

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

Our origin story

- This is the first year as hybrid course
- We encourage questions/engagement
- Priority is getting experience over ‘getting it right’

Developed Spring 2021 - online



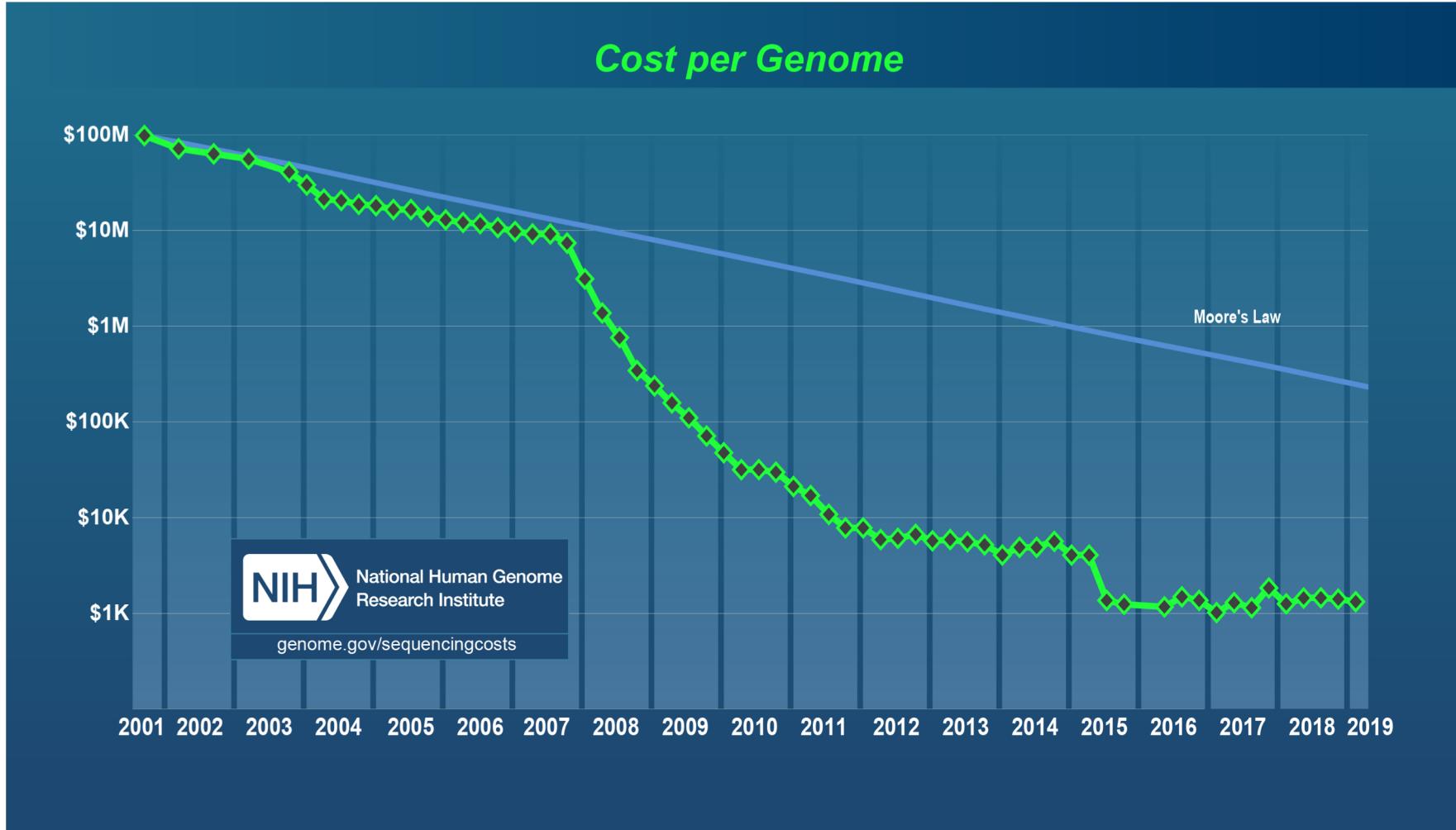
<https://baylab.github.io/MarineGenomics2022/>

<https://baylab.github.io/>

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)



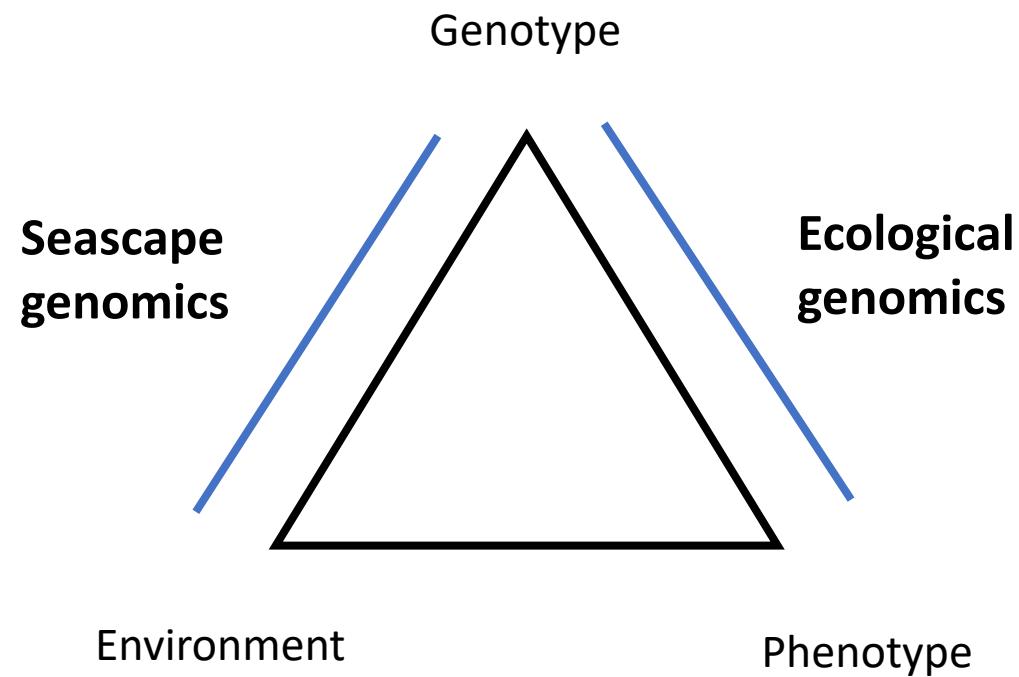
Evolutionary questions in Marine Biology

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?

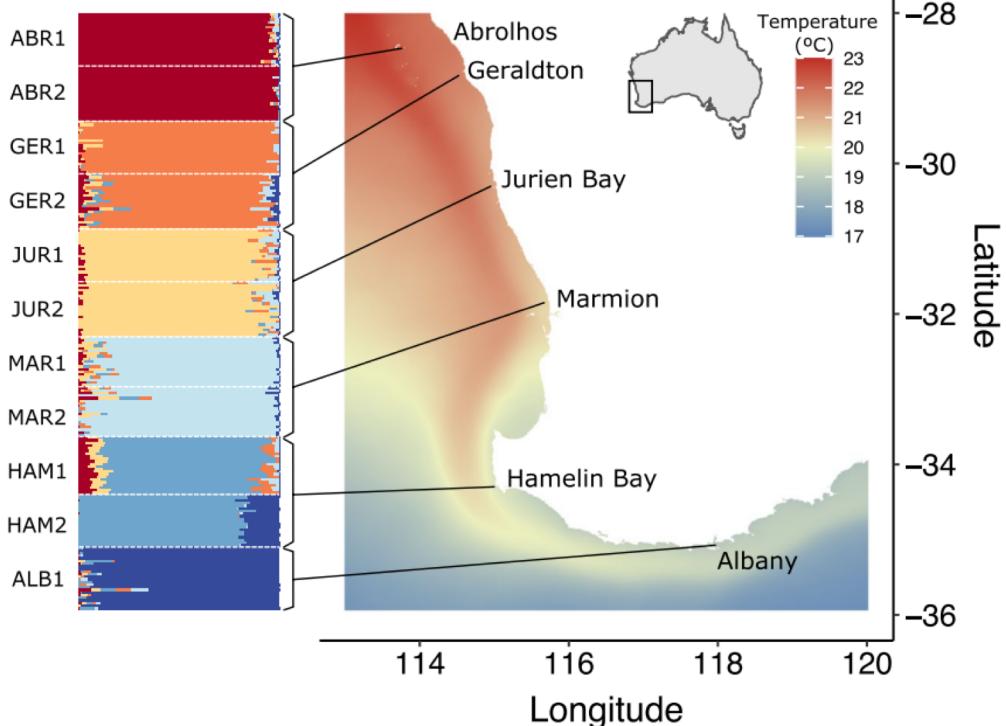


Genotype-Environment mismatch of kelp forests under climate change

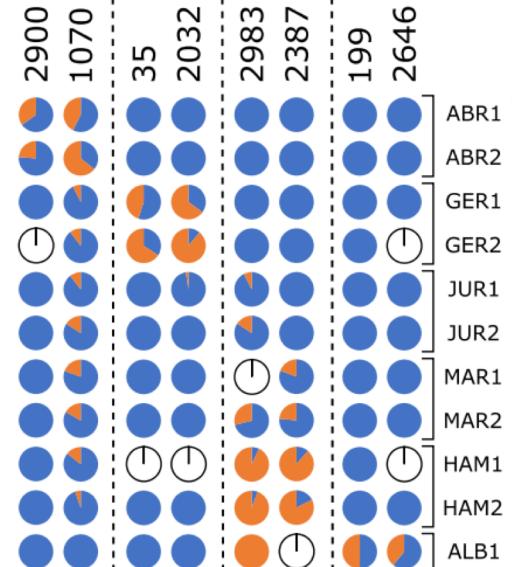
Sofie Vranken^{1,2} | Thomas Wernberg^{1,2,3} | Armin Scheben^{2,4} |
Anita Alice Severn-Ellis² | Jacqueline Batley² | Philipp Emanuel Bayer² |
David Edwards² | David Wheeler⁵ | Melinda Ann Coleman^{2,6,7}

3734 | WILEY MOLECULAR ECOLOGY

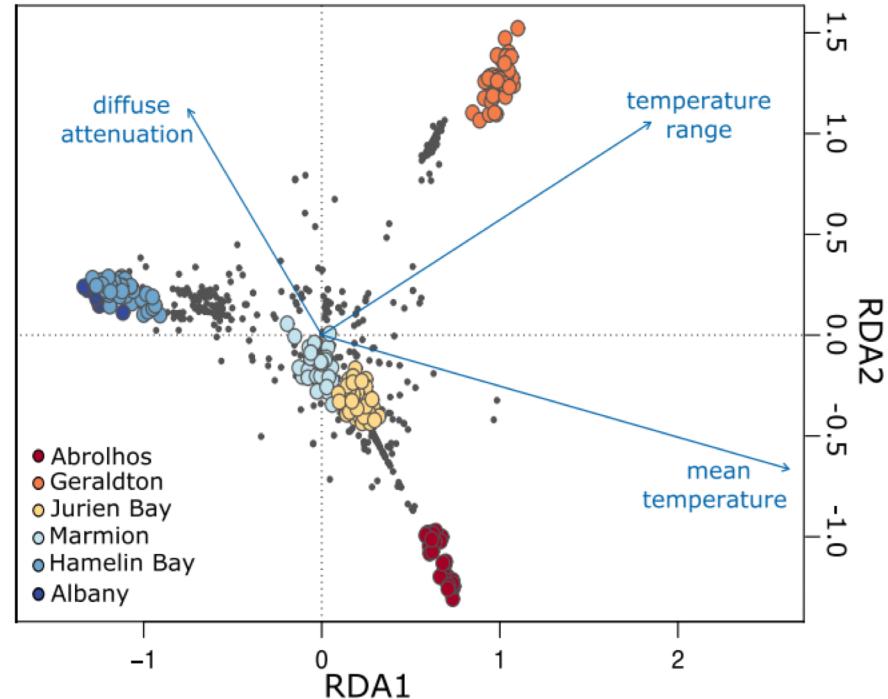
(a)



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}

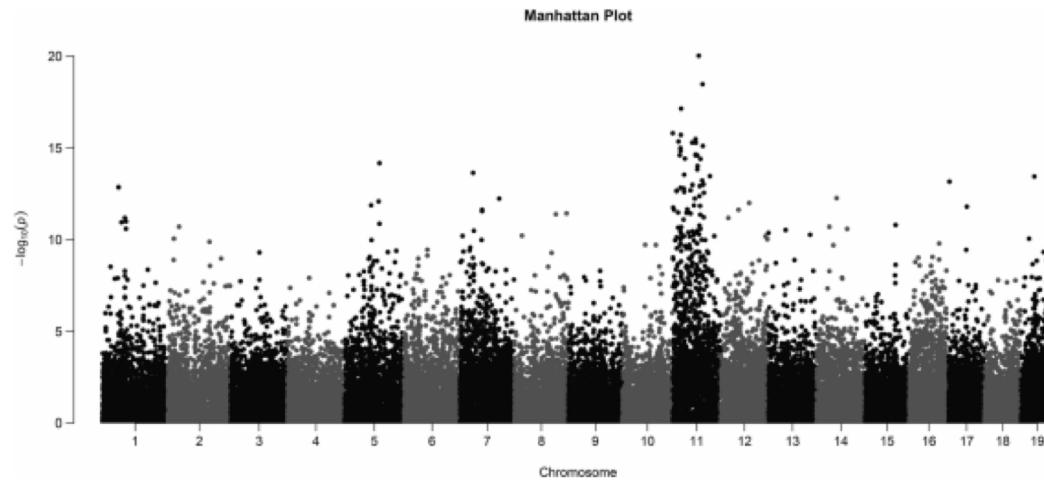


Fig. 2 Manhattan plot of $-\log_{10}(P)$ value for genome-wide association study

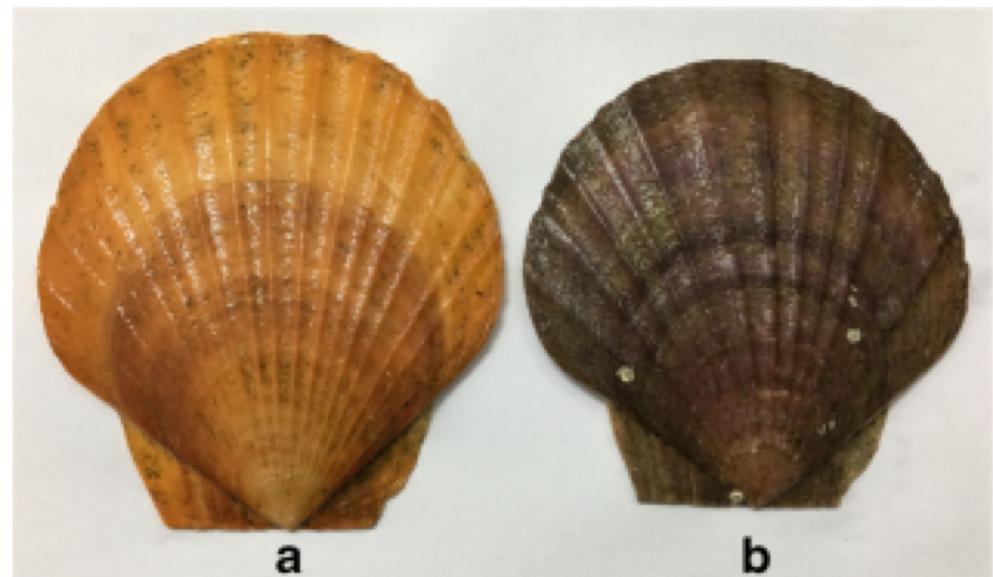


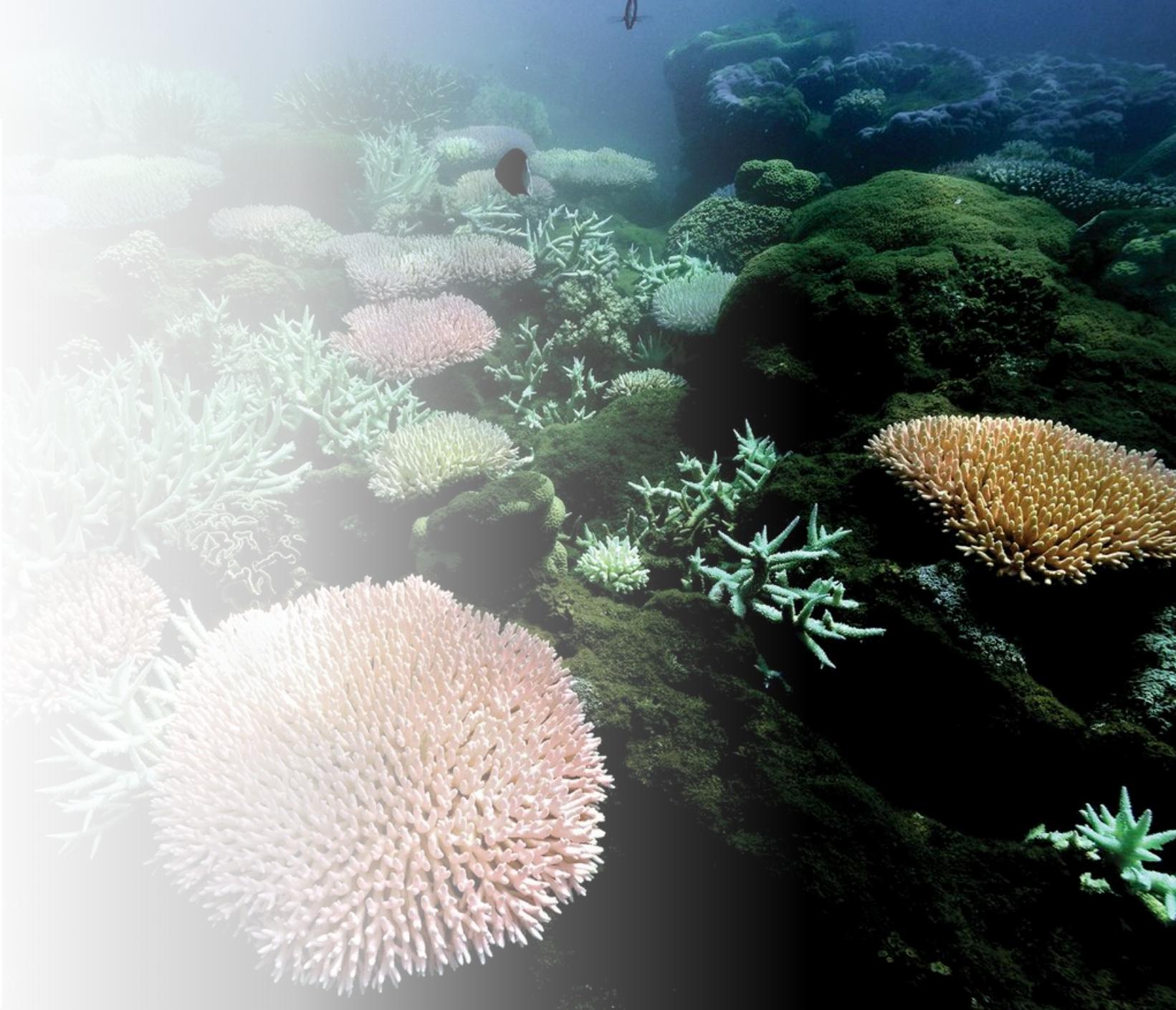
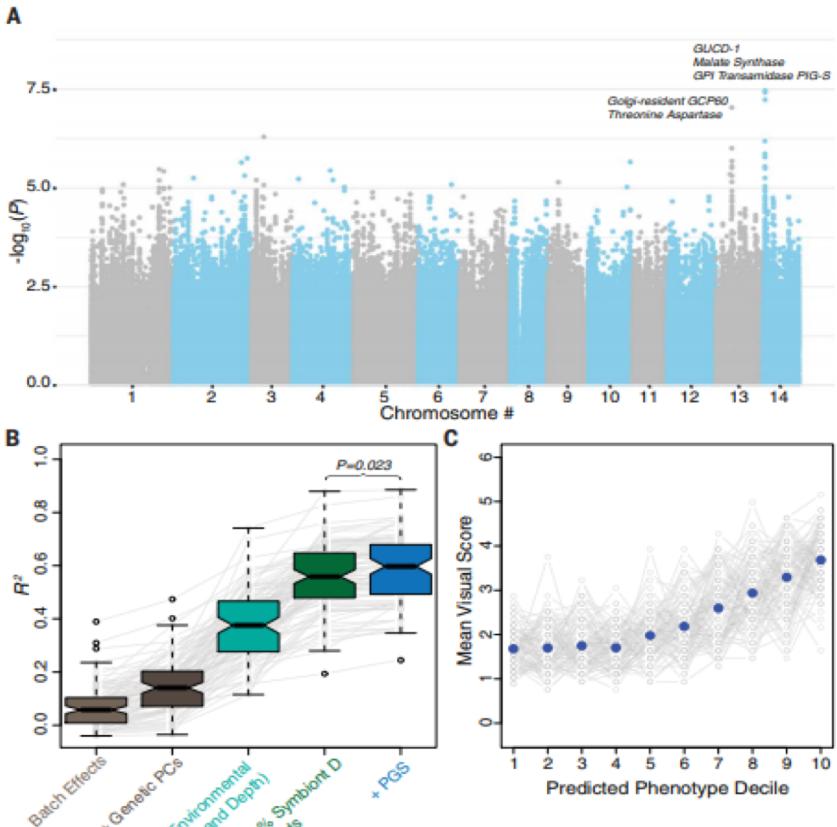
Fig. 1 Reddish-orange shell variant (a) and brown shell variant (b) of Yesso scallop, *Patinopecten yessoensis*

RESEARCH ARTICLE SUMMARY

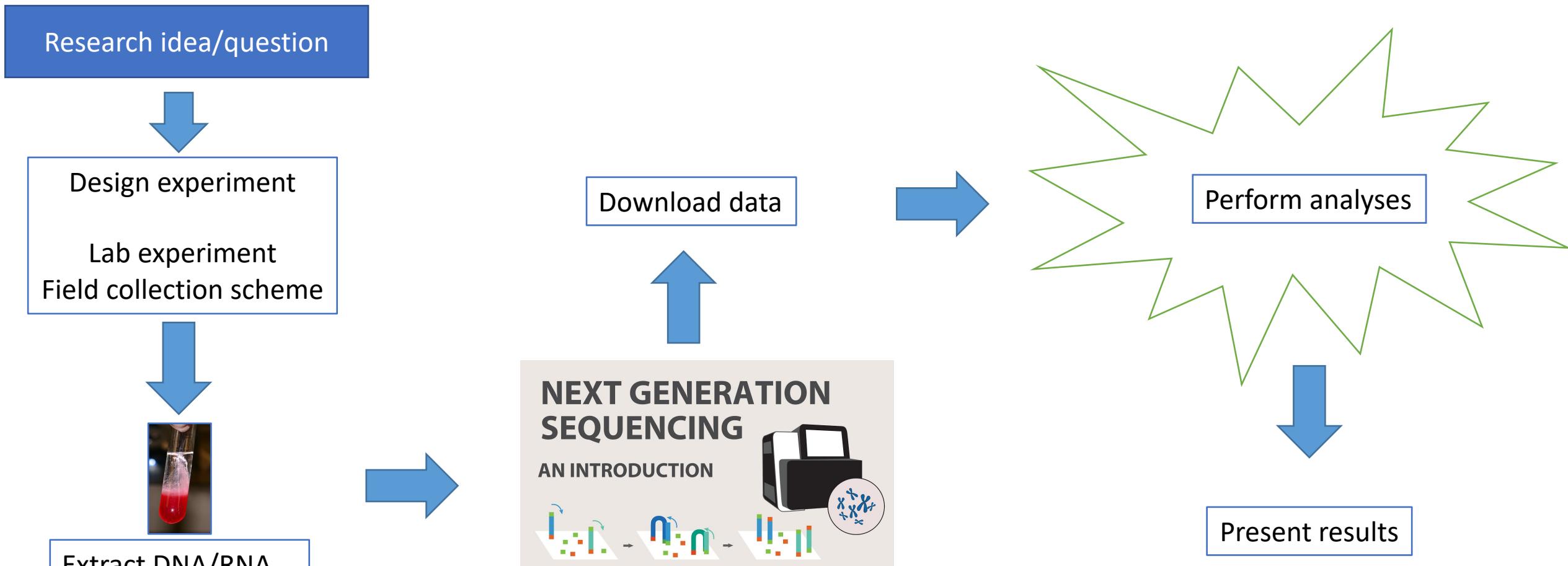
CORAL GENOMICS

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*†



How do we do marine genomics?



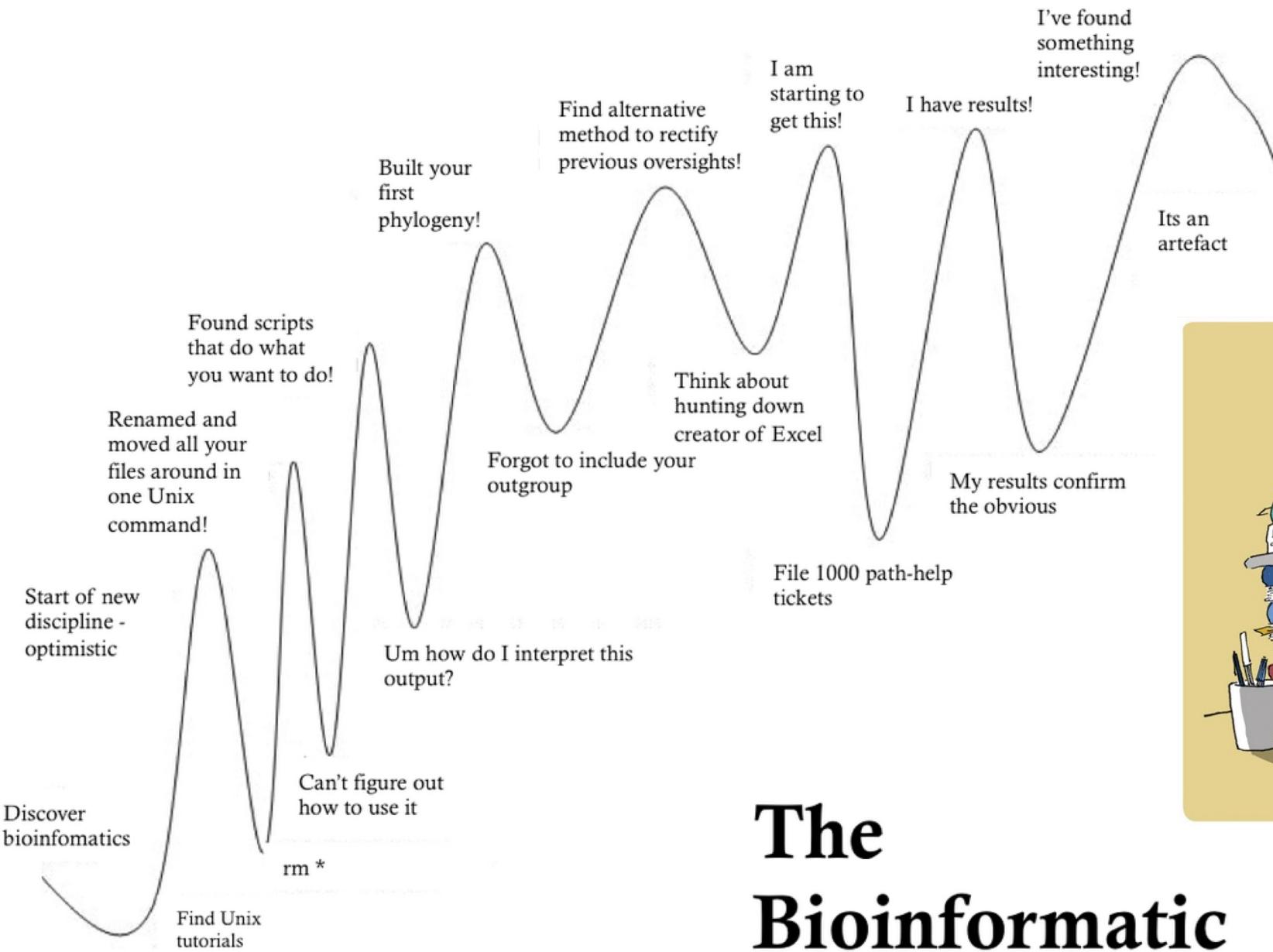
We use bioinformatics to answer these questions

We'll cover two main areas:

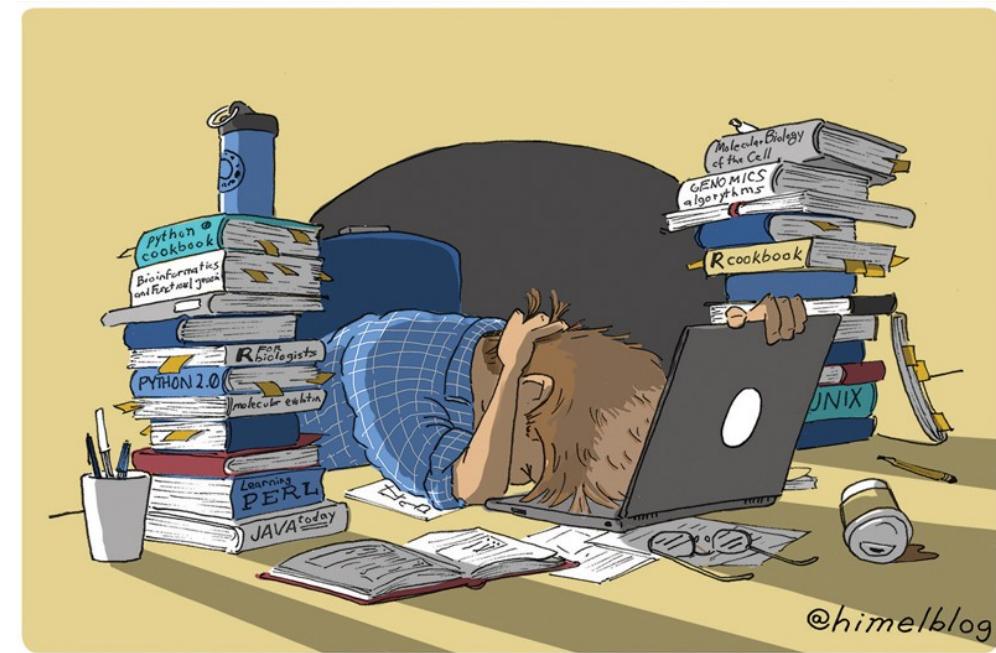
- The shell or Bash/UNIX
- R

Many of these analyses are very computationally intensive

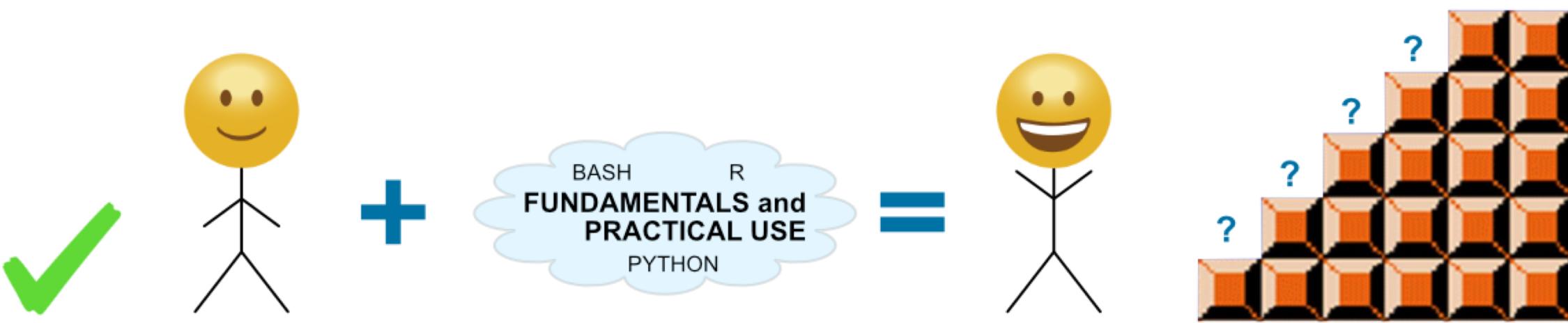
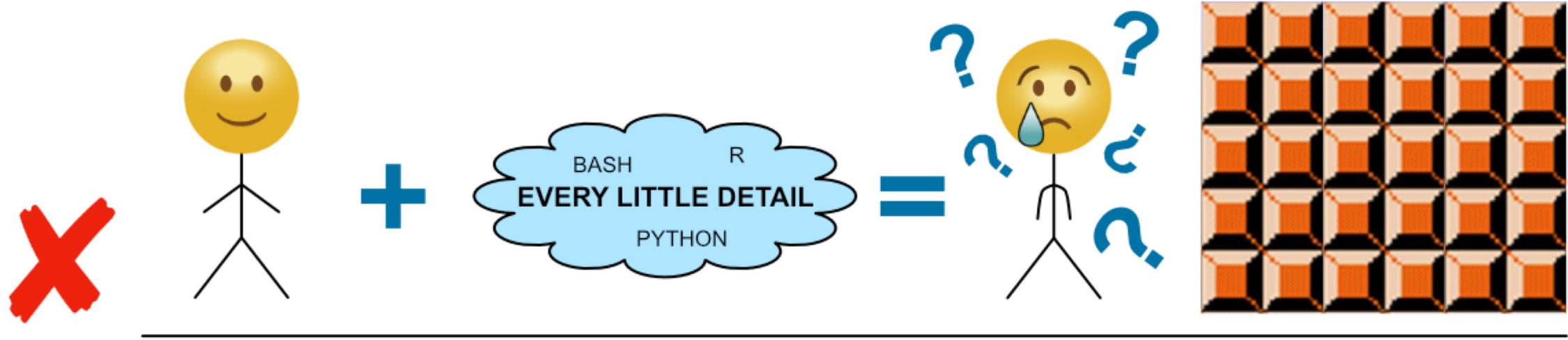




Source: <https://www.nature.com/articles/d41586-021-01485-y>



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

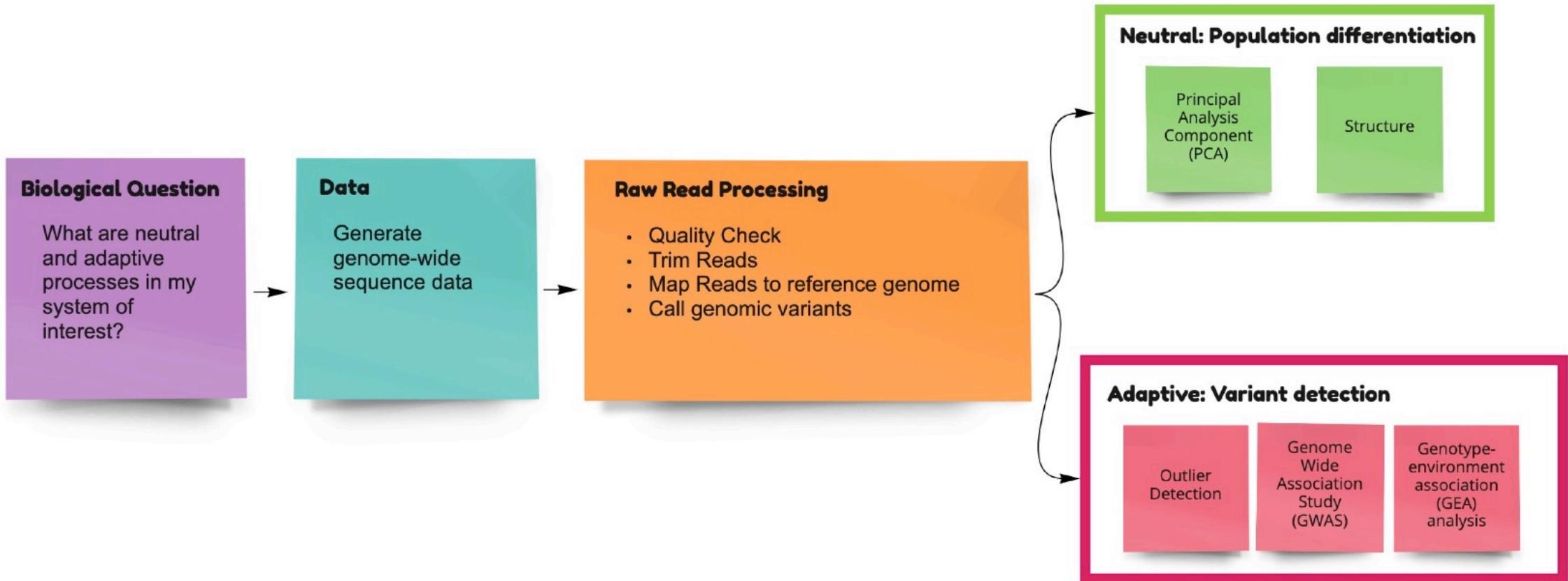


You're **scientific advisor** to aquaculture company interested in farming sea cucumbers

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



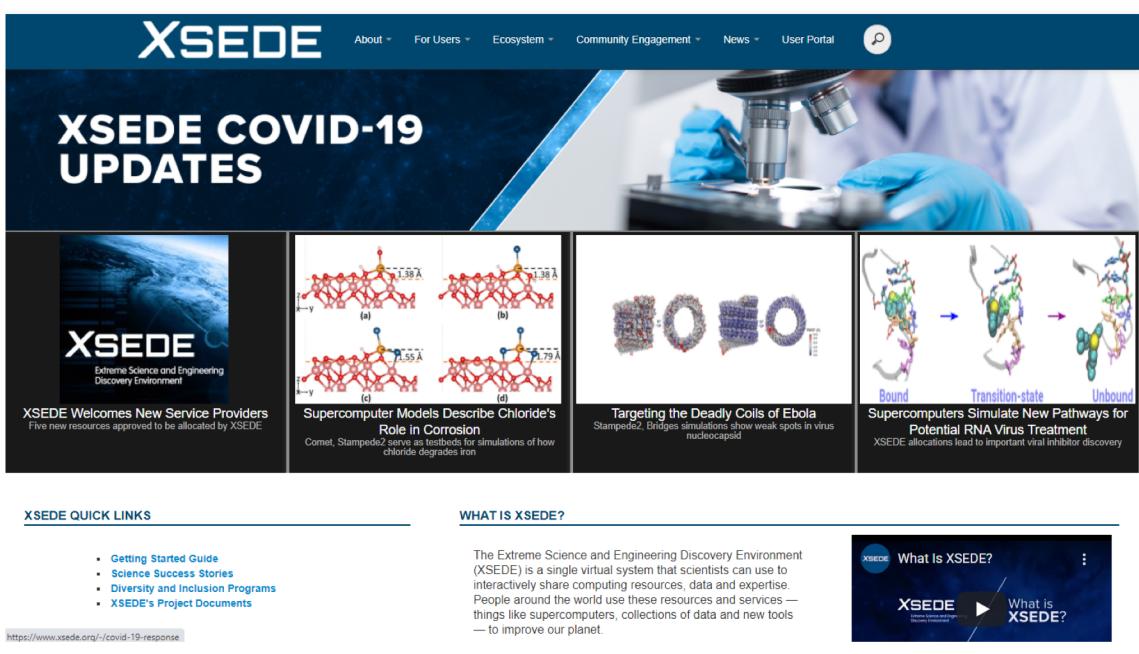
We do this via shell computing

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

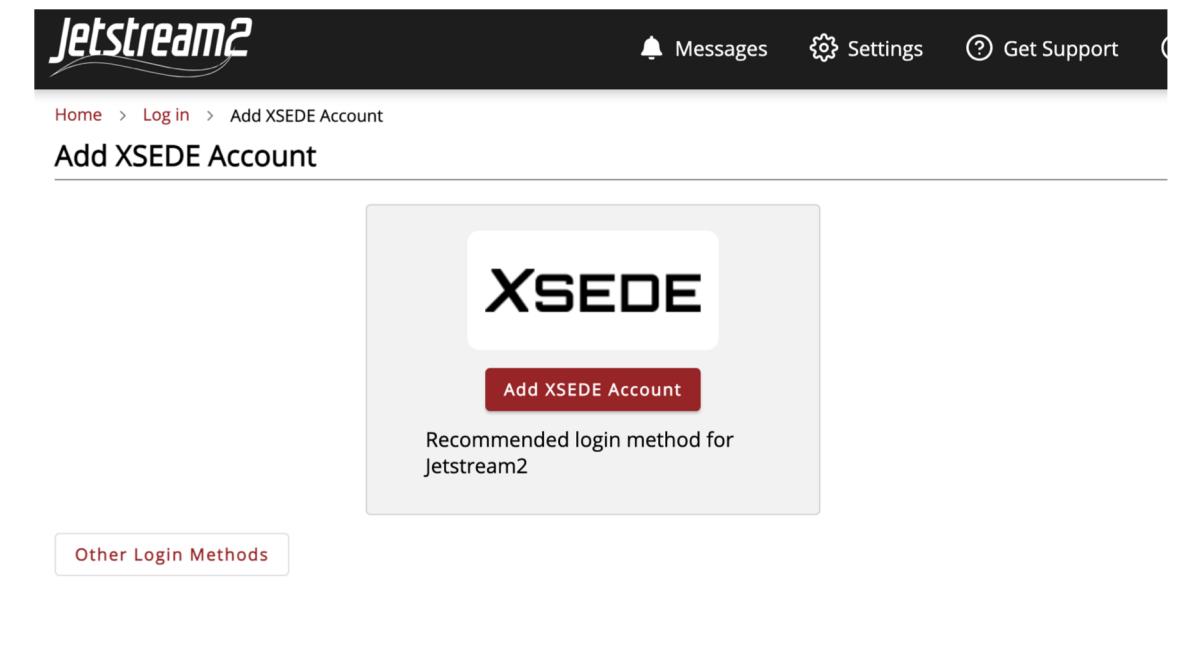
- Getting Started Guide
- Science Success Stories
- Diversity and Inclusion Programs
- XSEDE's Project Documents

<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.

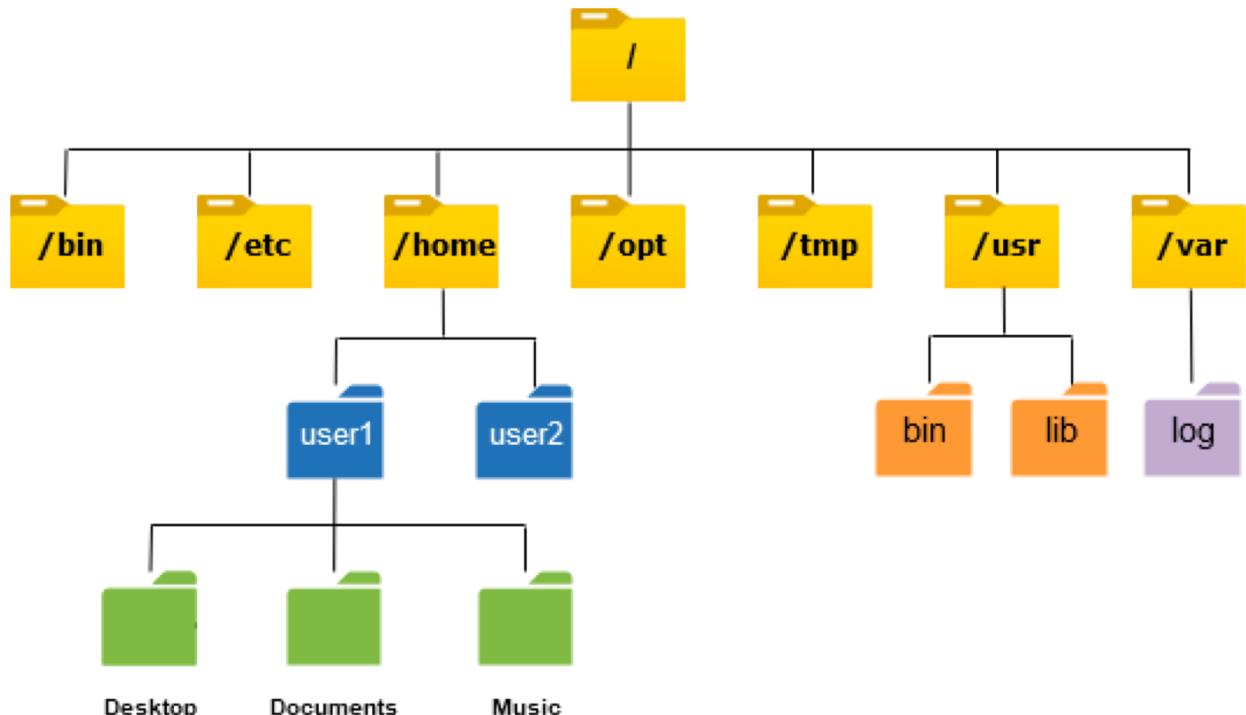
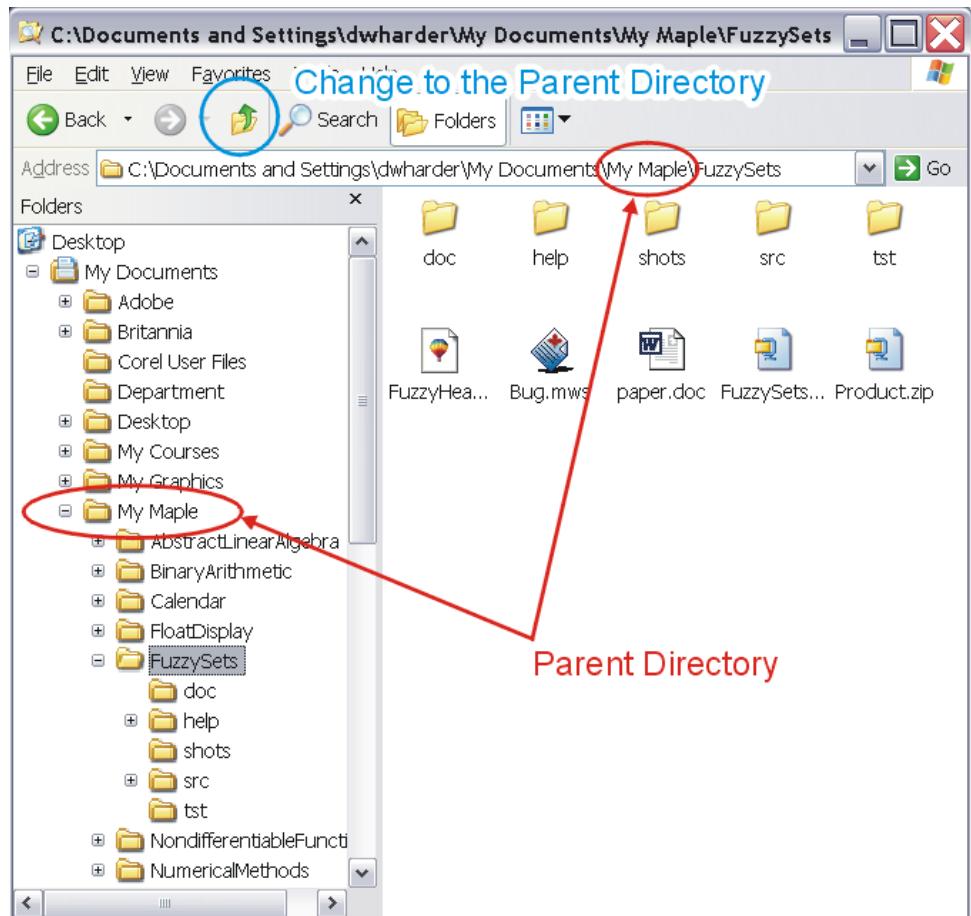
What Is XSEDE?



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.