

Introduction to Genomics in Natural Populations

Eve198

Week 1: January 7, 2025



Introductions

- Name
- Pronouns
- Year
- Major
- What drew you to this class?

Class outline

Week	Date	Topic
1	January 7th	Introduction to genomics, learning how to navigate FARM & introduction to coding
2	January 14th	Bash/UNIX coding: working with files
3	January 21st	Bash/UNIX coding: working with files continued
4	January 28th	Mapping to a Genome, Calling Variants and Calculating Allele Frequencies
5	February 4th	Intro to R: Introduction and Data Manipulation
6	February 11th	Intro to R: Plotting and Making Figures
7	February 18th	Population Structure
8	February 25th	Allele Frequencies and PCAs
9	March 4th	Fst outliers
10	March 11th	Taking Bioinformatics beyond the class

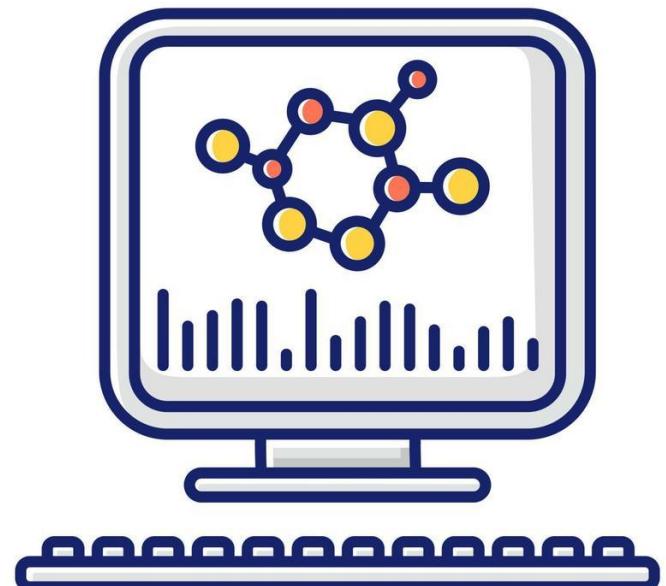
Grading:

- Attend class
- Participate in group coding activity
- Submit individual canvas assignment before the next class



Learning Objectives

- Use computing resources at UC Davis
- Write basic scripts in bash
- Perform genomic analyses modifying template scripts in R
- Describe the general bioinformatics pipeline
- Evaluate figures from published literature.

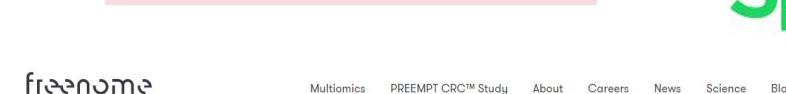


Why learn bioinformatics?

Data in Ecology and Genomics are getting bigger and bigger!

Students gain many transferable skills!

- Data science
- Personalized medicine
- NGO agency scientist
- Research scientist

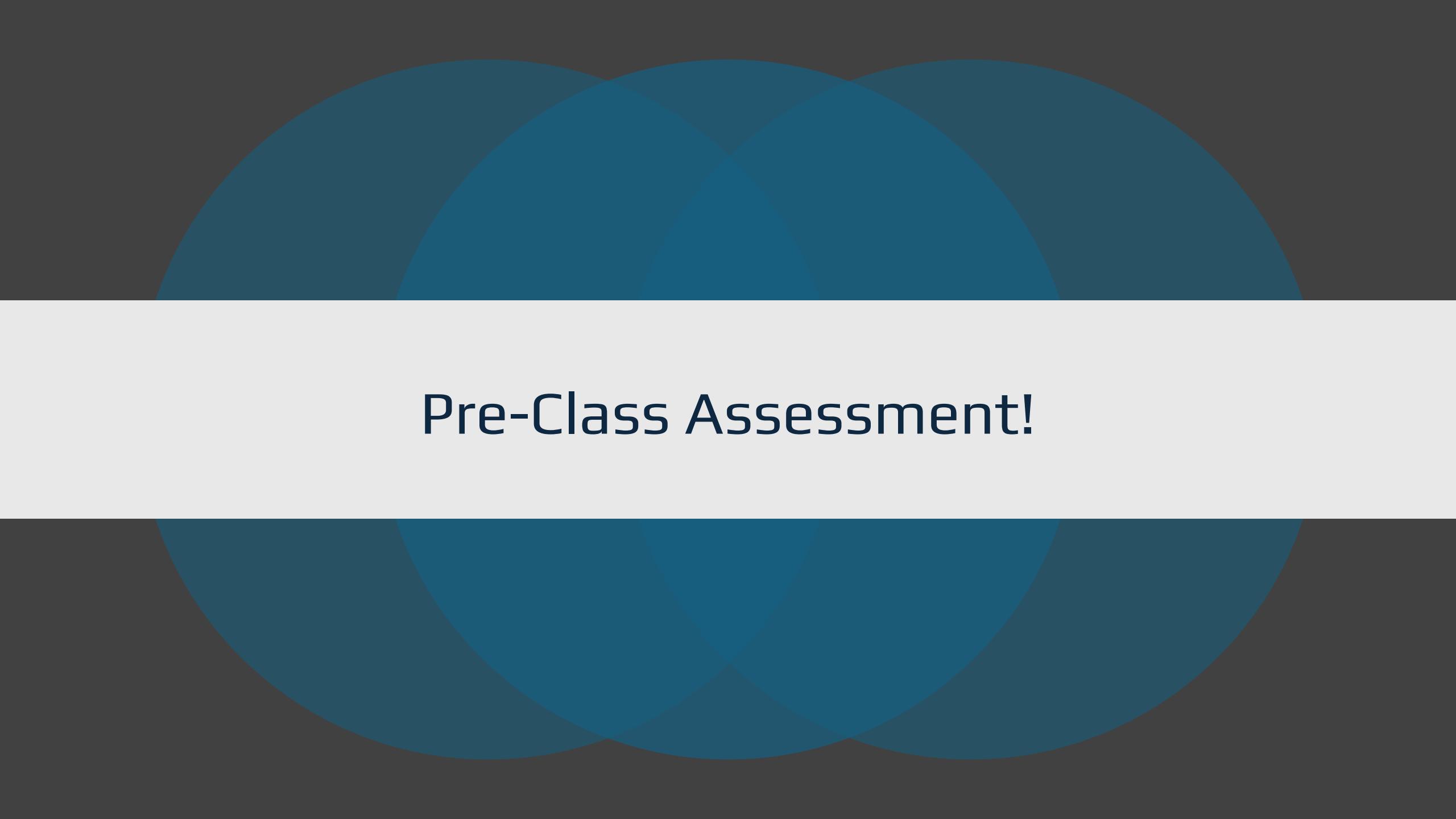


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Week 1 Objectives:

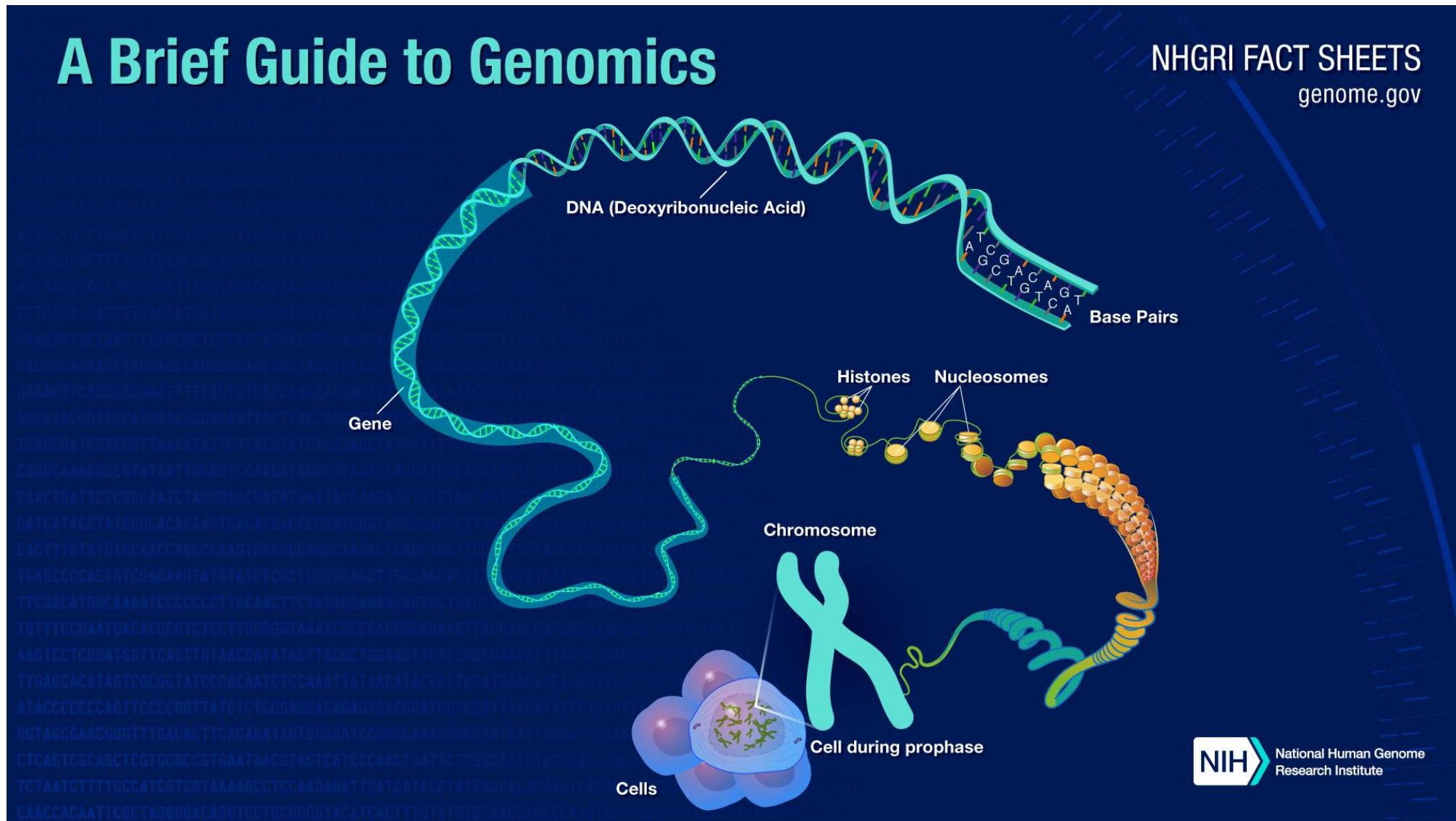
- Take Pre-class assessment
- Introduction to genomics & shell computing
- Accessing terminal via Farm OnDemand
- Learn how to use the command line interface to move around in your file system



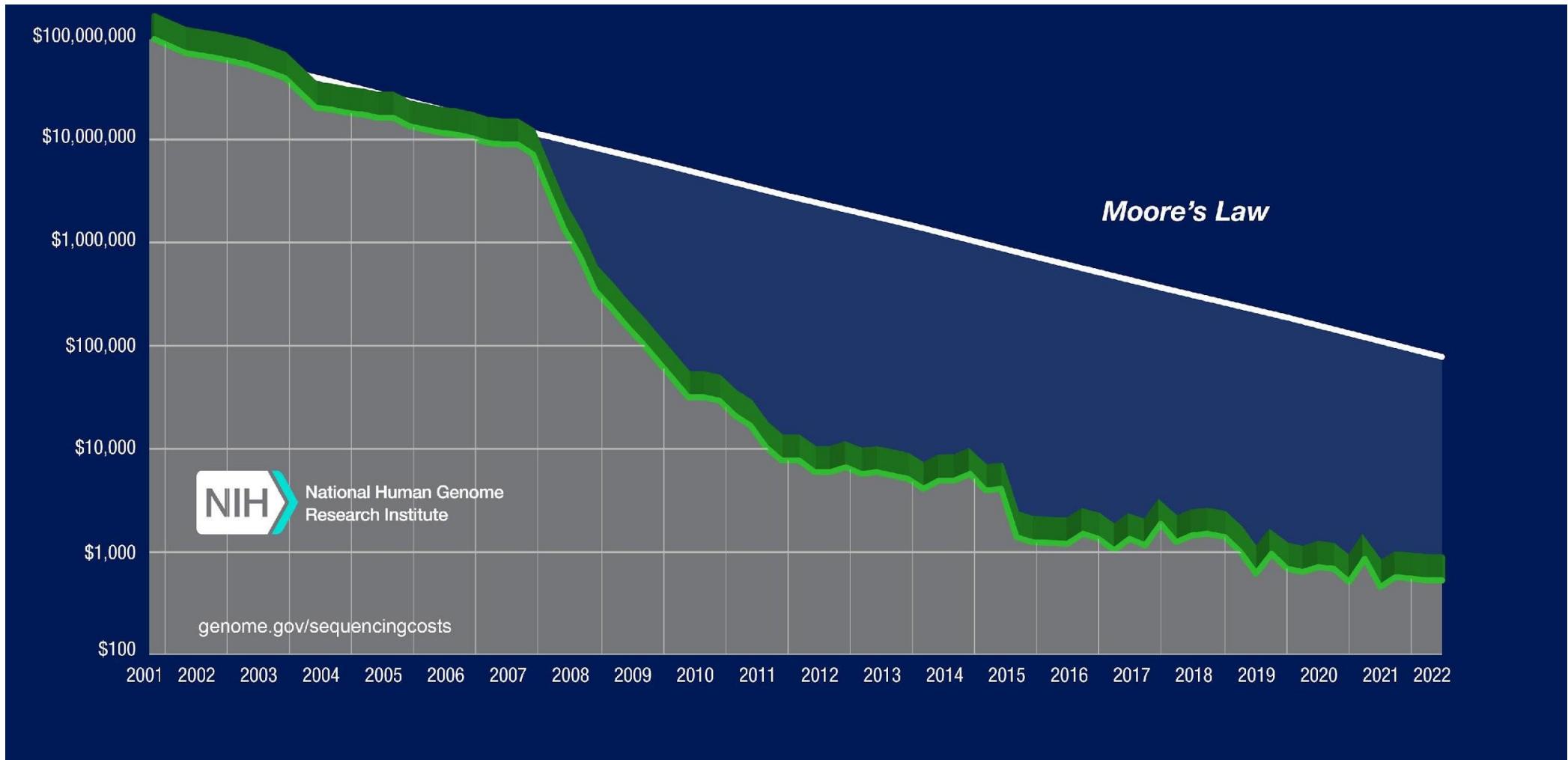
The background of the slide features a decorative pattern of overlapping blue circles. There are four large, semi-transparent circles in a medium shade of blue, arranged in a staggered pattern across the center. A smaller, darker teal circle is positioned at the top center. The overall effect is a clean, modern, and professional look.

Pre-Class Assessment!

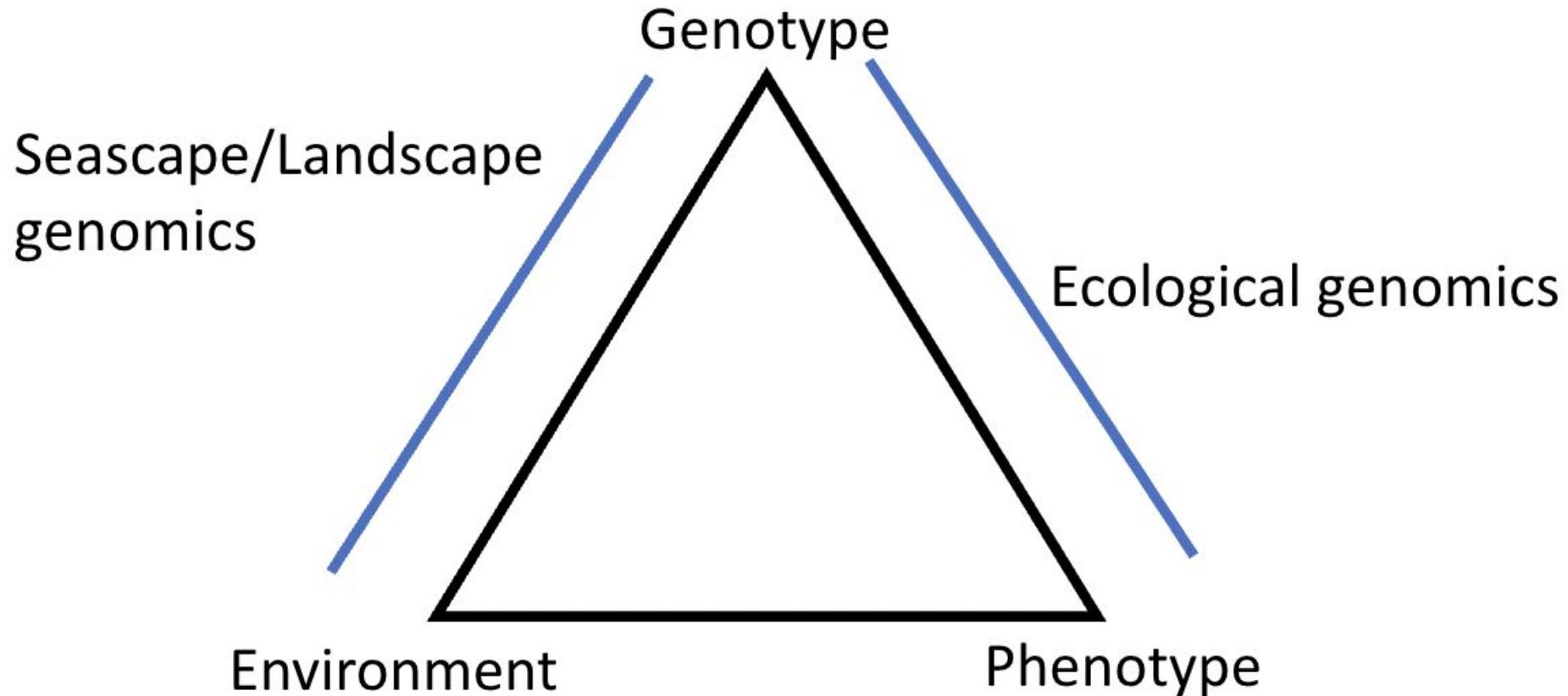
What is Genomics?



Genomics data is becoming more accessible & cheaper!



Pairing genetic data with environmental/phenotypic data



The tuatara genome reveals ancient features of amniote evolution

<https://doi.org/10.1038/s41586-020-2561-9>

Received: 5 December 2019

Accepted: 26 June 2020

Published online: 5 August 2020

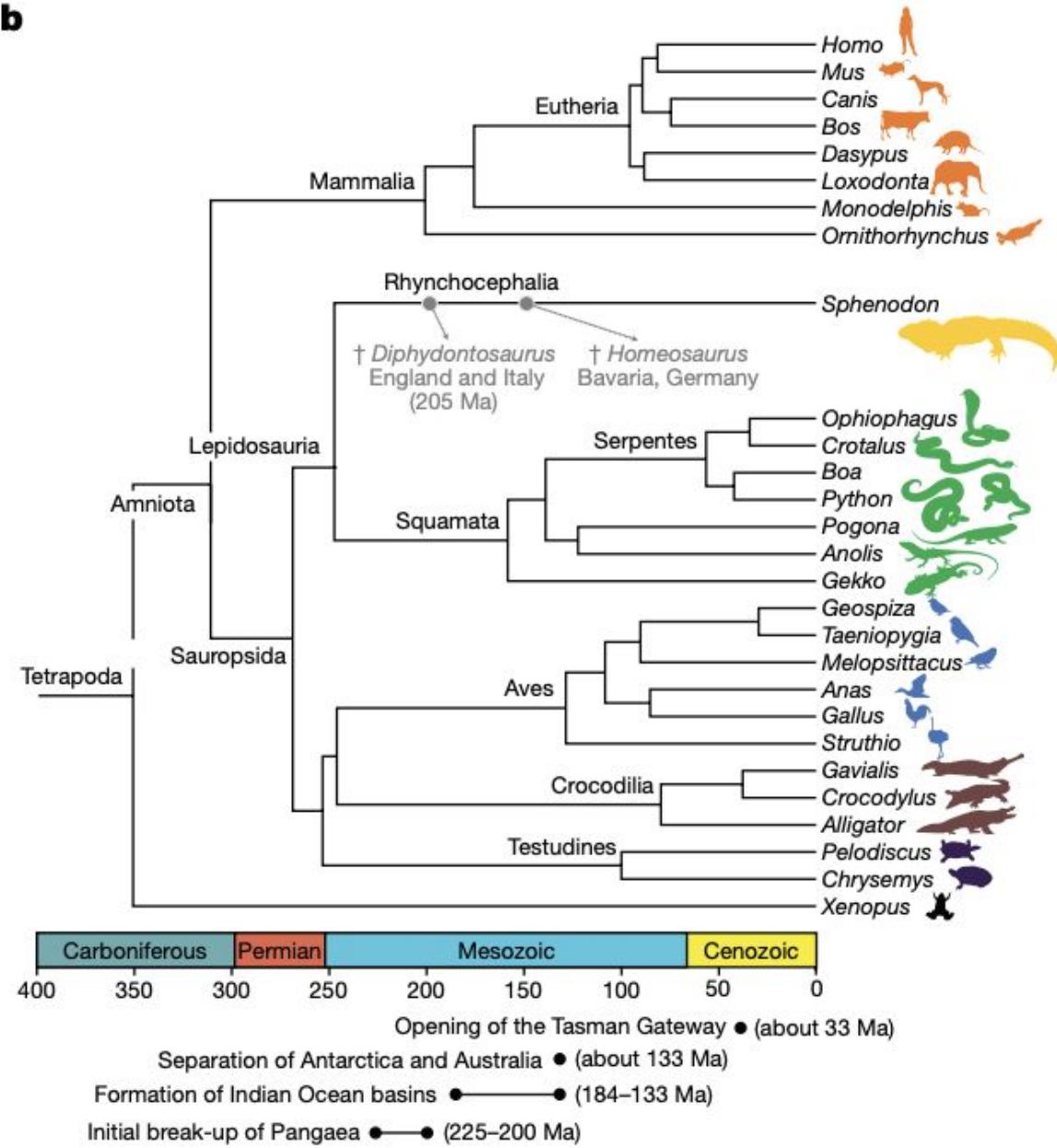
Open access

Check for updates

a



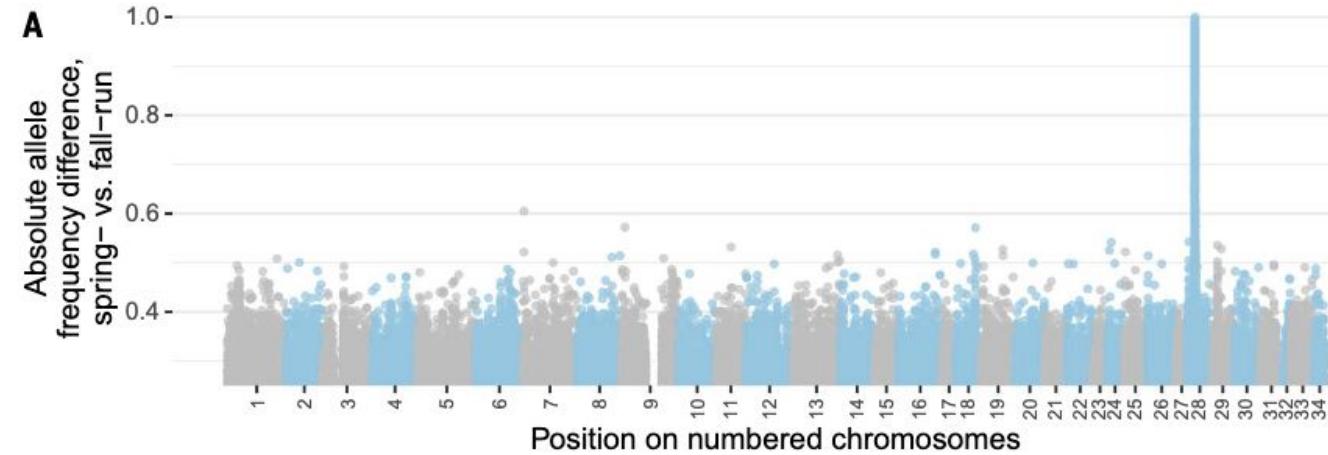
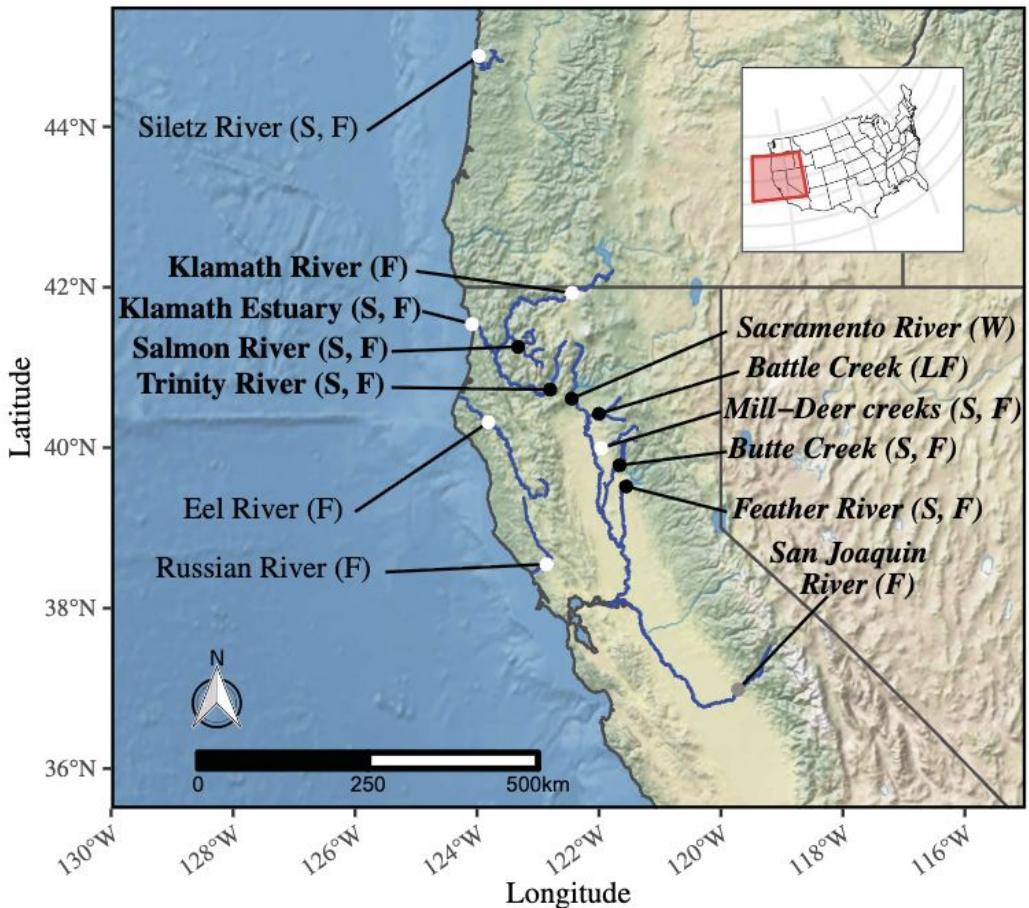
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MIGRATION

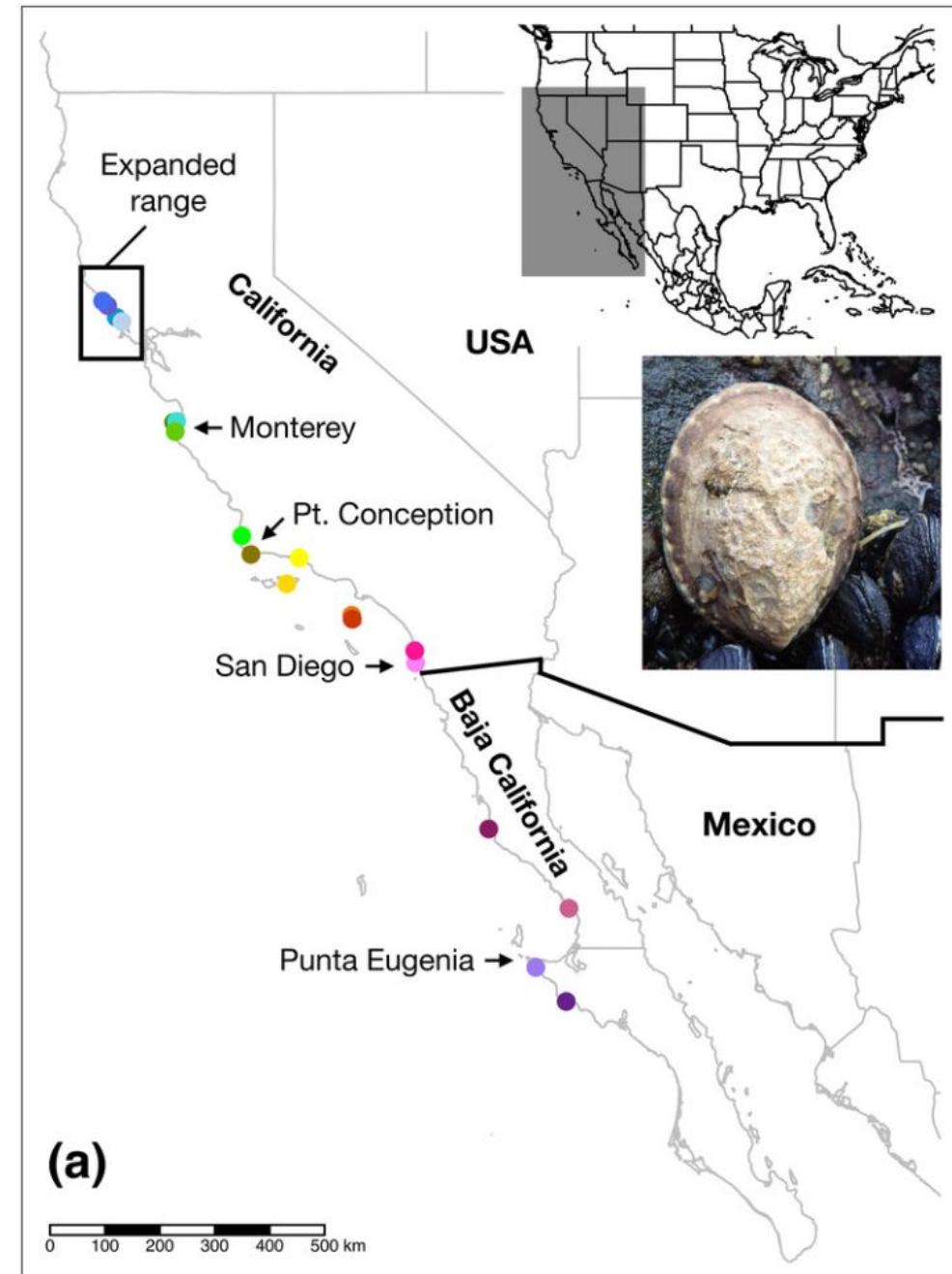
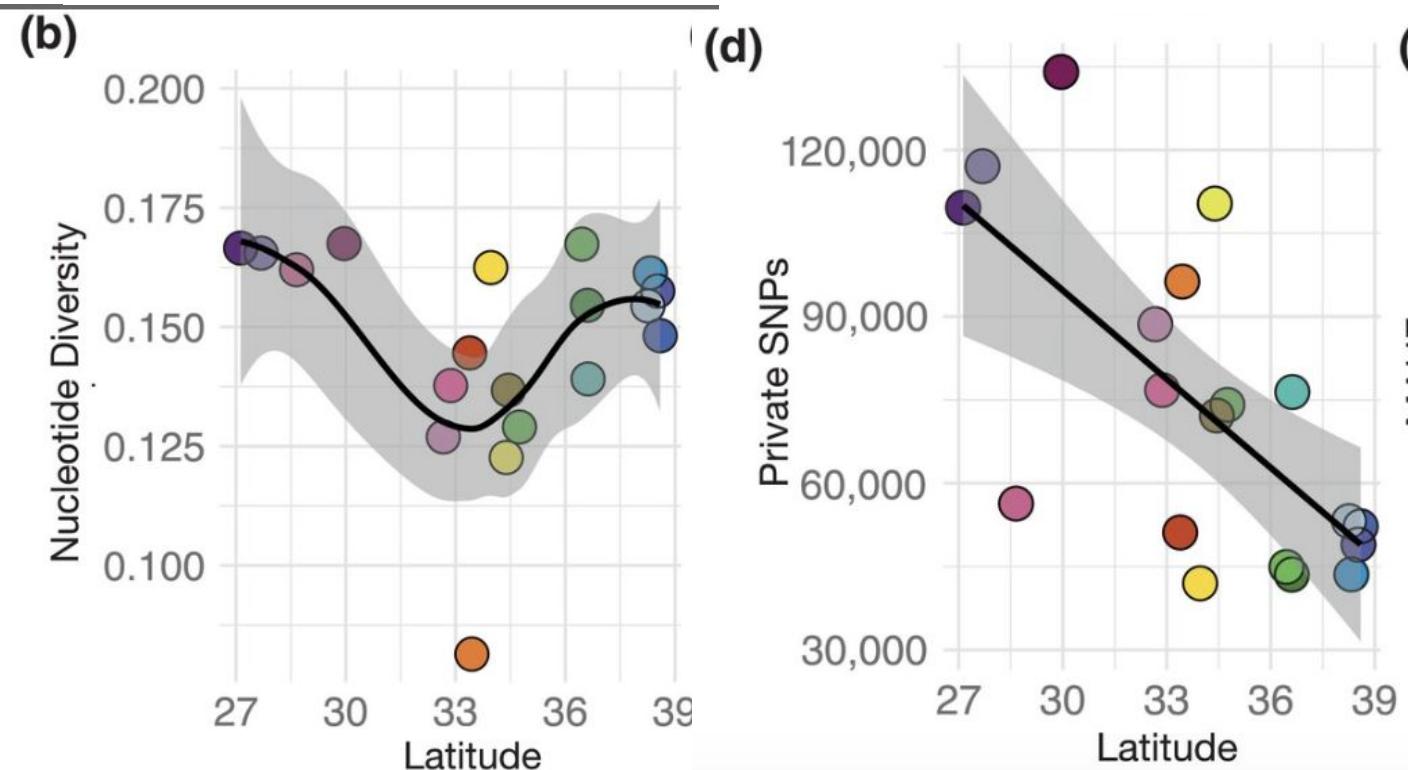
A complex phenotype in salmon controlled by a simple change in migratory timing

Neil F. Thompson^{1,2,3*}, Eric C. Anderson^{2,3,4*}†, Anthony J. Clemento^{2,3}, Matthew A. Campbell^{2,3,5}, Devon E. Pearse^{3,5}, James W. Hearsey⁶, Andrew P. Kinziger⁶, John Carlos Garza^{1,2,3*}†



Pushed waves, trailing edges, and extreme events: Eco-evolutionary dynamics of a geographic range shift in the owl limpet, *Lottia gigantea*

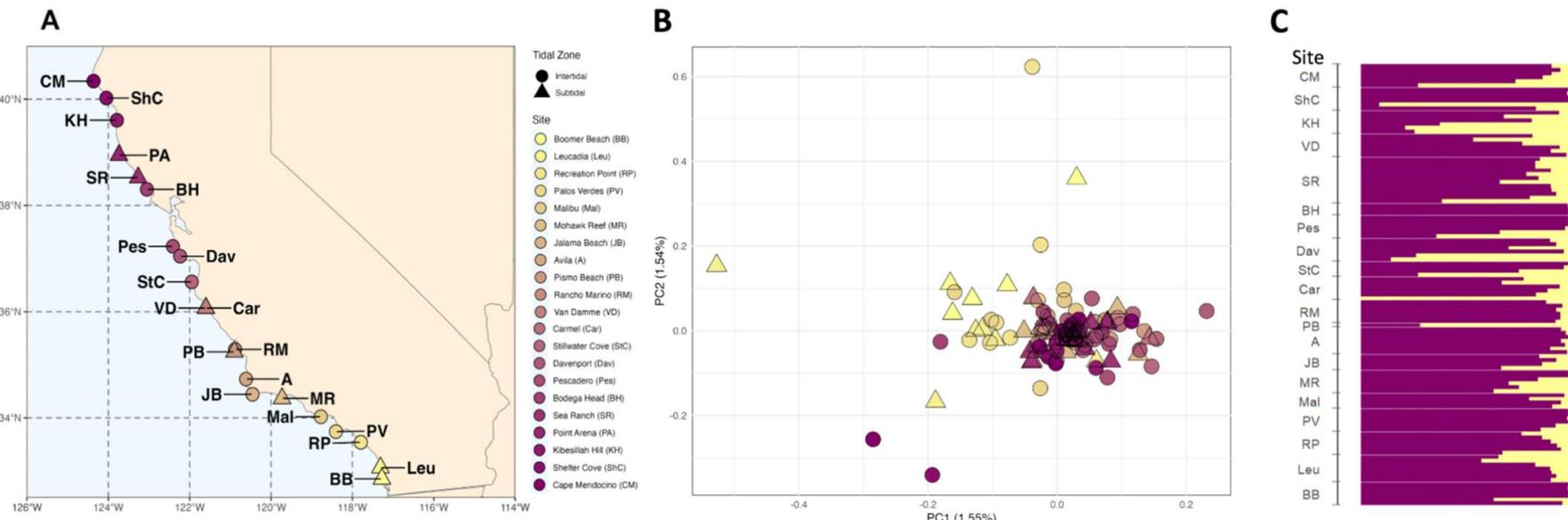
Erica S. Nielsen¹ | Samuel Walkes^{1,2} | Jacqueline L. Sones³ | Phillip B. Fenberg⁴ |
David A. Paz-García⁵ | Brenda B. Cameron¹ | Richard K. Grosberg¹ |
Eric Sanford^{1,2} | Rachael A. Bay¹



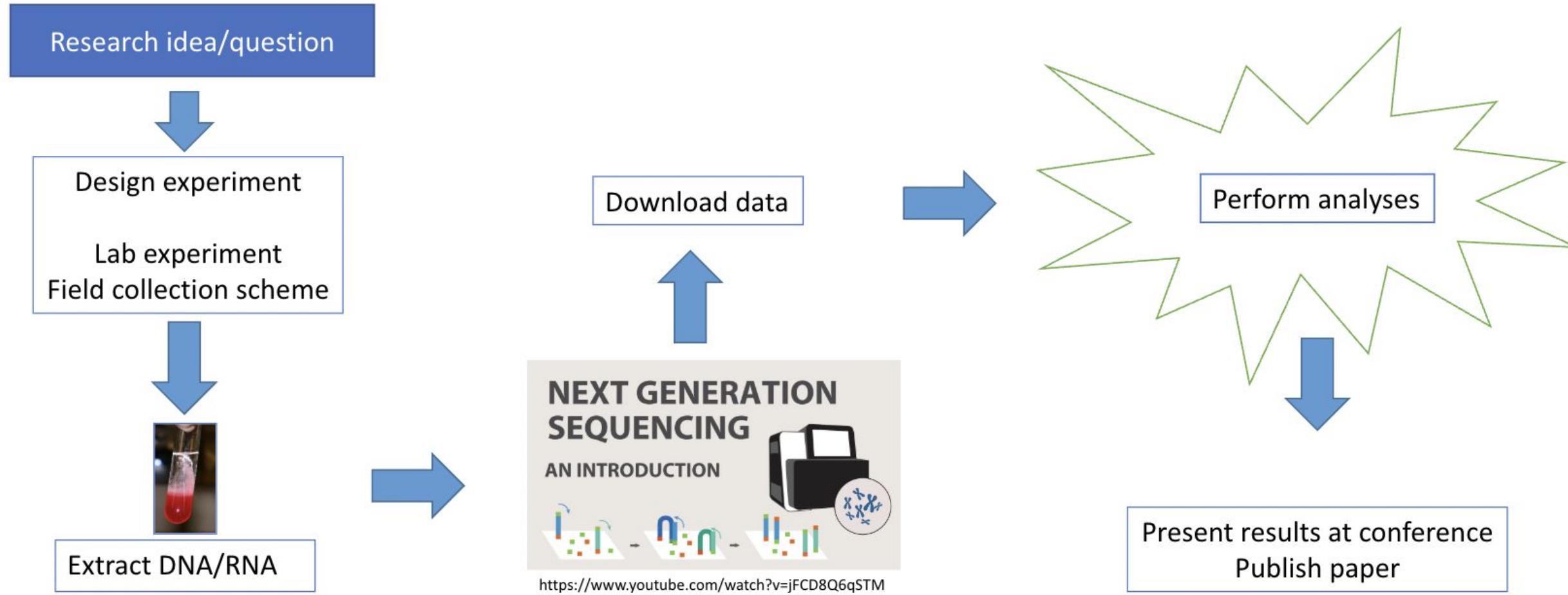
Selection Over Small and Large Spatial Scales in the Face of High Gene Flow

Camille Rumberger, Madison Armstrong, Martin Kim, Raquel Ponce, Josue Melendez, Melissa DeBiasse, Serena Caplins, Rachael Bay

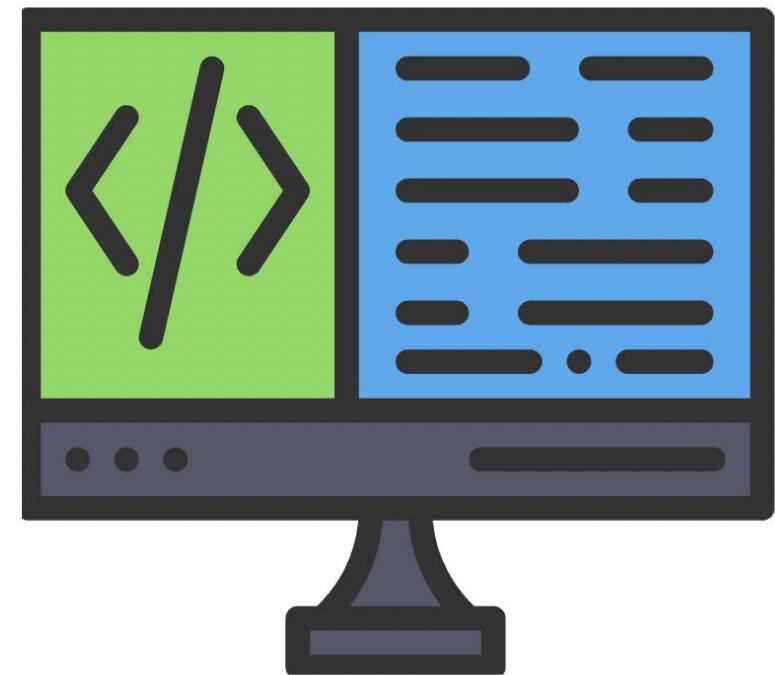
First published: 19 February 2025 | <https://doi.org/10.1111/mec.17700>



How do we do it?

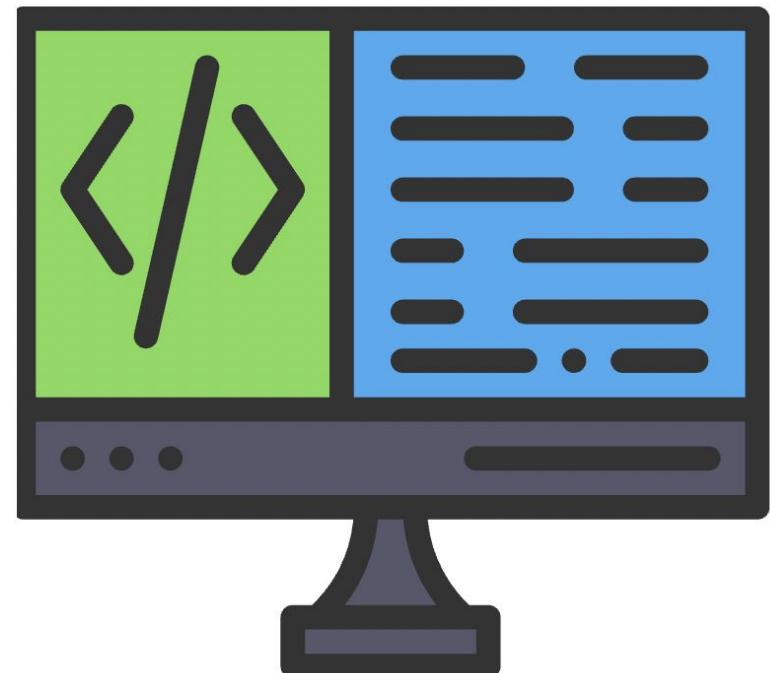


Shell Computing: Why is it useful?



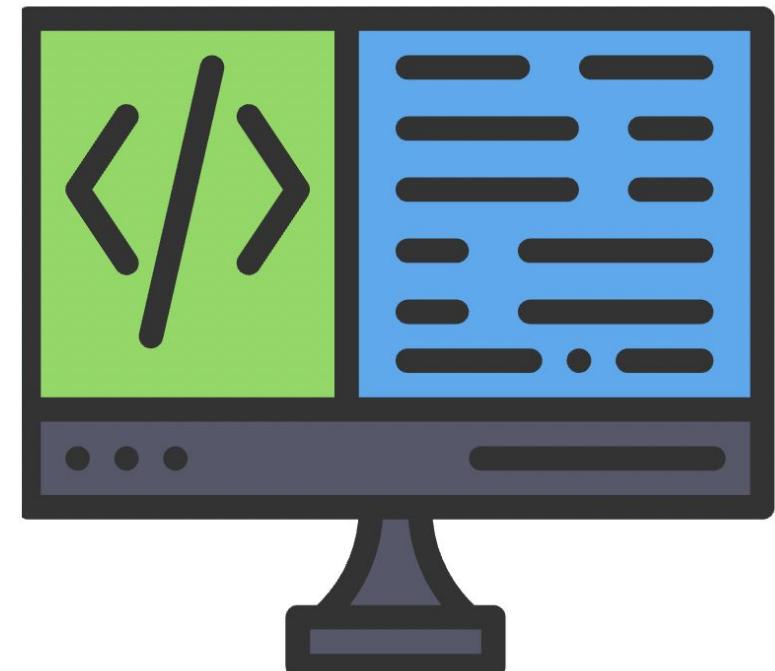
Shell Computing: Why is it useful?

- Accessibility of tools



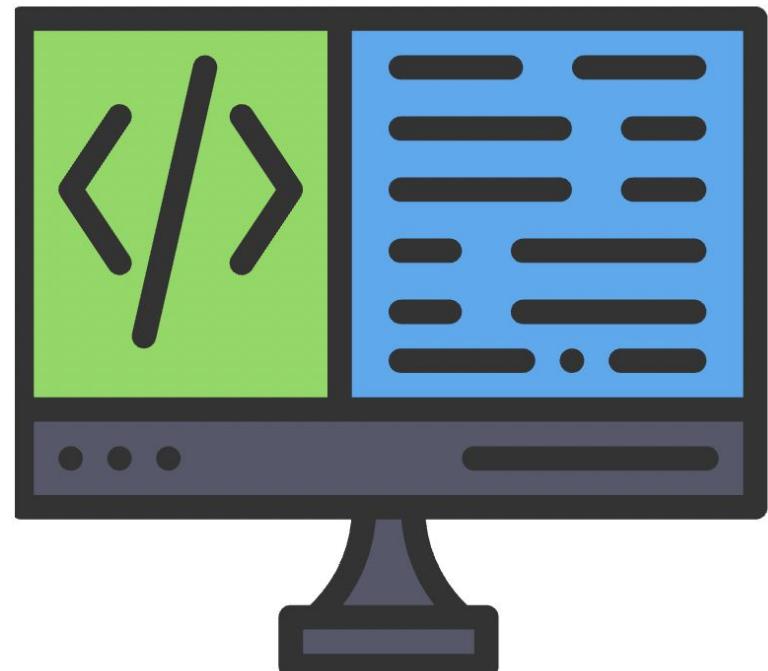
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- Automate repetitive tasks aka less boring!



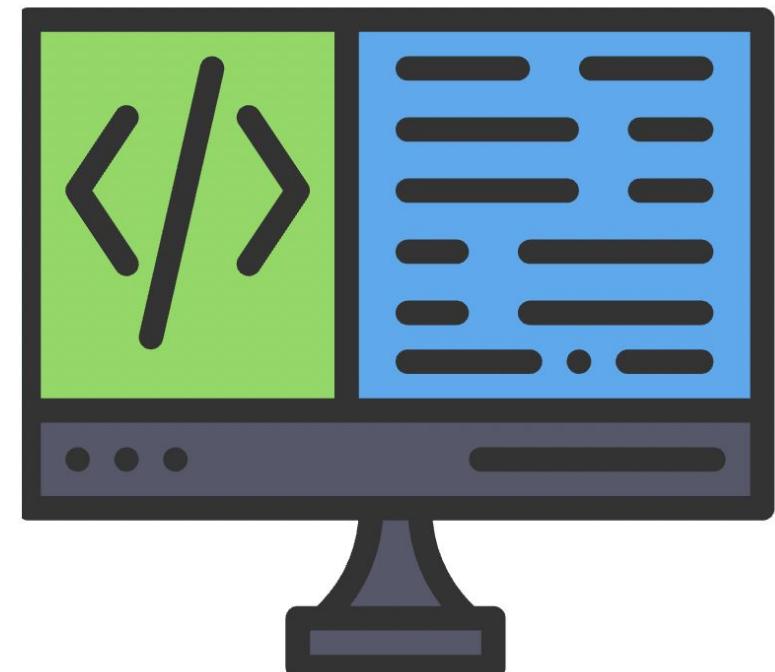
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- Makes your work less error prone

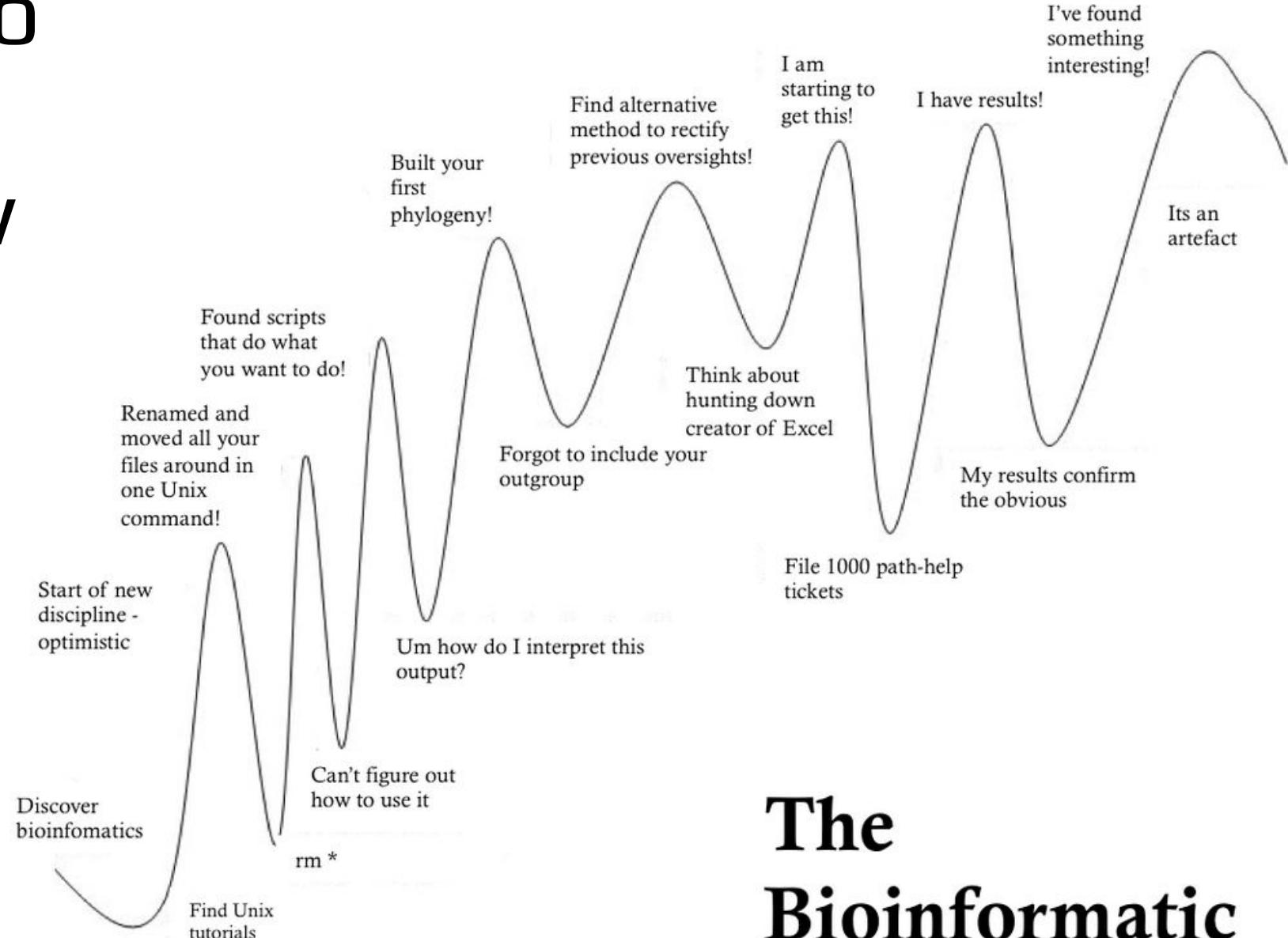


Shell Computing: Why is it useful?

- Accessibility of tools
- Automate repetitive tasks aka less boring!
- Makes your work less error prone
- Makes your work more reproducible



Let's navigate to Farm OnDemand now and our course website for the rest of class!



The Bioinformatic learning curve