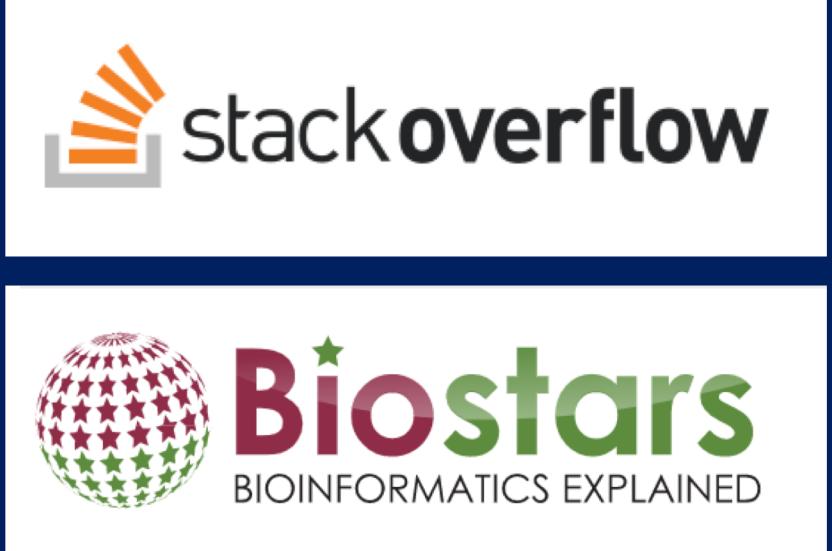




Source: <https://www.nature.com/articles/d41586-021-01485-y>



The Bioinformatic learning curve



Why learn bioinformatics?

Gain many transferable skills!

- Data science
- Personalized medicine
- NGO agency scientist

Undergraduate degree
Grad school

- Postdoc
 - Professor
 - Research scientist in industry

freenome

Multomics PREEMPT CRC™ Study About Careers News Science Blog

f t in



Spot the pattern,
treat
the cancer.

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



What's on the menu?

P. californicus

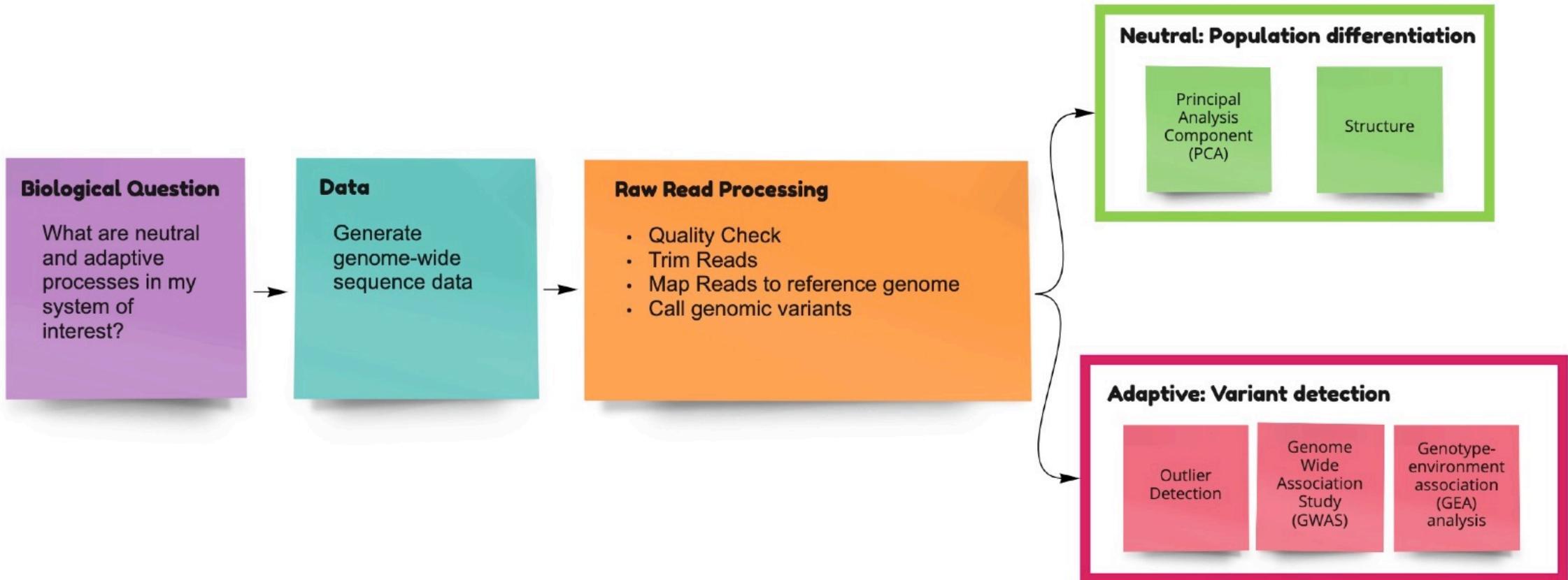


You're **scientific advisor** to aquaculture company interested in farming sea cucumbers

They want to know:

- Are there different populations?
- If so, is one population better suited to be grown in warmer conditions?
- Which genes will lead to suitable growth traits?

The power of the pipeline



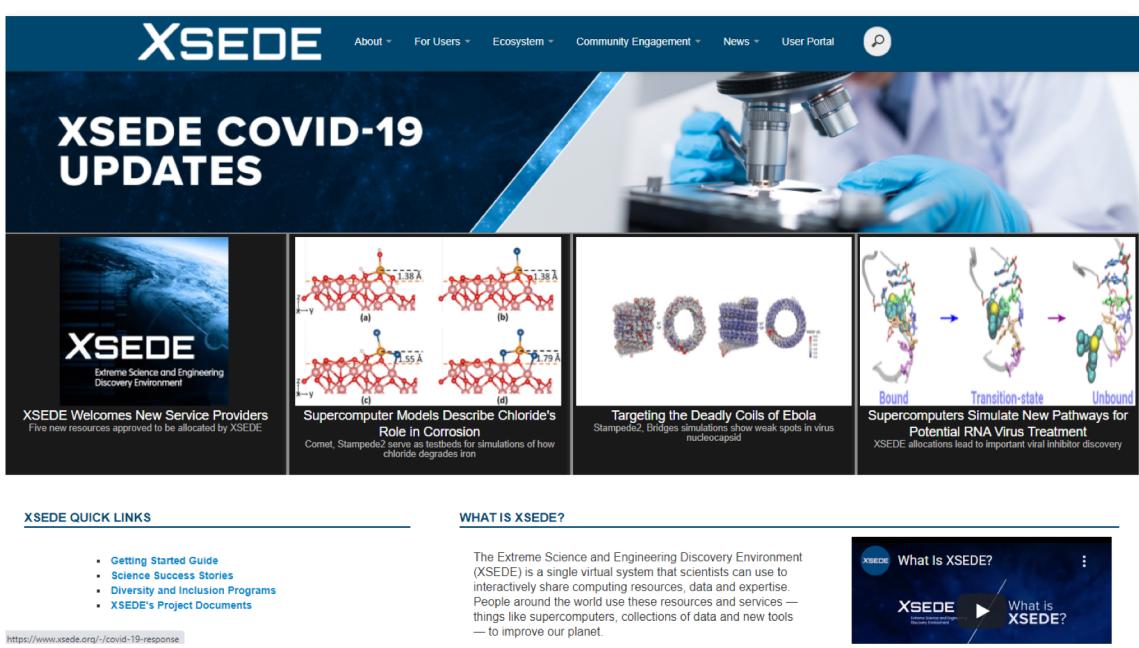
We do this via shell computing

Reasons for using
command line:

- More efficient
- Less error-prone
- Reproduceable



Jetstream via xsede



The XSEDE COVID-19 Updates page features a banner with a scientist in a lab coat and gloves using a microscope. Below the banner are several news cards:

- XSEDE Welcomes New Service Providers**: Five new resources approved to be allocated by XSEDE.
- Supercomputer Models Describe Chloride's Role in Corrosion**: Comet, Stampede2 serve as testbeds for simulations of how chloride degrades iron.
- Targeting the Deadly Coils of Ebola**: Bridges simulations show weak spots in virus nucleocapsid.
- Supercomputers Simulate New Pathways for Potential RNA Virus Treatment**: XSEDE allocations lead to important viral inhibitor discovery.

XSEDE QUICK LINKS

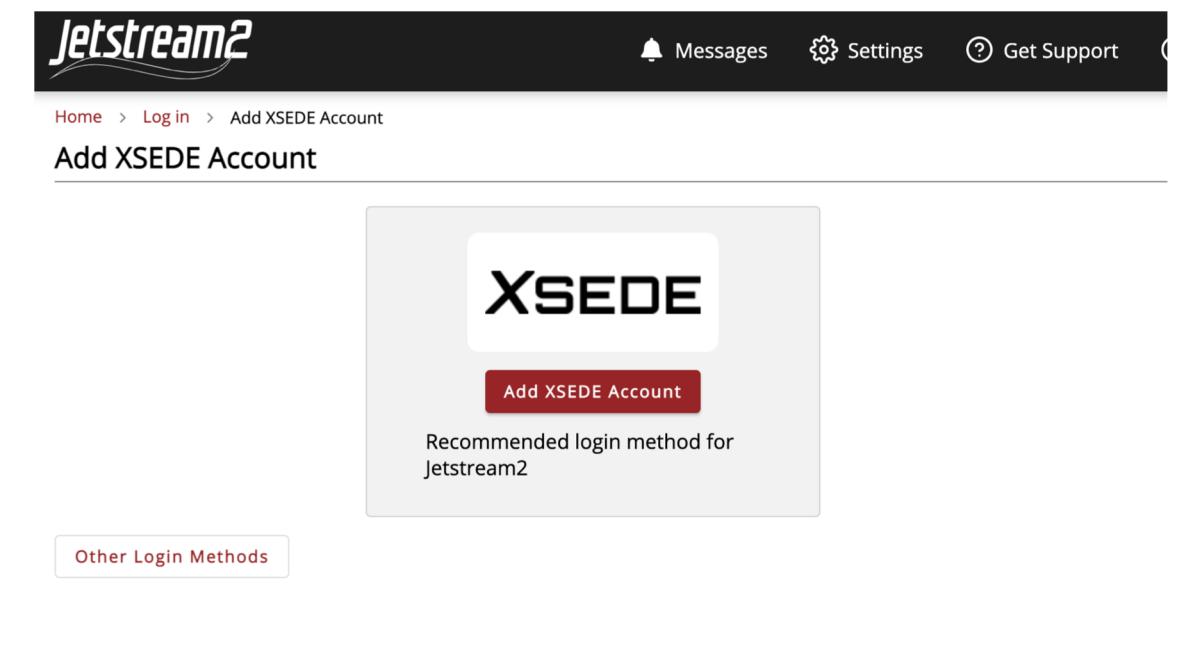
- Getting Started Guide
- Science Success Stories
- Diversity and Inclusion Programs
- XSEDE's Project Documents

<https://www.xsede.org/-/covid-19-response>

WHAT IS XSEDE?

The Extreme Science and Engineering Discovery Environment (XSEDE) is a single virtual system that scientists can use to interactively share computing resources, data and expertise. People around the world use these resources and services — things like supercomputers, collections of data and new tools — to improve our planet.

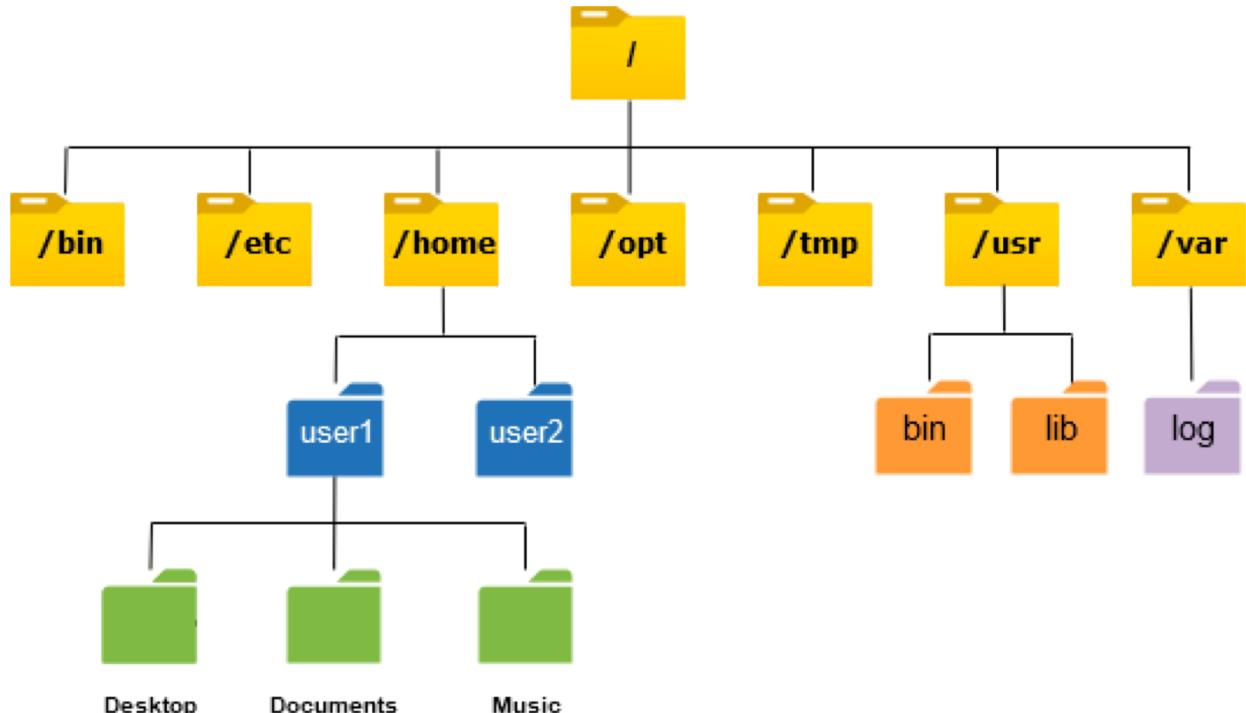
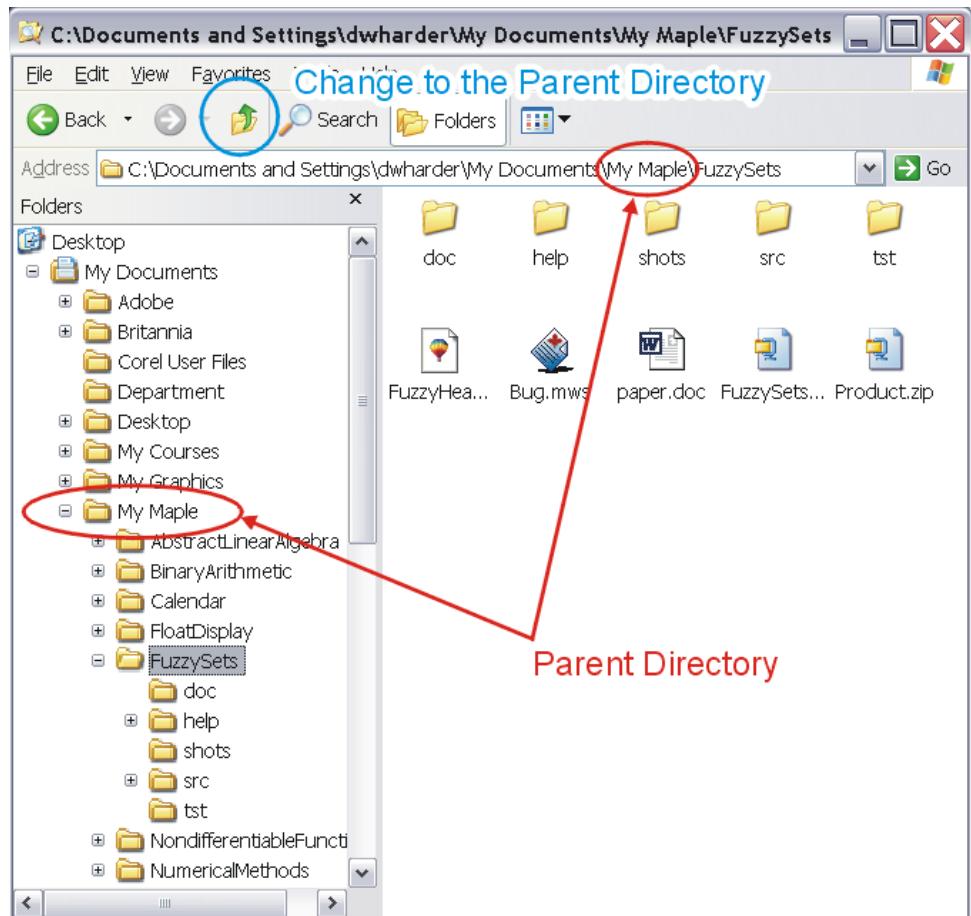
What Is XSEDE?



The Jetstream2 Add XSEDE Account page has a header with "Jetstream2", "Messages", "Settings", "Get Support", and a user icon. The main content area includes:

- Add XSEDE Account** button
- XSEDE** logo
- Add XSEDE Account** button
- Recommended login method for Jetstream2**
- Other Login Methods** button

Navigating directories



```
exouser@smoothly-epic-skink:~$ To run a command as administrator (user "root"), use "sudo <command>". See "man sudo_root" for details.
```