

Geog 4/563

Analytical Workflows in Earth Sciences
Oregon State University

James R. Watson, Spring 2025

Week 2

During week 2 we will start a discussion about doing scientific research in teams, and go over the “digital infrastructure” often used to perform collaborative (code-based) research. We will spend time setting this digital infrastructure up for your term projects.

Lecture 1 - Monday

- Introduce James (15 mins)
- Discuss how to run collaborative coding projects (5 mins)
- Introduce required digital infrastructure (15 mins)
- Class activity 1: setup digital infrastructure (20 mins); have your “first” team meeting

Week 2

Lecture 2 - Wednesday

- Setup your team's digital infrastructure
- Introduce R and Rstudio (15 mins)
- Install R and Rstudio and make sure everyone has it working (15 mins)
- Make a GitHub repository for term project (10 mins)
- Co-write readme with your team. Learn how to push/pull/branches/merge (10 mins)

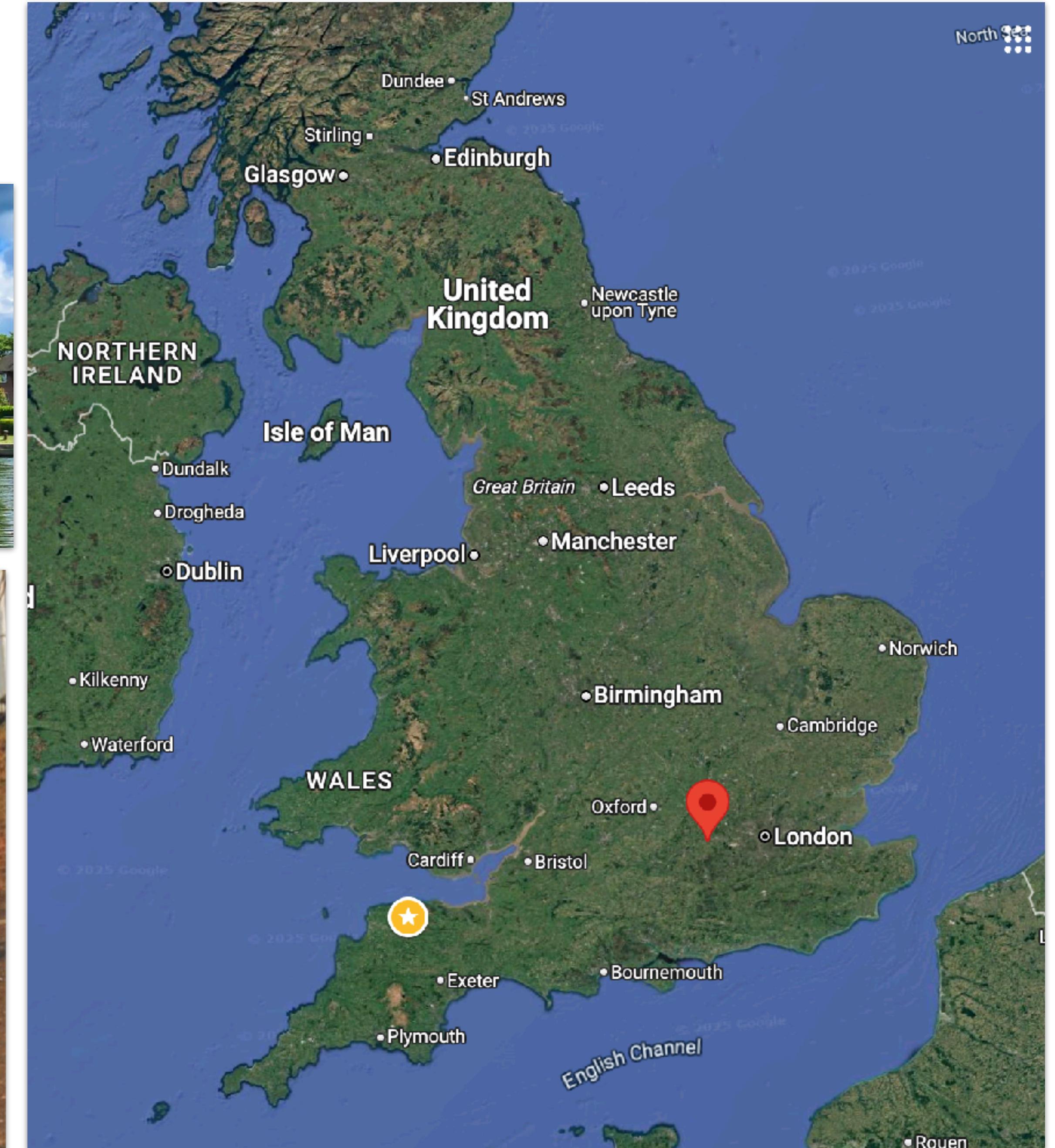
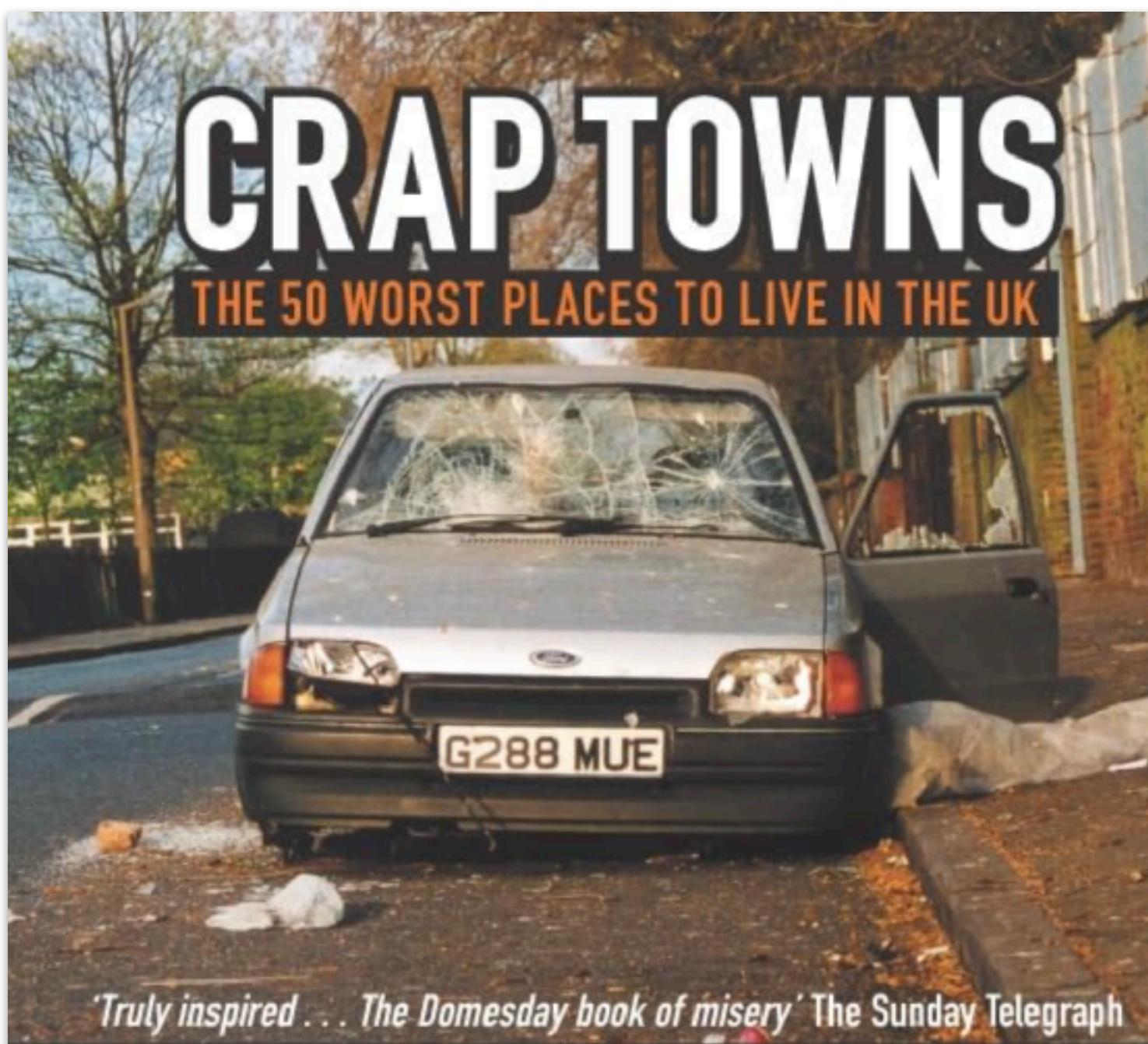
Week 2

Lab - Thursday

- Coding challenge: develop R code to simulate a predator-prey system, involving a for-loop, involving using ChatGPT as a coding co-pilot, involving making time series figures
- practice using collaborative digital infrastructure (drive, core docs, schedule, meeting, roles and responsibilities, collaborative coding).
- co-developing a GitHub repo

Lets talk about me

Maidenhead, UK



Bristol, UK



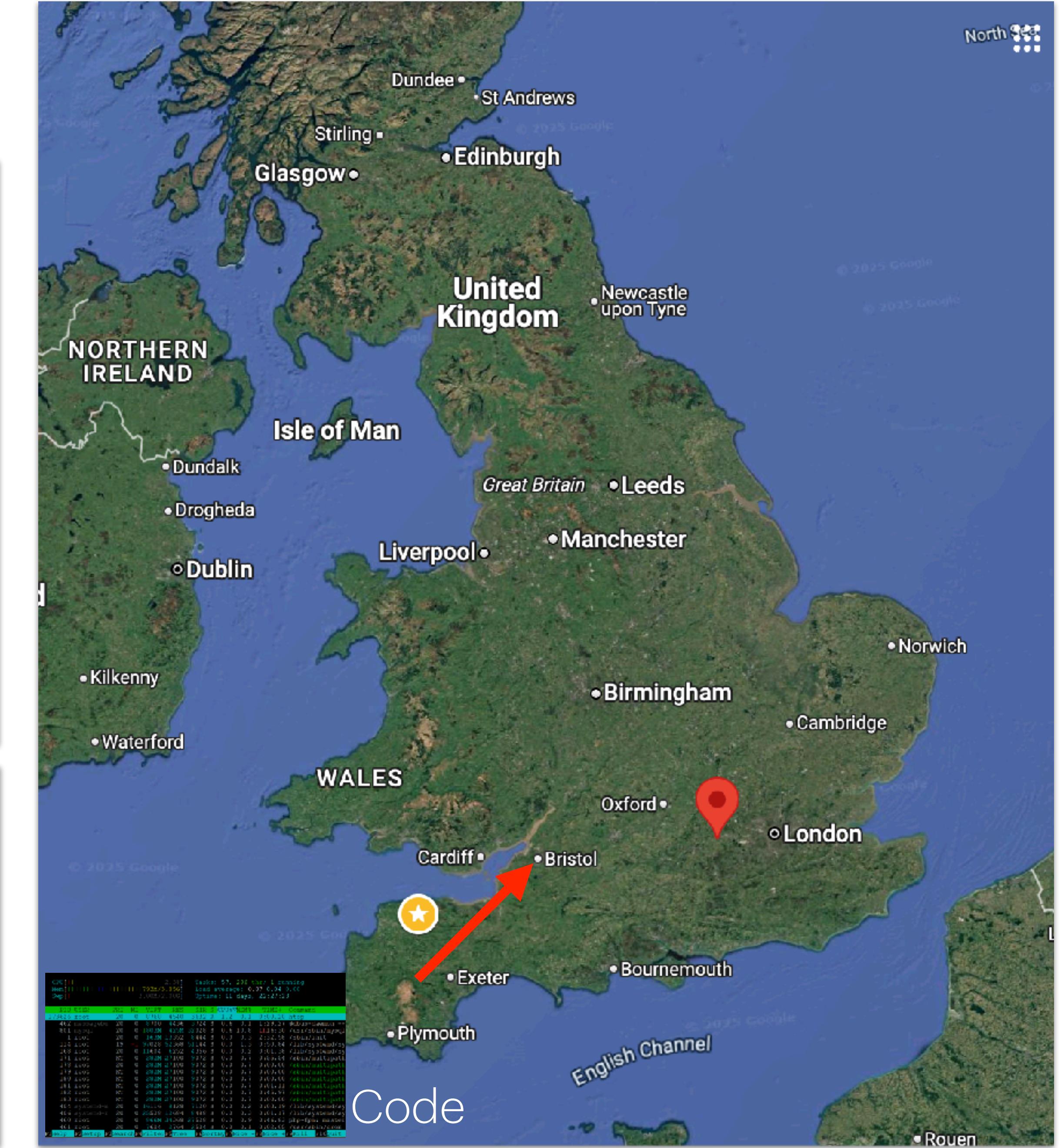
Bristol University: I
studied Biochemistry



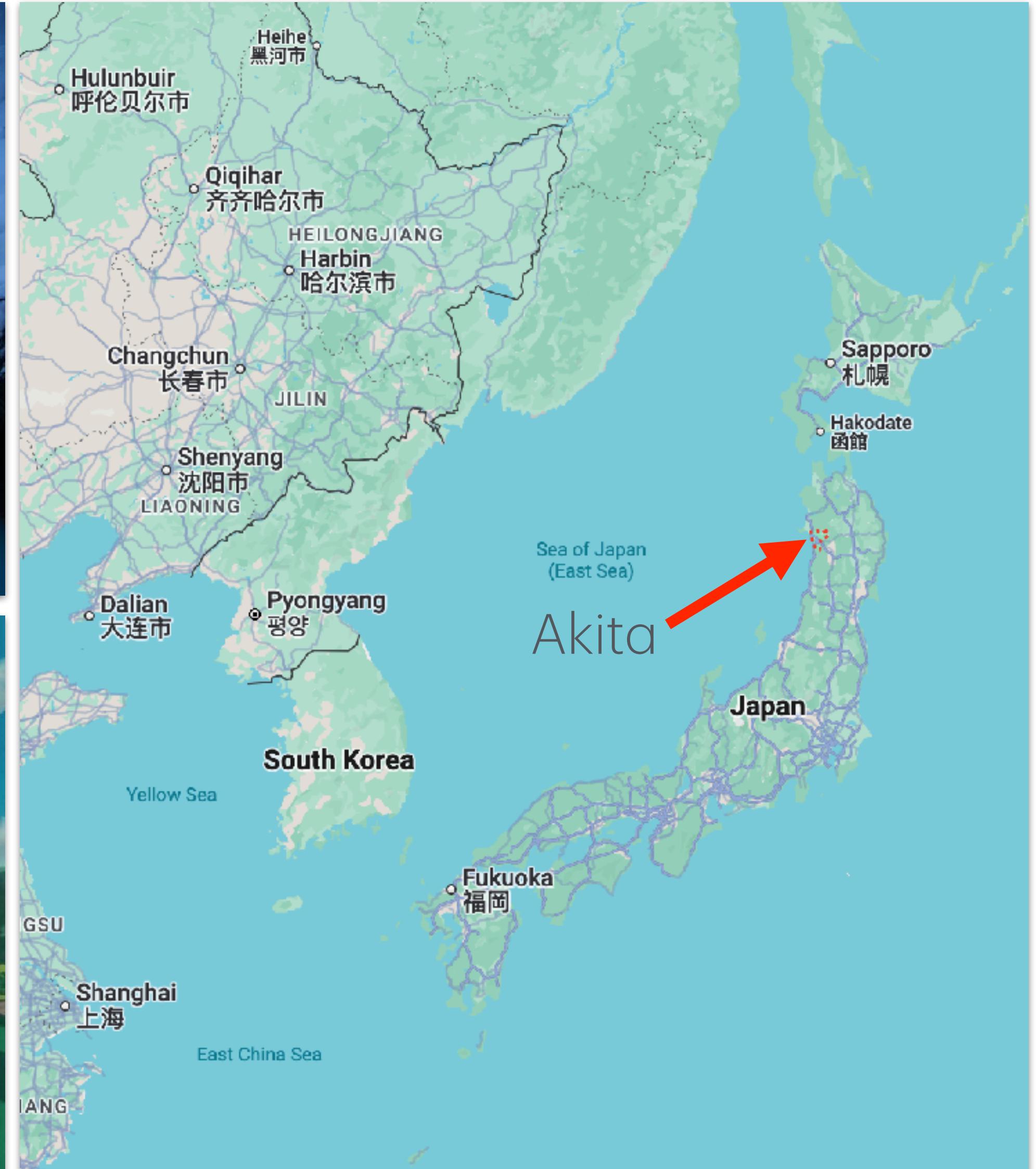
Banksy



Code



English teaching, Japan



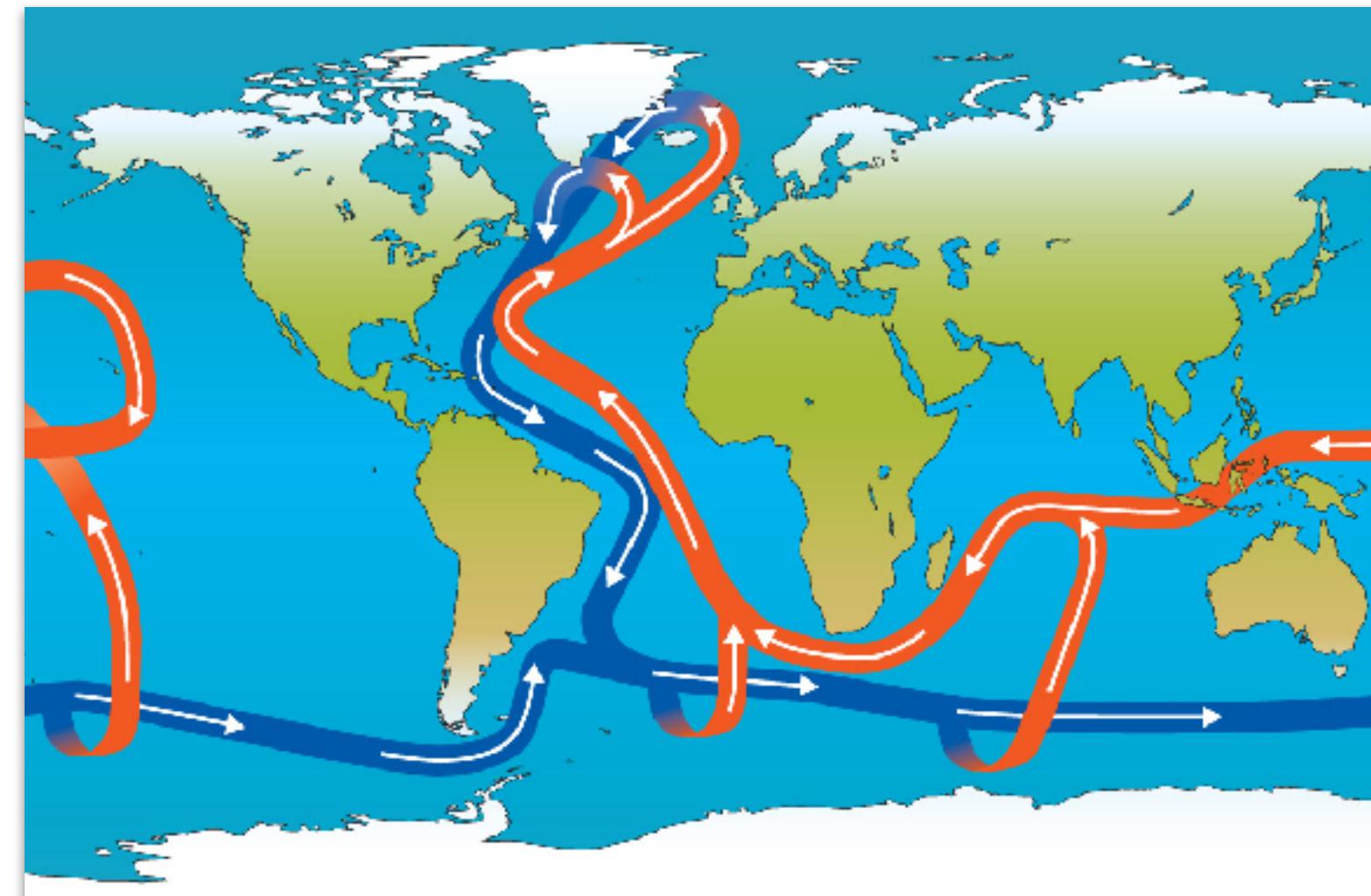
Biked around NZ



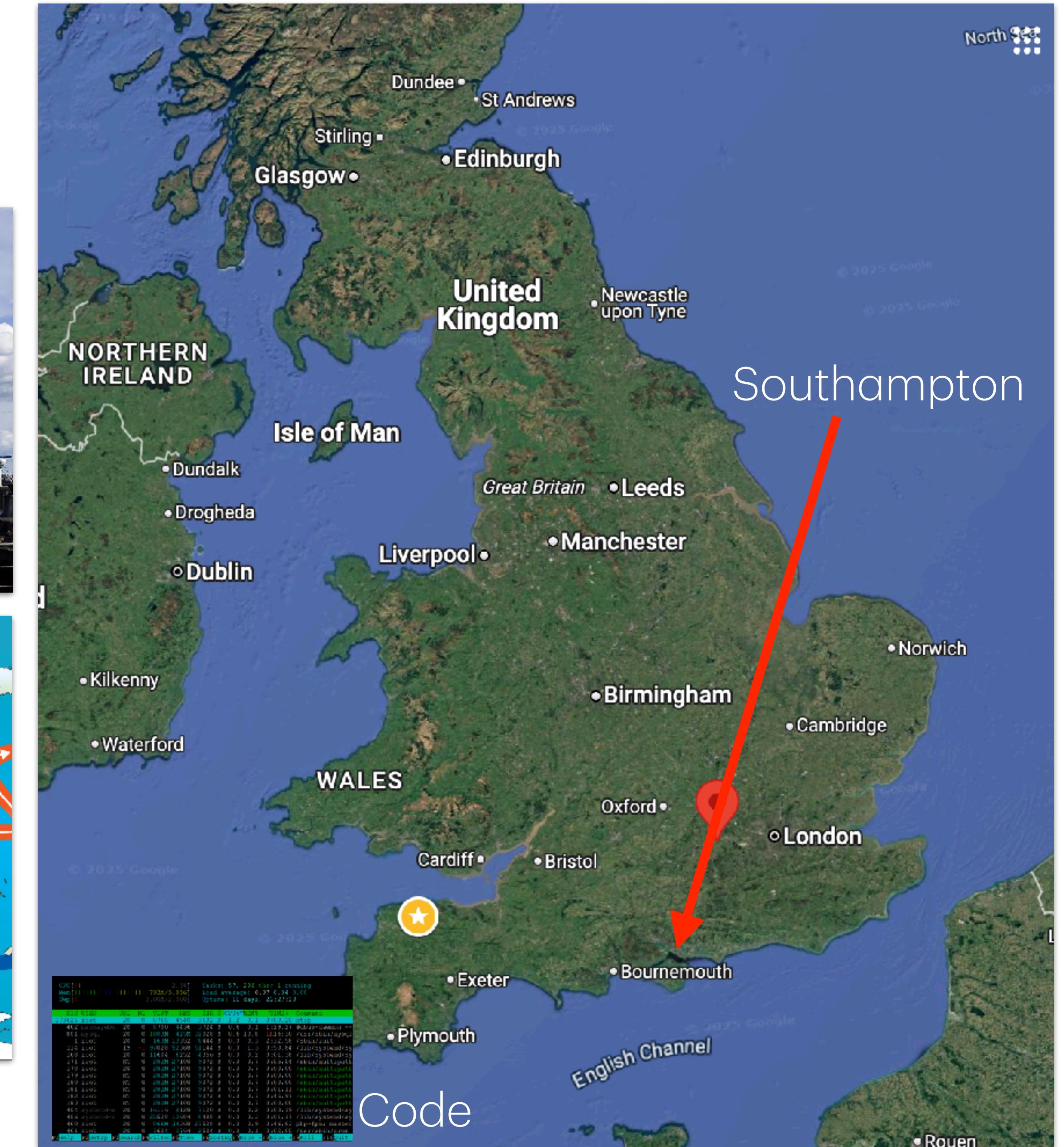
Southampton, UK



MS in
Oceanography at
the National
Oceanography
Center in the UK

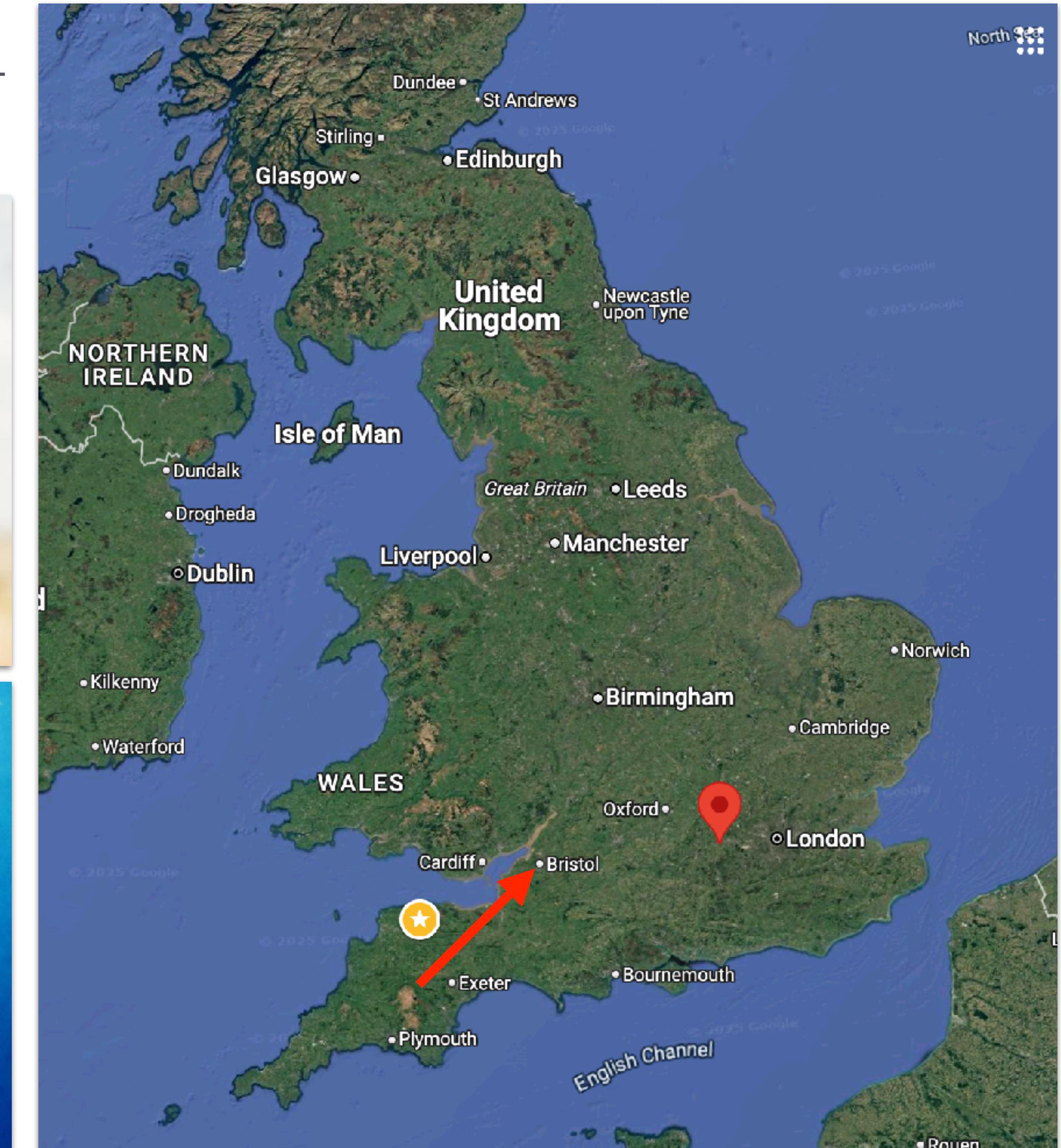
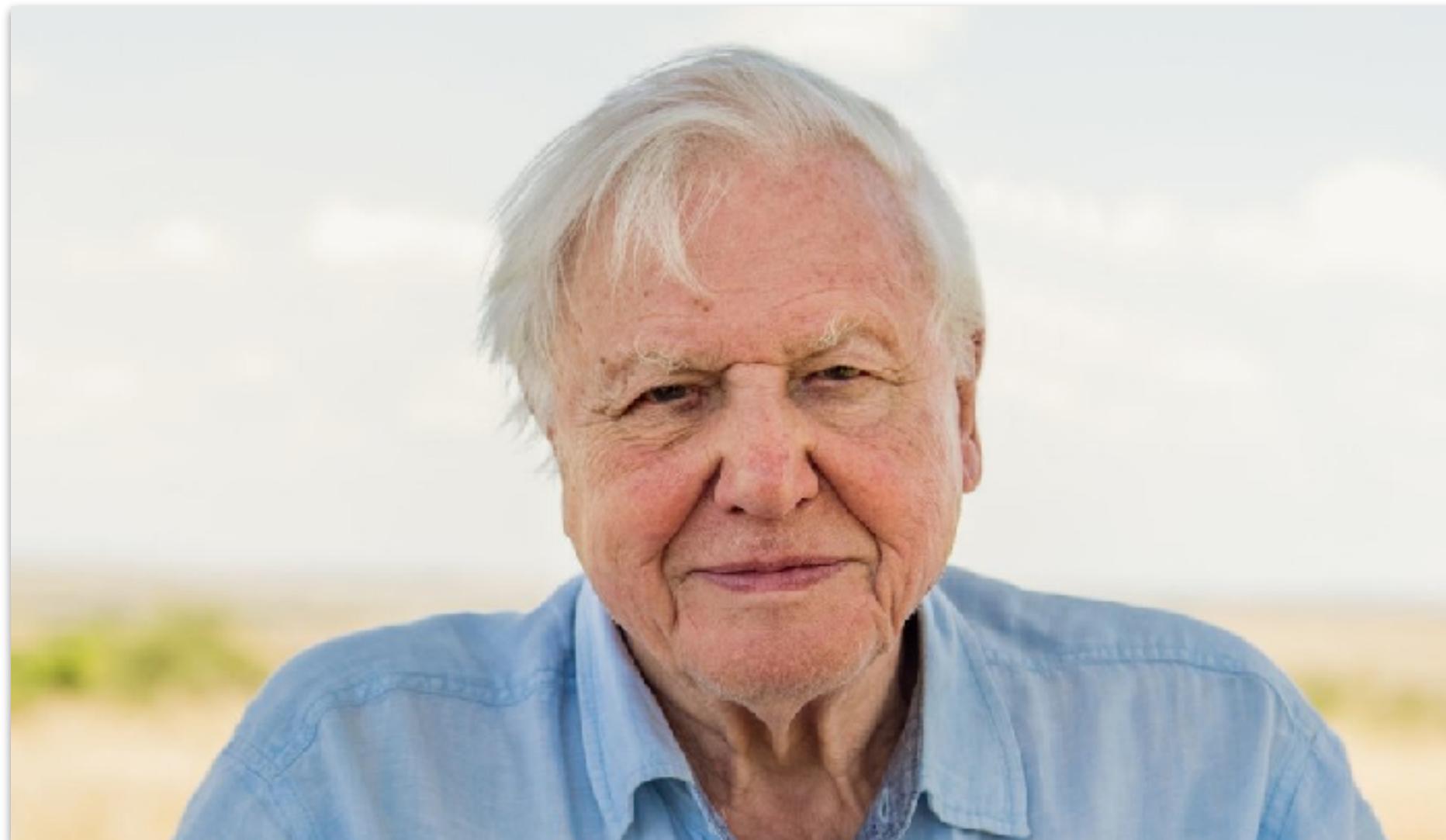


I worked on this (guess this)

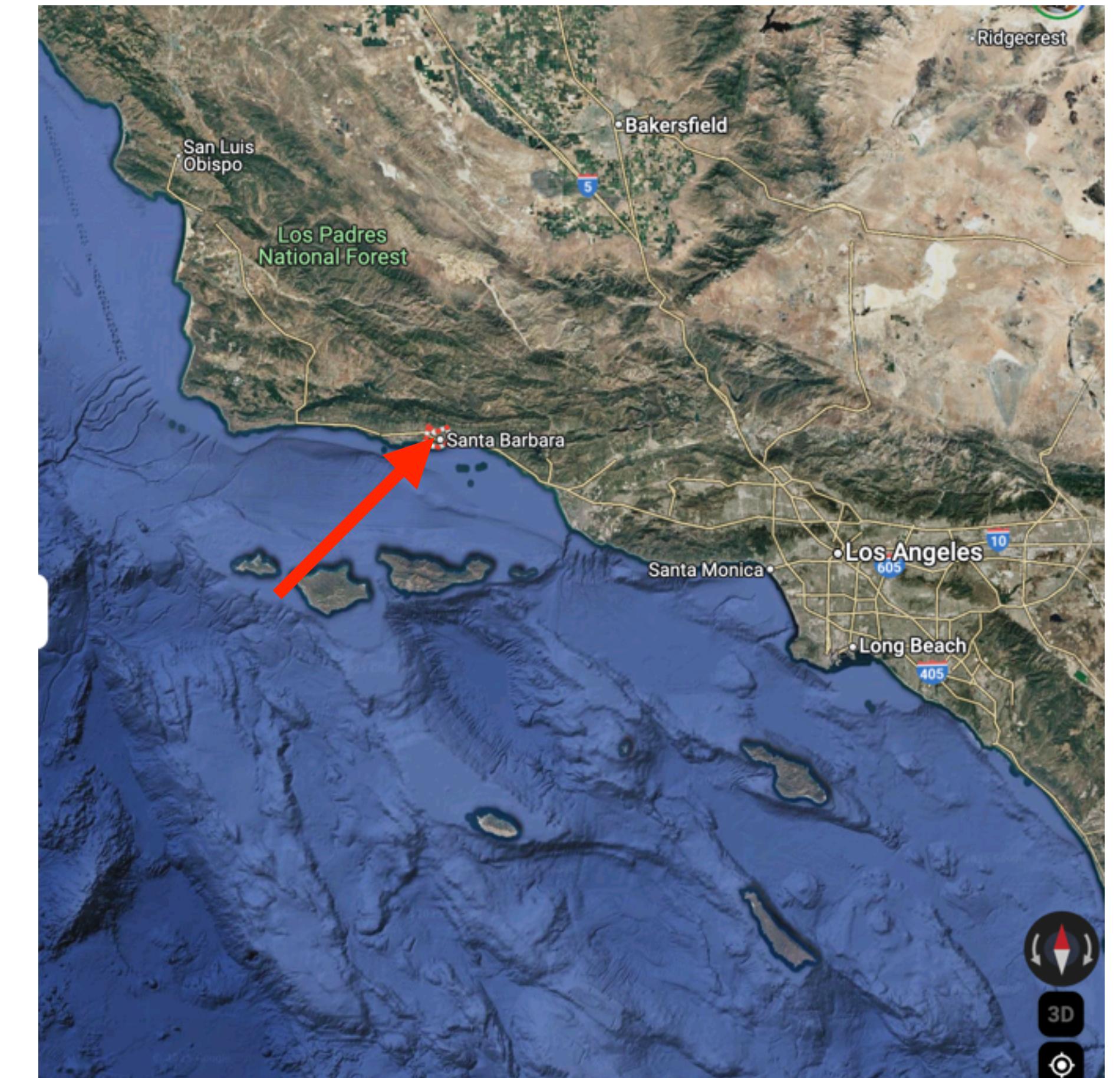
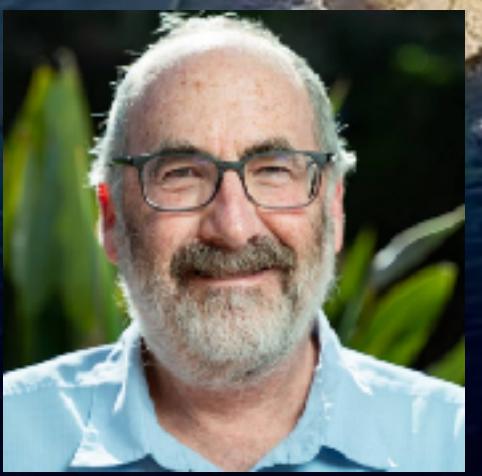


Code

BBC, Natural History

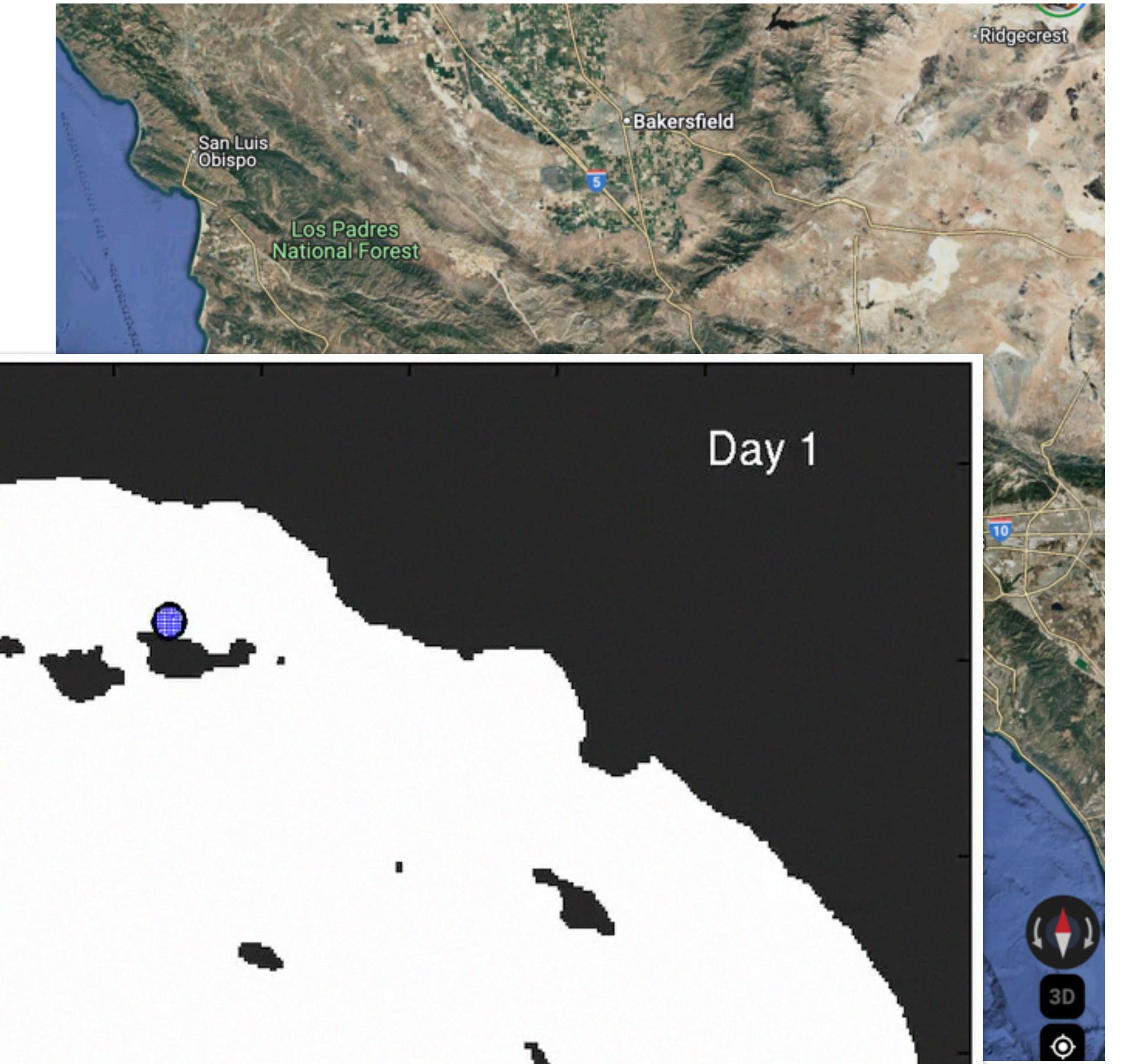
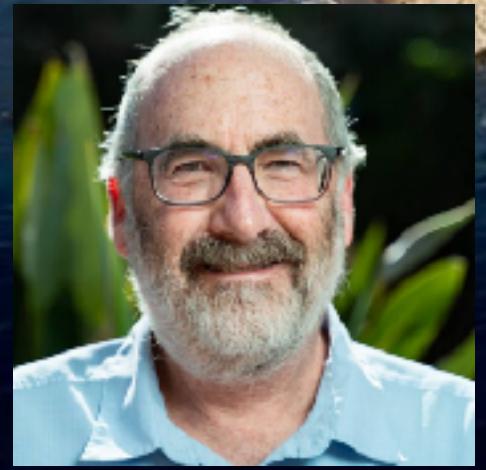


Santa Barbara, CA



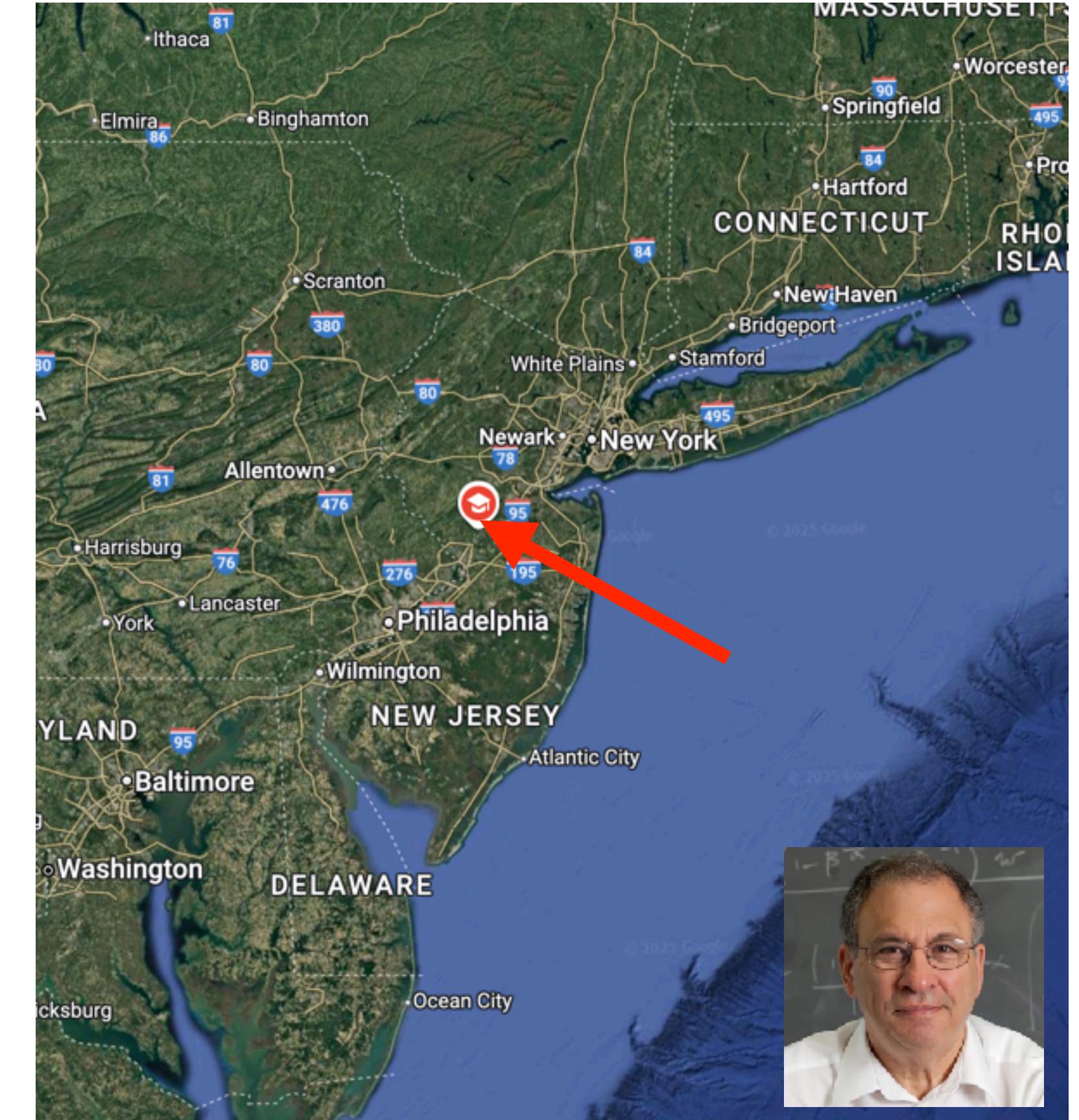
I studied Marine Science at UC Santa Barbara (in a Geography department): focusing on quantifying marine habitat connectivity and marine protected area design

Santa Barbara, CA



I studied Marine Science at UC Santa Barbara (quantifying marine habitat connectivity and mo

Princeton, NJ



I worked at Princeton University with theoretical ecologists: collective and complexity scientists on behavior of fishermen

Stockholm, Sweden



I worked at the Stockholm Resilience Center with sustainability scientists like Johan Rockstrom, on planetary boundaries and ecosystem regime shifts

What I really do



Oregon State
University



The point of this:

- Everyone's path is different
- **You don't need a degree in CS to do quantitative code-based research**
- The most important thing is that you ask important / interesting questions

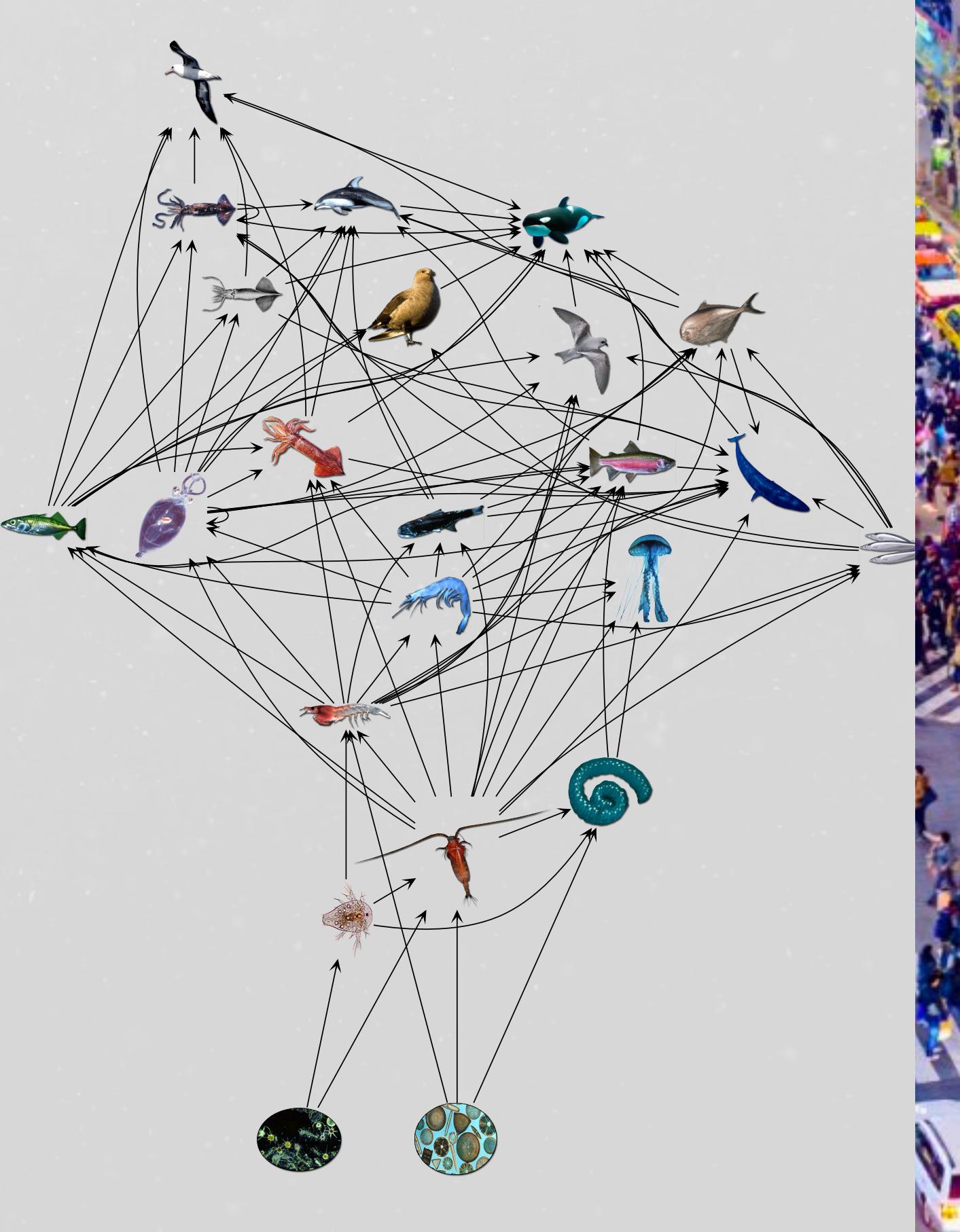
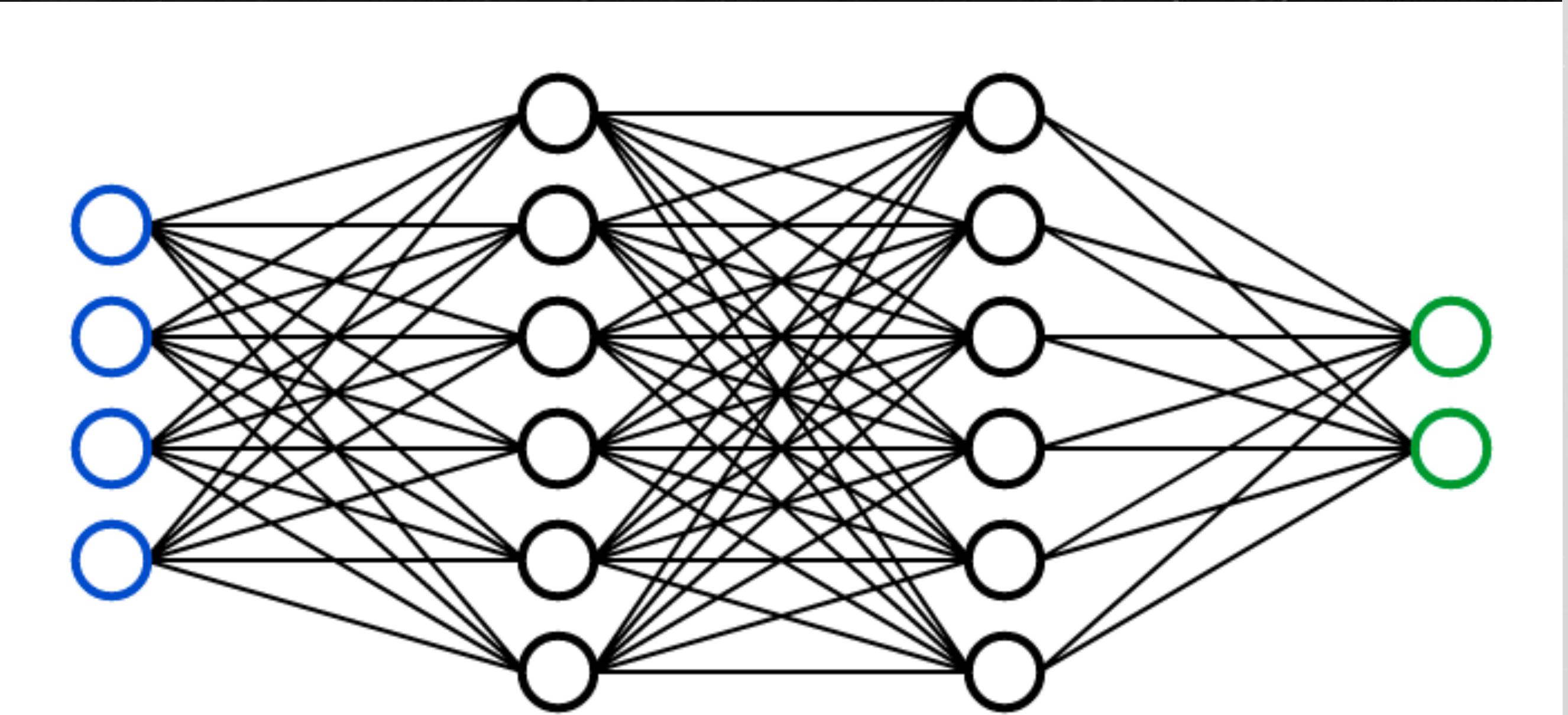
Lets talk about you

- Introduce yourself (10s)
- Tell the class about your goals for this year (30s)
- Tell the class about your research project (30s)

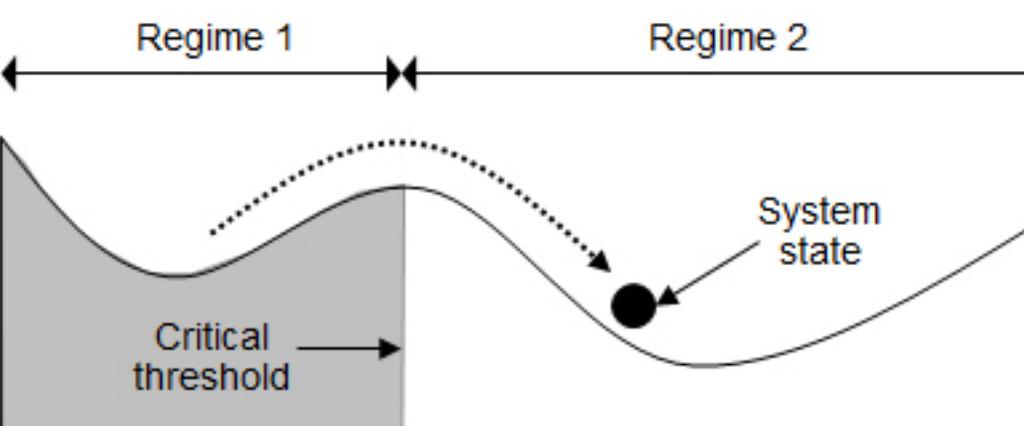
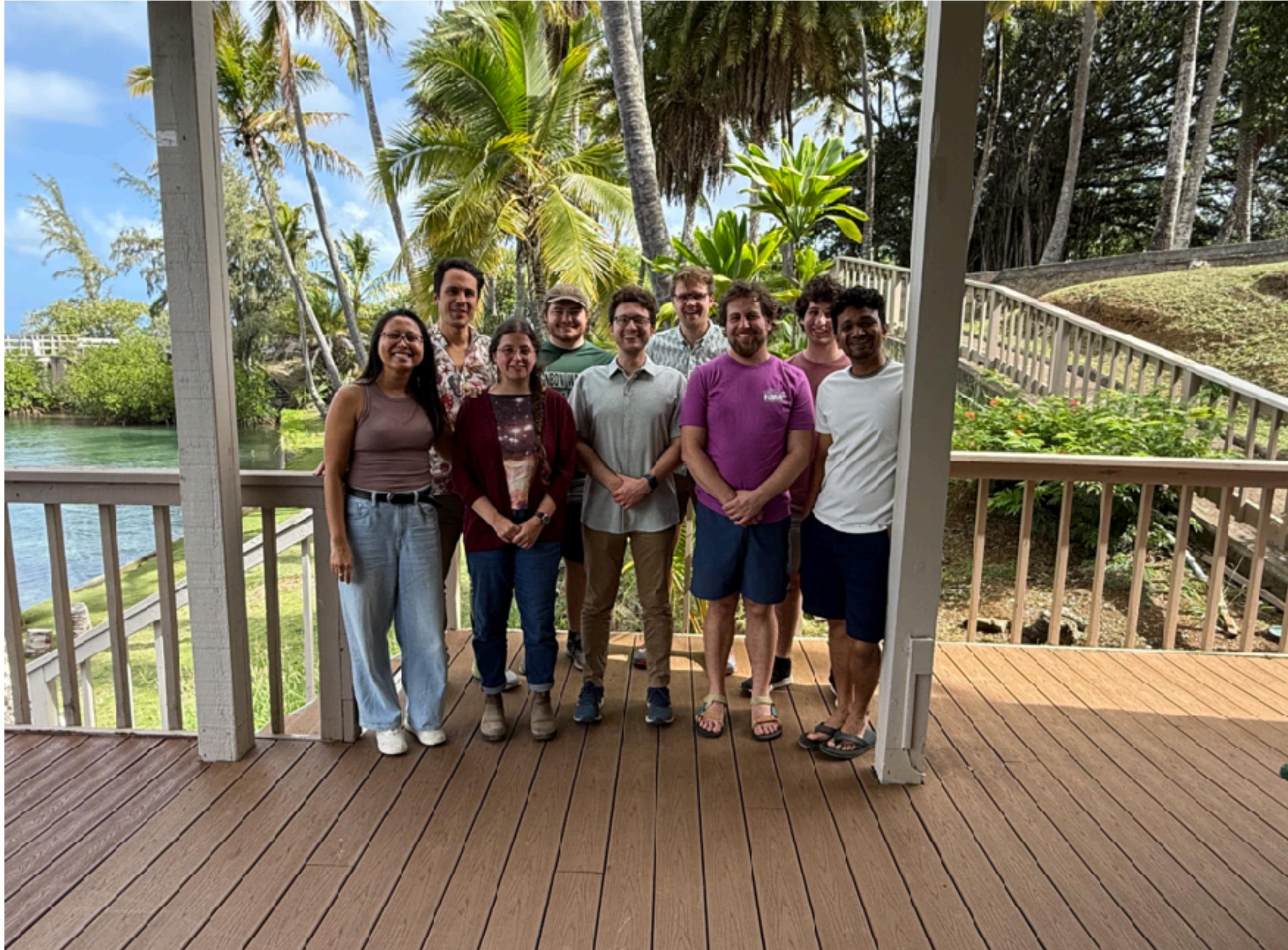
Lets talk about my work

Lets talk about my work

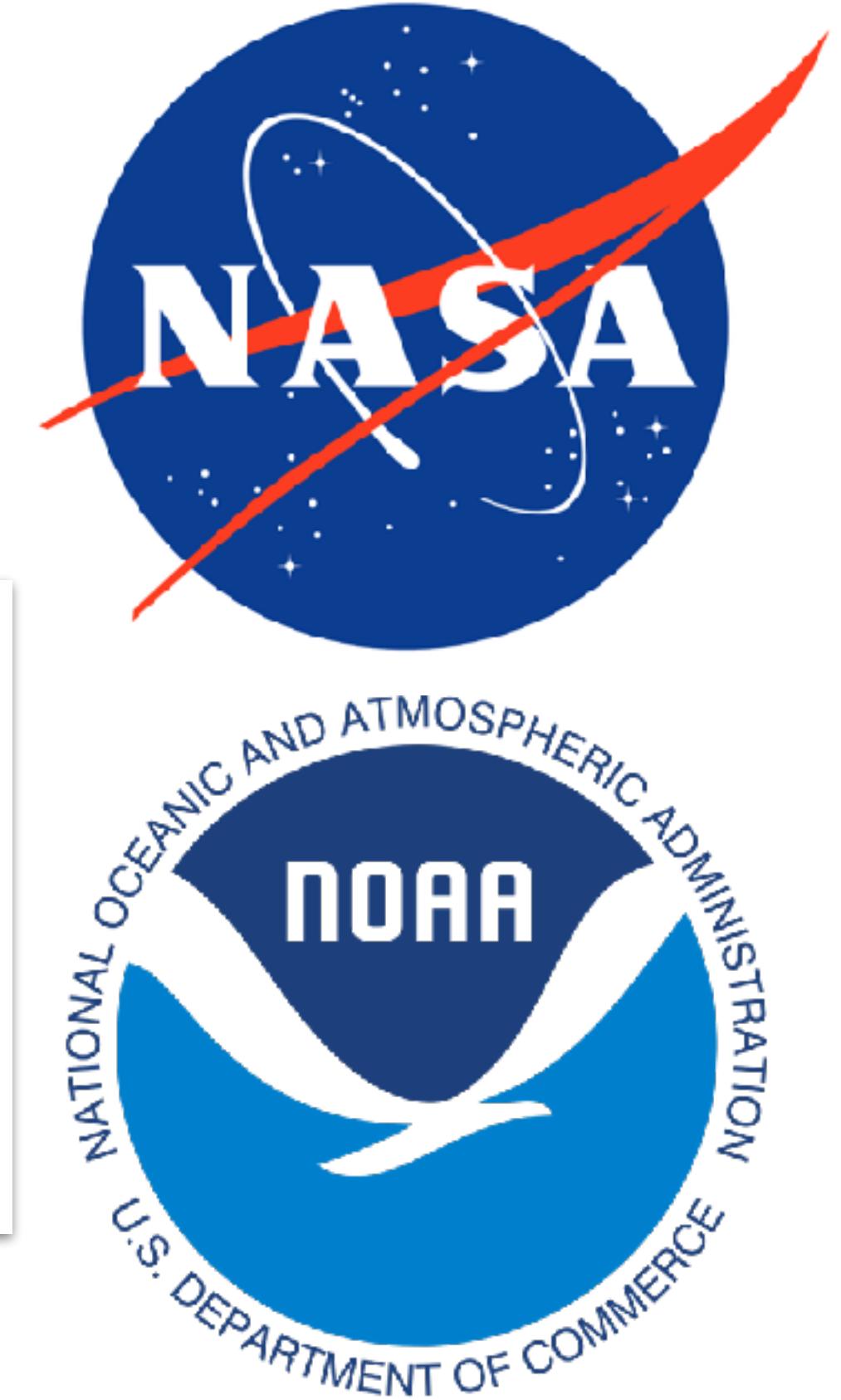
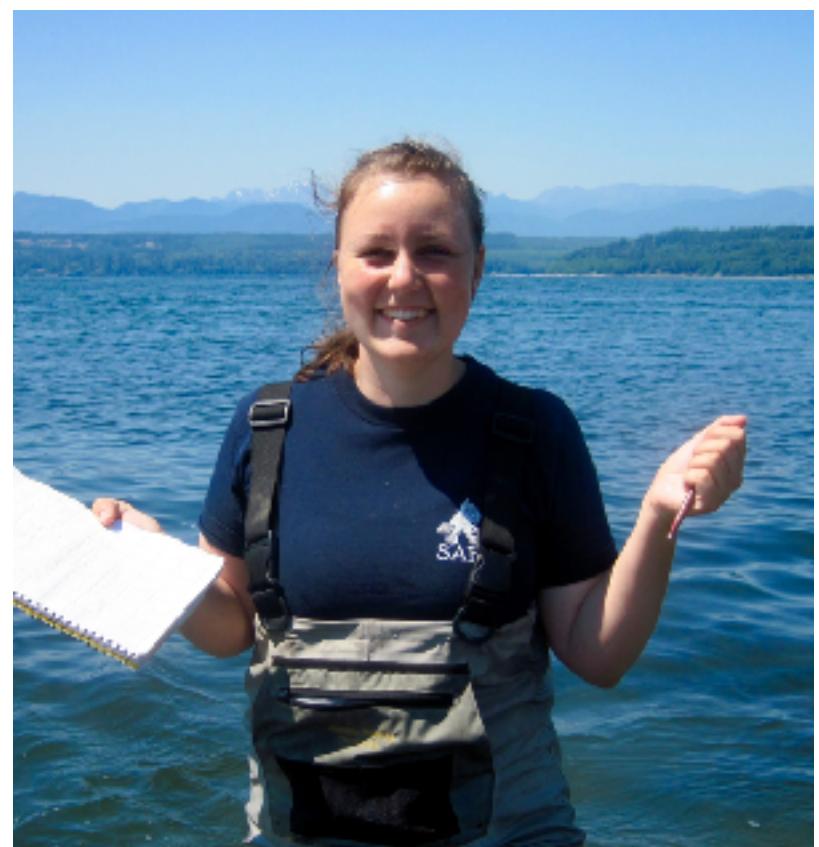
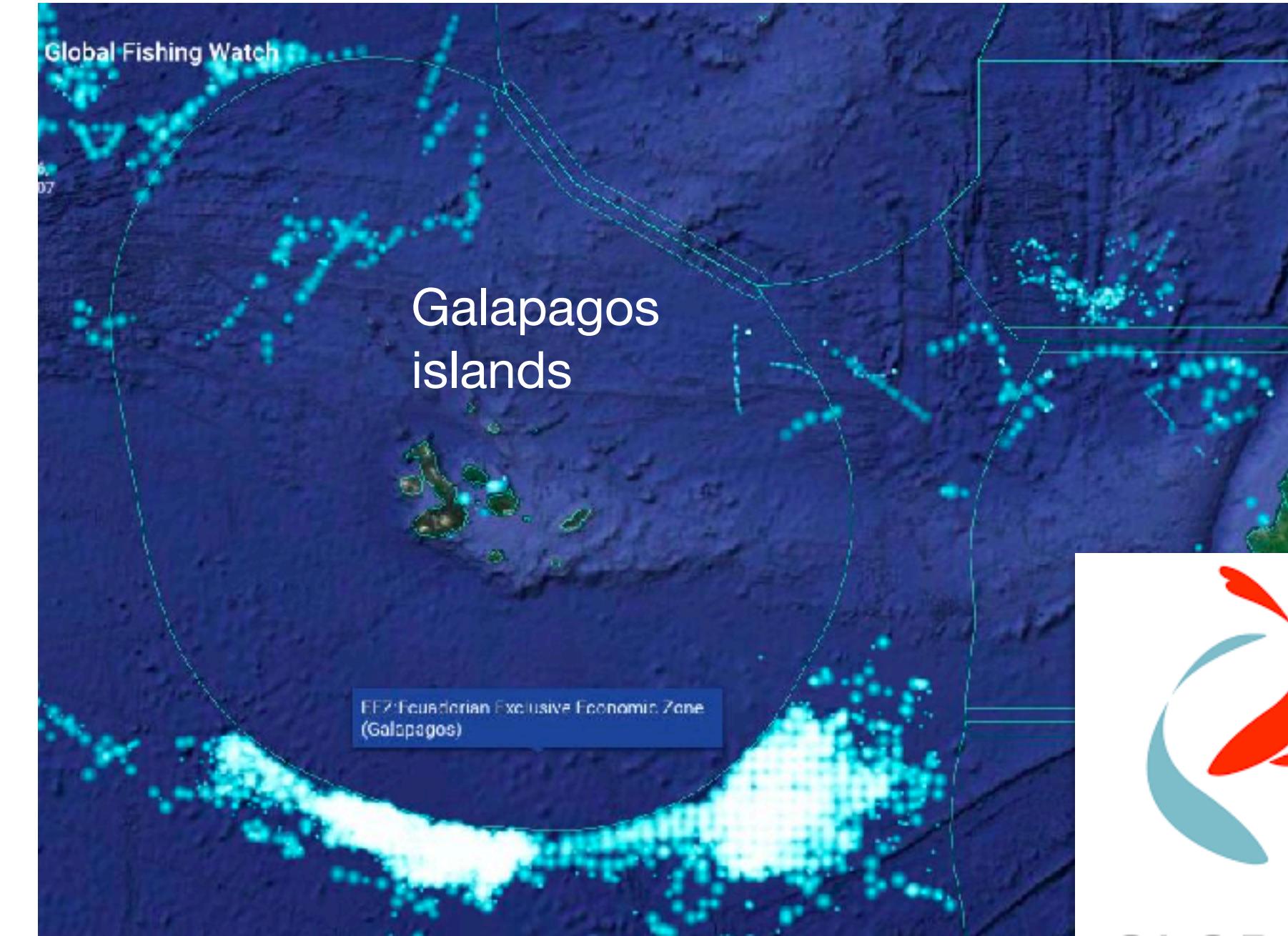
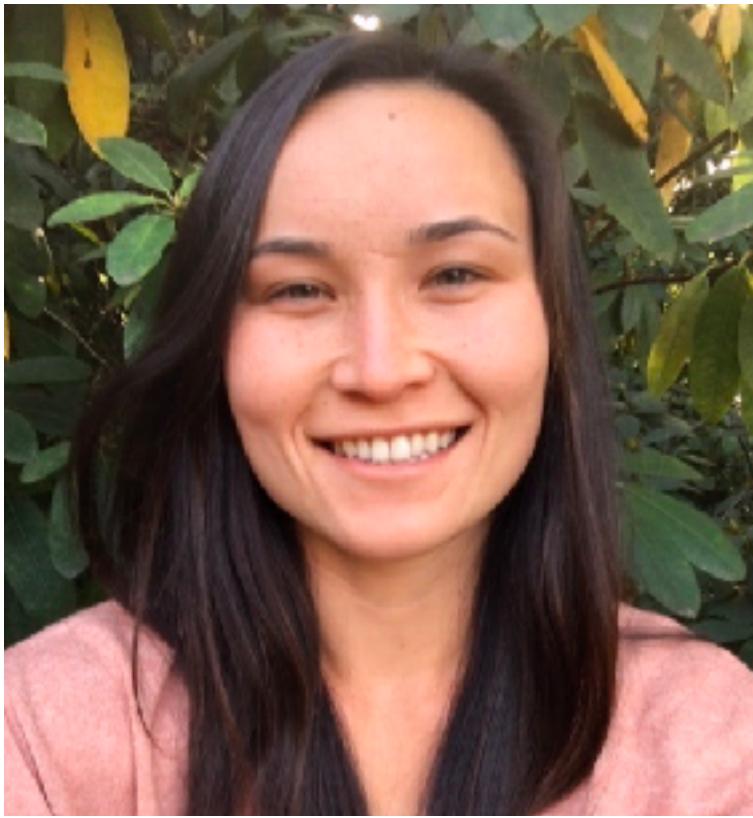




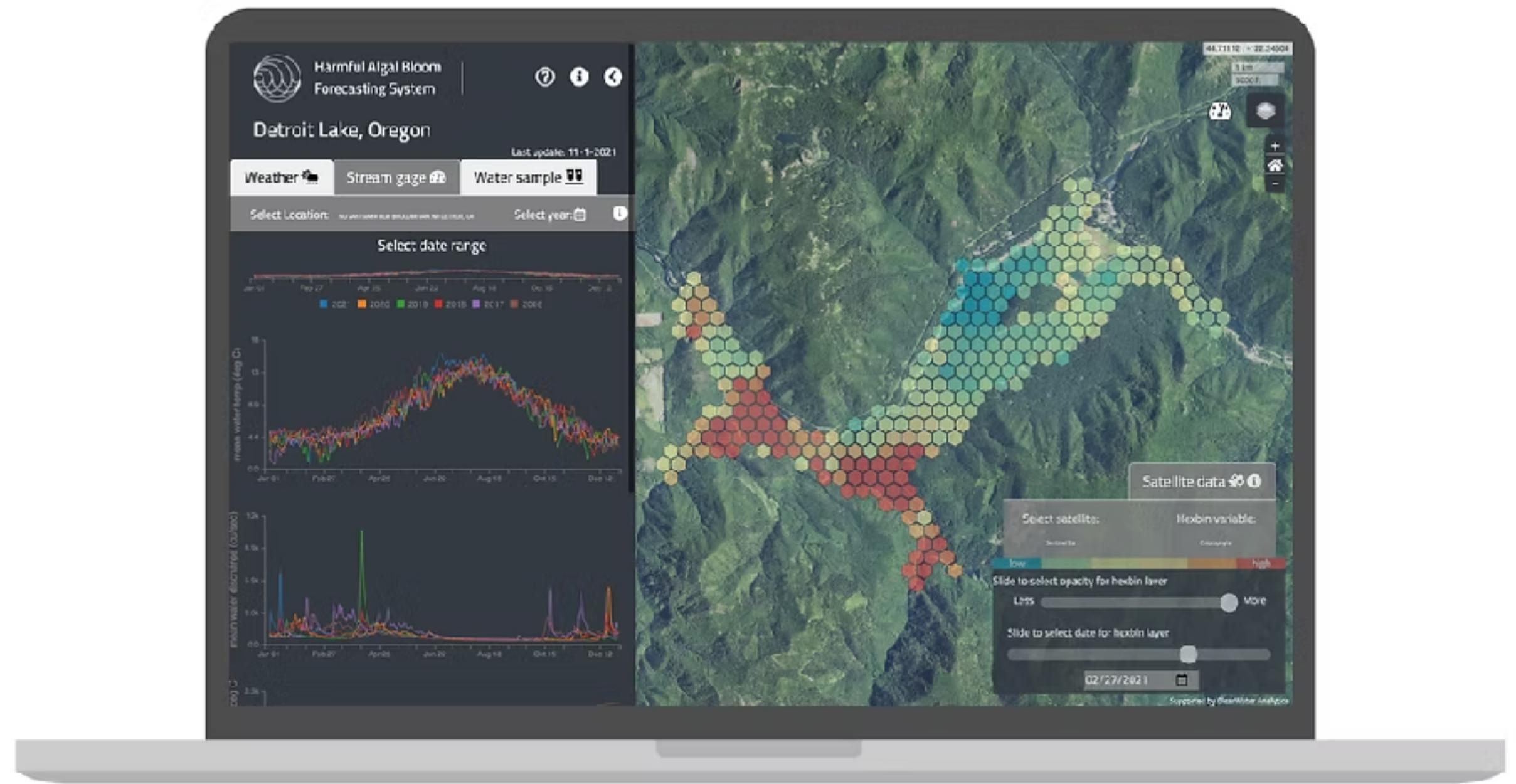
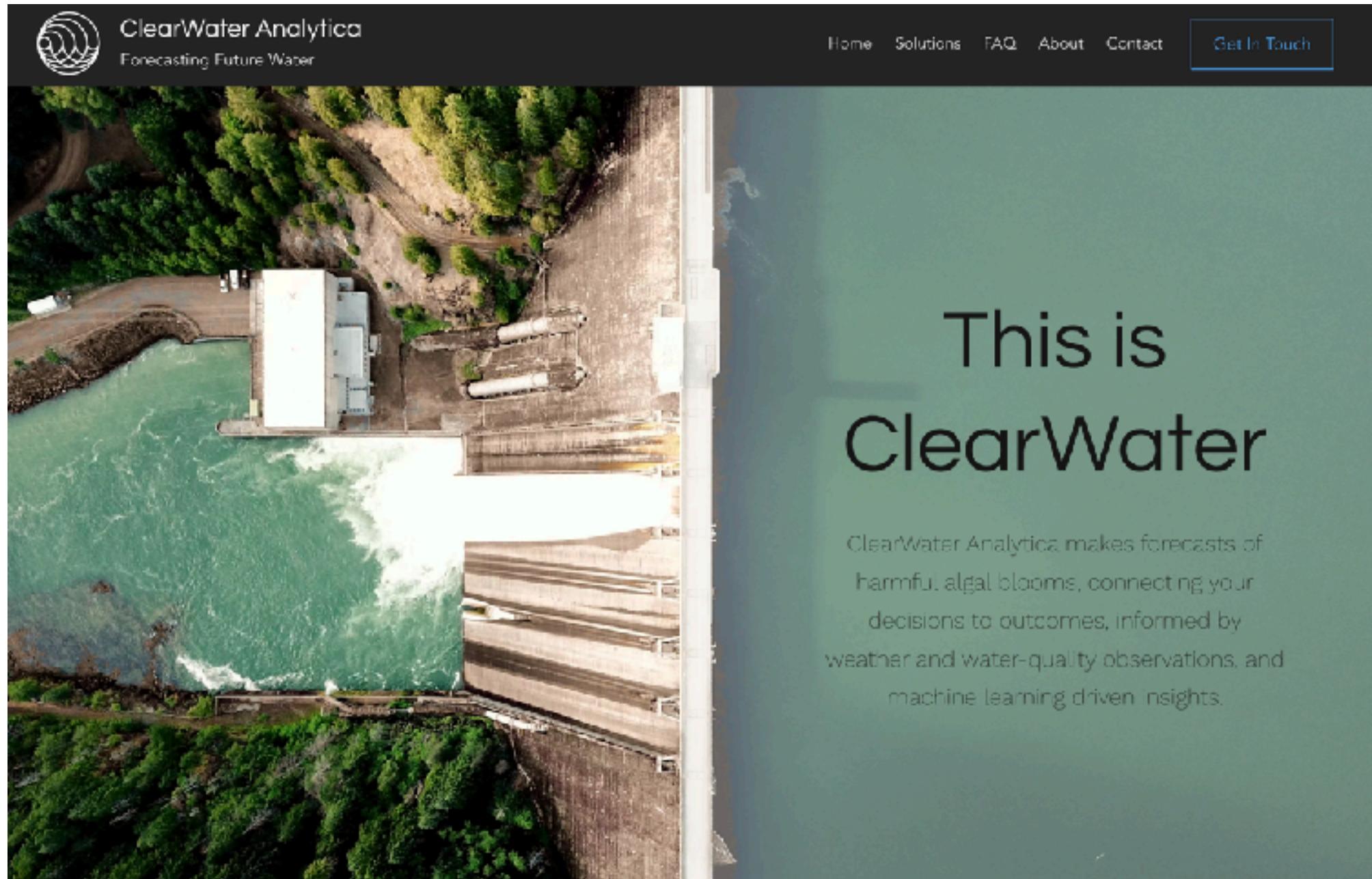
NSF: Scientific ML for predicting regime shifts



NOAA+NASA: predicting illegal fishing



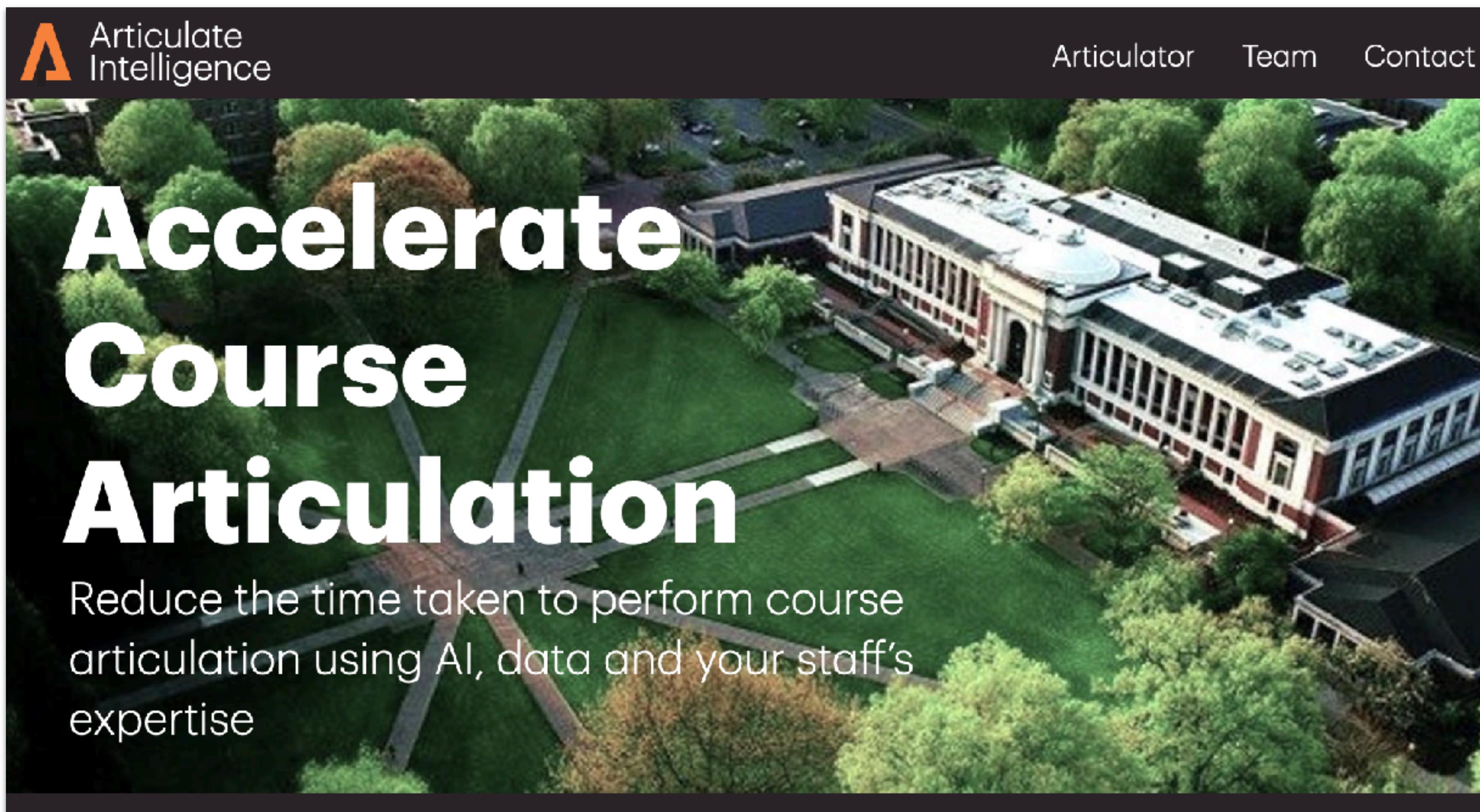
Clearwater Analytica



A screenshot of the "Our Team" section of the website. It features two circular profile pictures of team members: Mathew Titus, CTO, and John Woodill, Senior Data Scientist. Both profiles are set against a background of handwritten mathematical equations.

A web-app dashboard for real-time monitoring of harmful algal blooms in lakes

Articulate Intelligence



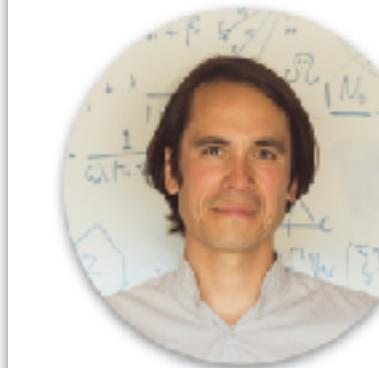
Articulate Intelligence

Accelerate Course Articulation

Reduce the time taken to perform course articulation using AI, data and your staff's expertise

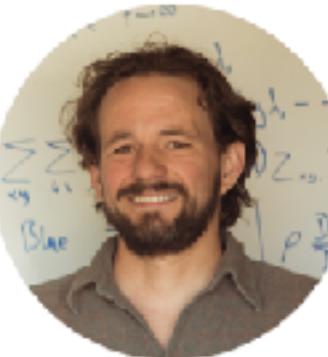
Articulator Team Contact

Team



James Watson
Co - Founder and
Chief Executive
Officer

M in



John Woodill
Co - Founder and
Chief Technology
Officer

M in

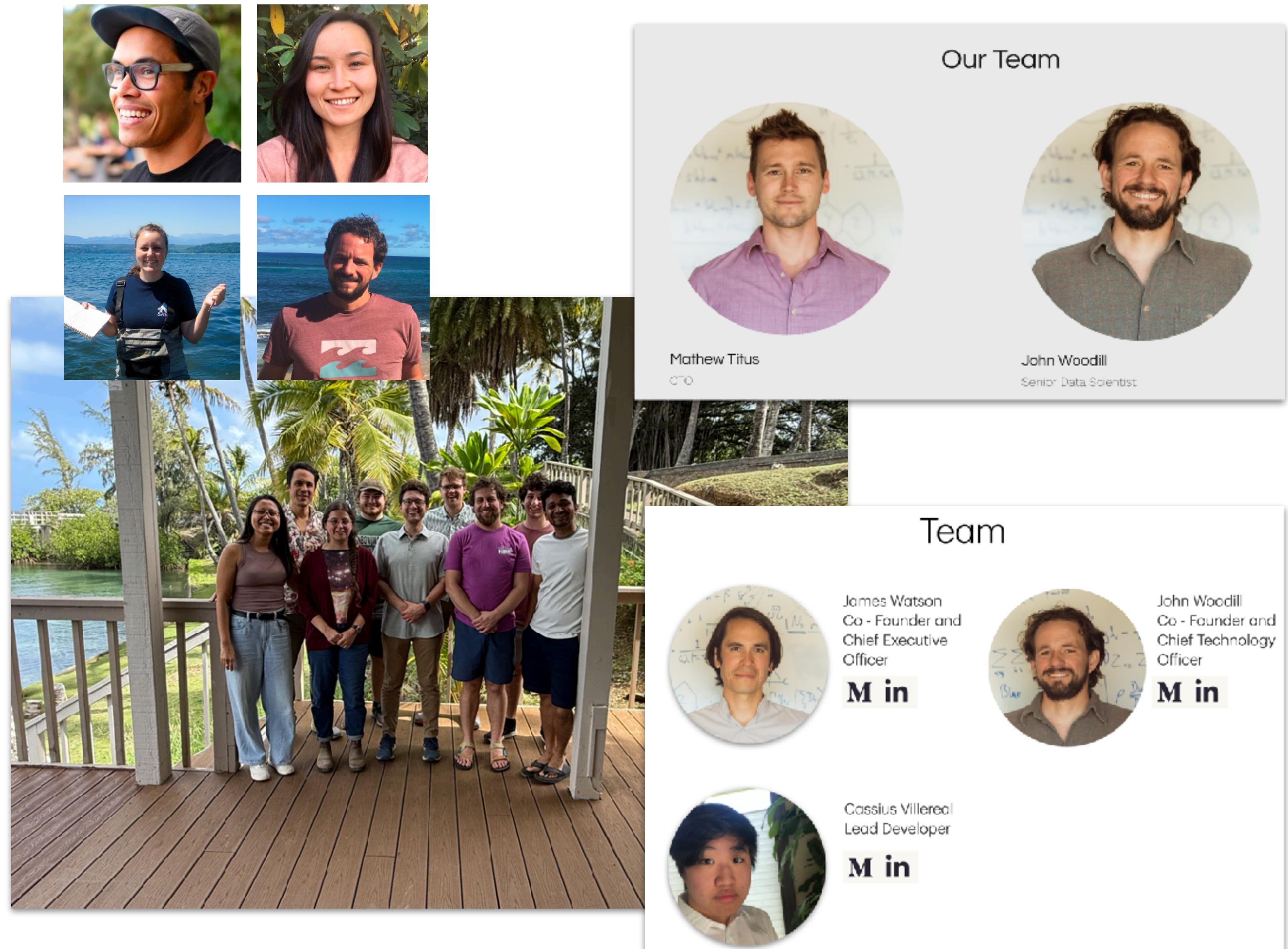


Cassius Villereal
Lead Developer

M in

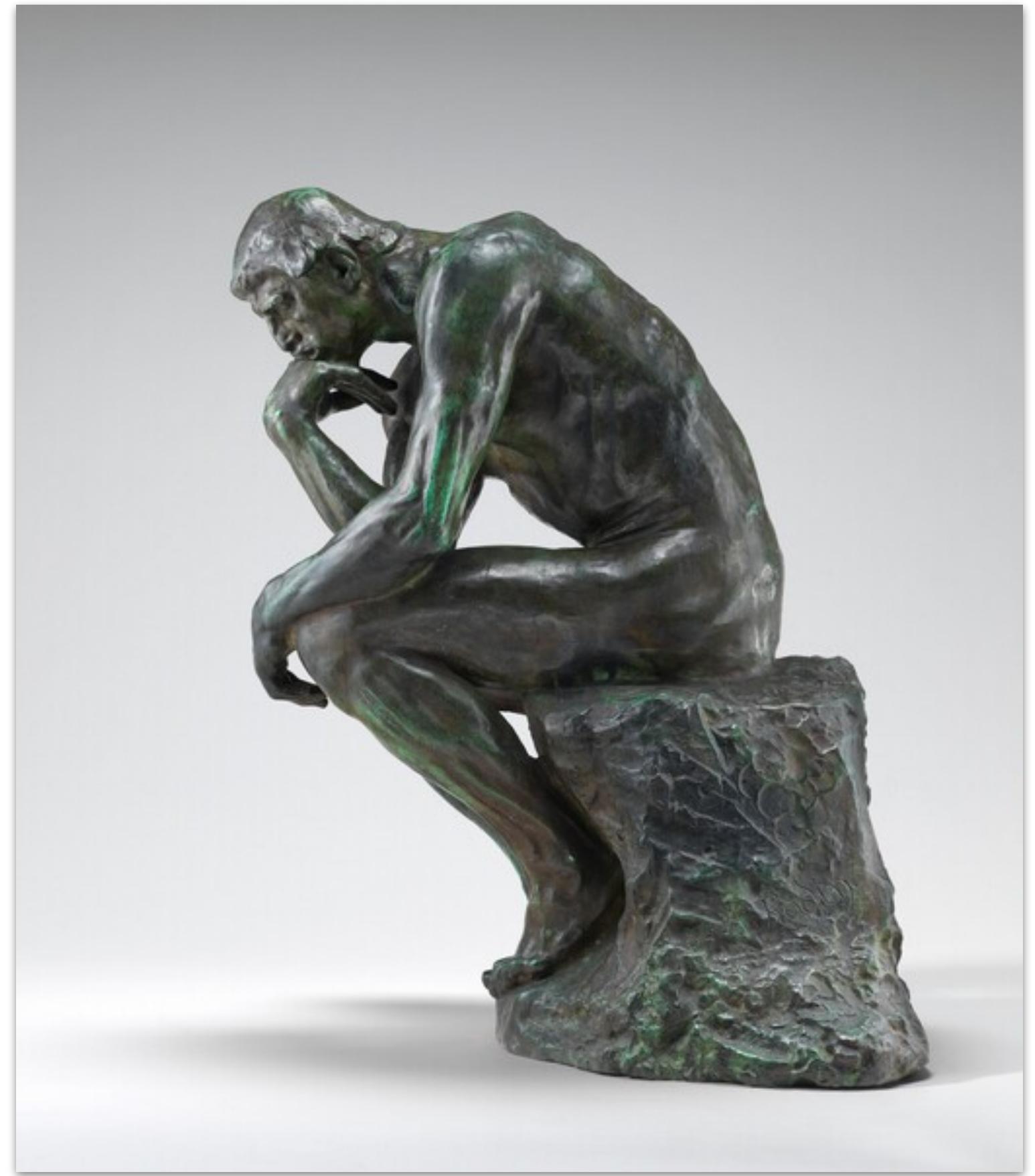
The point of this:

- **Team work (2 - 15 people)**
- Mathematics > Modeling
- AI > Machine Learning > Statistics
- Data > Code

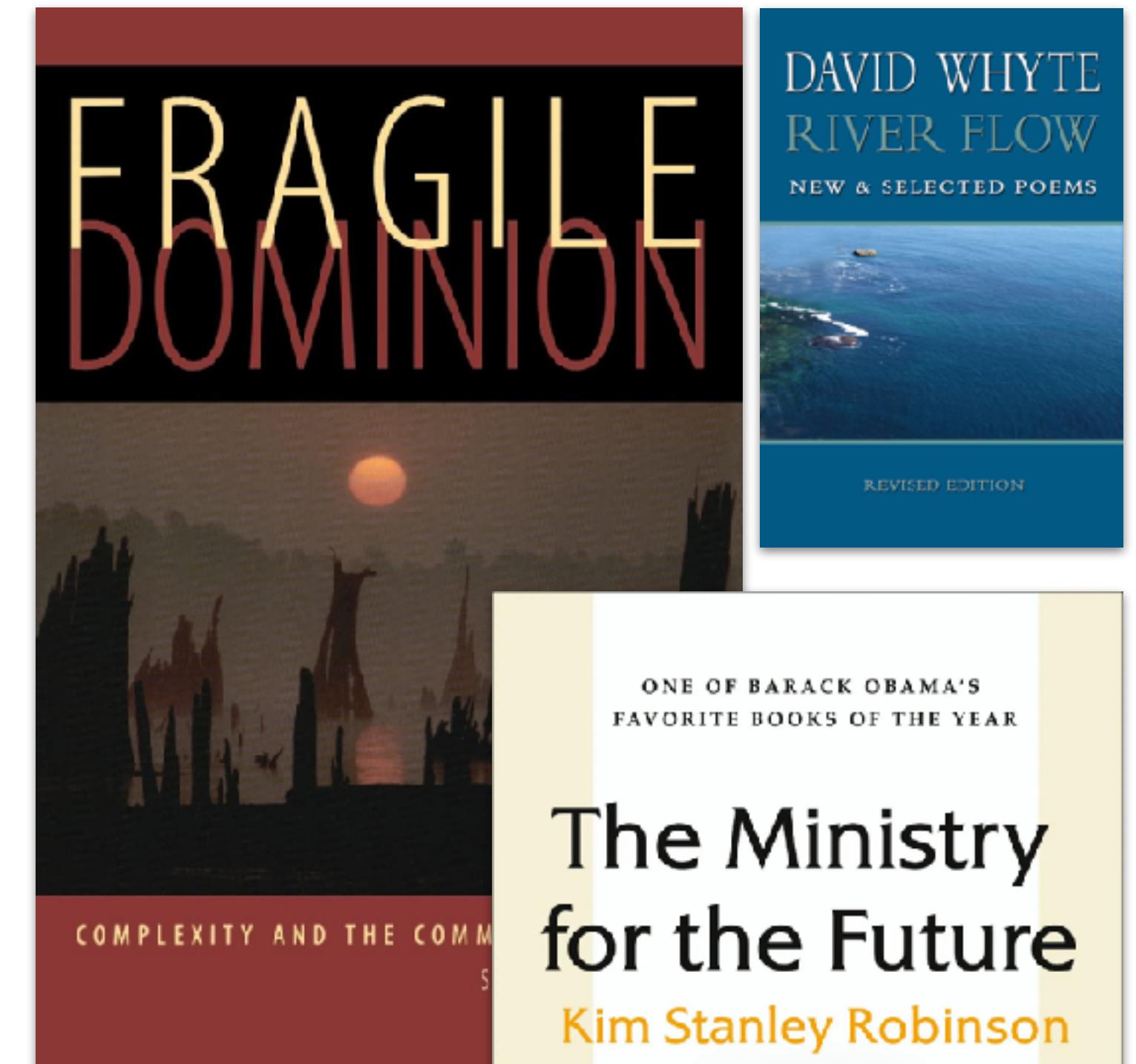
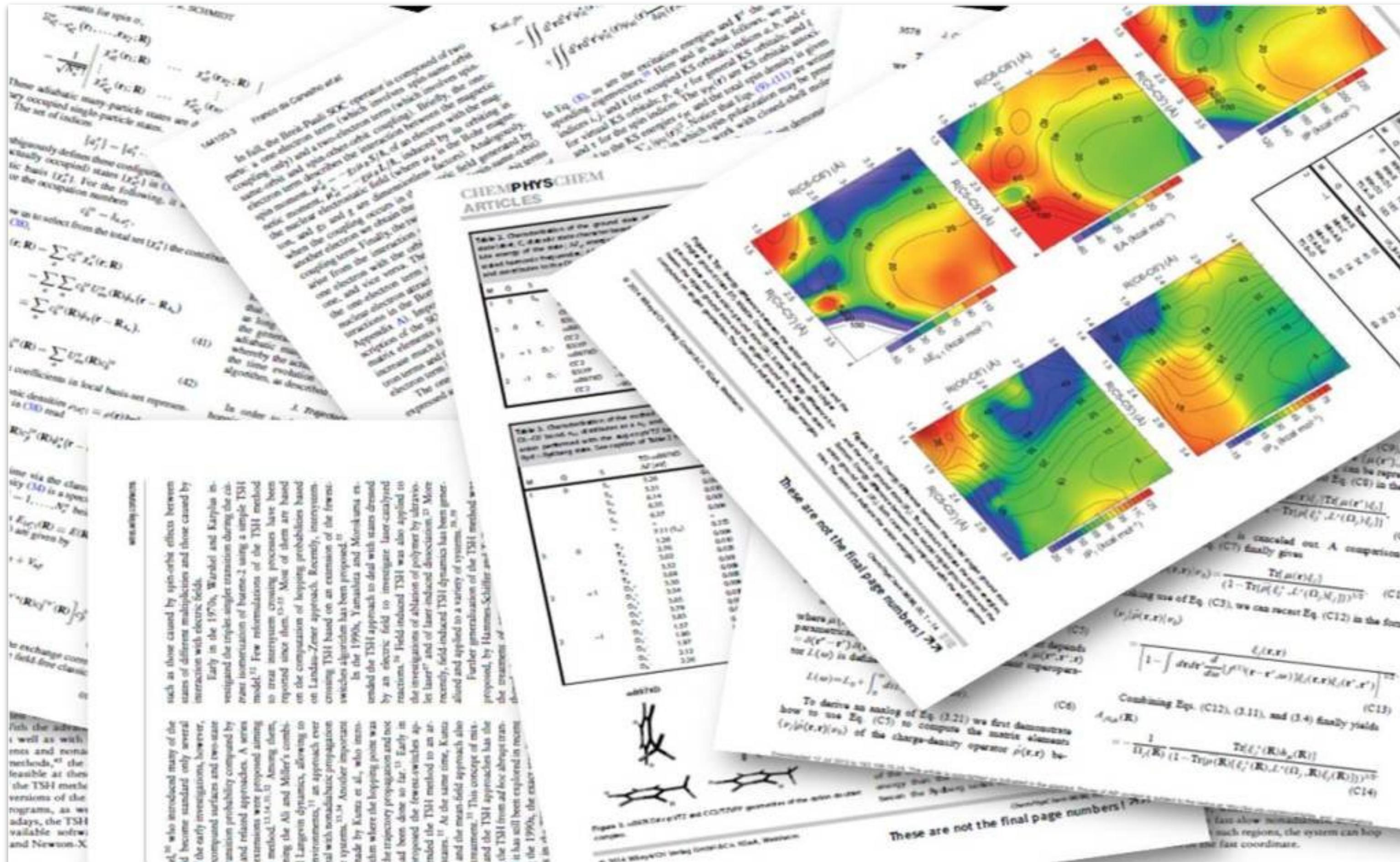


Lets talk about my process

Think



Read



The Ministry
for the Future

Kim Stanley Robinson



"The best science fiction
nonfiction novel I've ever read."

—JONATHAN LETHEM

Research



Google Drive

Overleaf

Julia
computing



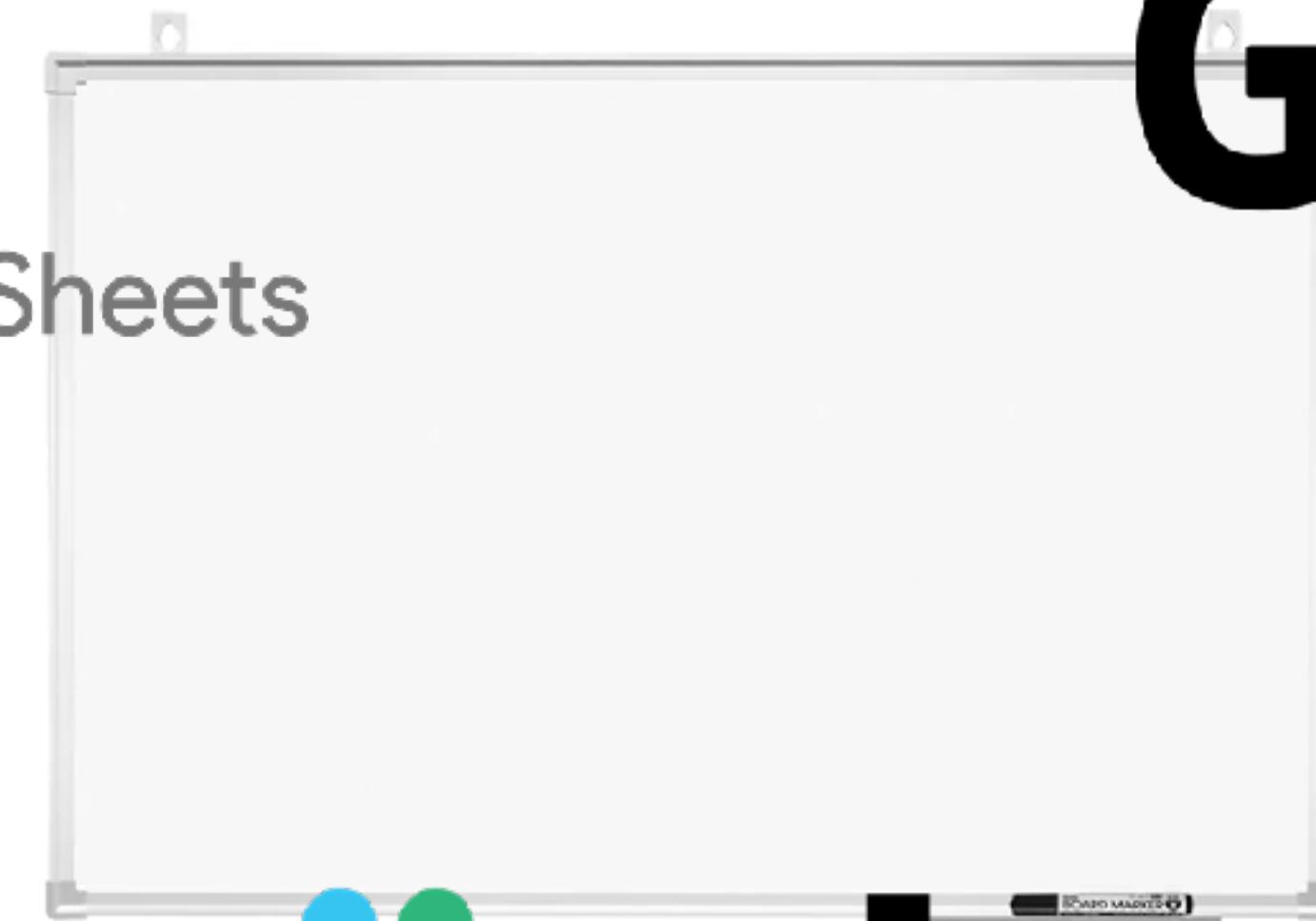
GitHub



Google Sheets



Google Docs



Trello



python



slack



R Studio®

Write

COLLABORATIVE RESEARCH: MODEL ENABLED MACHINE LEARNING (MnML) FOR PREDICTING ECOSYSTEM REGIME SHIFTS

Overview
 Machine learning coupled with ecological theory can overcome three of the biggest challenges in biology at the ecosystem level, specifically the apparent uniqueness of every ecosystem at local spatial scales, the often-strict limitations in data availability, and our need to predict nonlinear dynamics, often exhibited as large and abrupt or "regime shifts" in ecosystem structure and function. Countless examples describe a repeated story: an ecosystem undergoes a regime shift, one that impacts critical ecosystem services such as the provision of food and income. The data available was insufficient to forewarn of the shift, and theoretical models developed to describe such phenomena were too abstract to provide any actionable information to managers and stakeholders. There is a need for methods -- new bioinformatics and cyberinfrastructure more broadly -- that can predict these regime-shifts, and for identifying the drivers of such changes so that policies and technologies can be developed to help avoid them. Here, in this **cyberinfrastructure innovation** project we will advance Model Enabled Machine Learning (MnML) as a new bioinformatics tool for forecasting ecosystem regime shifts.

Intellectual Merit
 MnML as new bioinformatic cyberinfrastructure will consist of novel methods that combine scientific understanding of ecological dynamics (i.e., theoretical models) with the predictive power of machine learning. MnML leverages Universal Differential Equations to advance the machine learning of ecological dynamics. The predictive skill of this proposed innovation will be compared to other state-of-the-art approaches, and our goal is to significantly improve upon existing methods for predicting regime shifts in the following ecosystems:

- 1) Tropical coral ecosystems that switch between coral- and algal-dominated states
- 2) Freshwater lakes that exhibit harmful algal blooms
- 3) Mangrove ecosystems that suffer from multiple stressors.

This project will be conducted in continuous collaboration with stakeholders from these case study systems. The user communities we will work with and whom we aim to impact include ecosystem scientists, water quality managers, coral and mangrove conservation groups, and tropical fisheries and coastal management agencies. The main project deliverable will be a scientific coding package, written in R and Julia, for predicting ecological regime shifts using new MnML methods.

Broader Impacts
 The potential of MnML as a new bioinformatic tool used by ecosystem managers lies not just in its predictive skill, but also in the clear interpretability it provides, which will maximize its utility as an operational tool. Importantly, MnML has the potential to promote **equitable science** by reducing the data requirements of machine learning driven predictions, giving stakeholders in data-poor systems a useful operational tool. In addition to this broader scientific impact, this project will result in the training of several junior researchers, and the confirmed team so far is comprised of a majority of persons that identify either as a person of color and/or an underrepresented groups in science. The results of this project will be embedded in courses taught by the PIs (~70 students per year) and a summer school will be conducted in the final year of the project, where ~10 undergraduate STEM students in Hawai'i will learn about machine learning and ecological theory, prioritizing local conservation issues. We will prioritize the recruitment of students from underrepresented minorities, recruiting from the UH system which includes 3 universities and 7 community colleges that are federally designated Asian American and Native American Pacific Islander-Serving Institutions.

Pitches (1p)

Model Enabled Machine Learning (MnML)

COLLABORATIVE RESEARCH: MODEL ENABLED MACHINE LEARNING (MnML) FOR PREDICTING ECOSYSTEM REGIME SHIFTS

OVERVIEW
 Ecosystems can change radically, suddenly and without warning (1,2). There are numerous examples of this in marine, lentic, and terrestrial systems. From African savannahs (3) to Californian kelp forests (4), these ecosystem "regime shifts" have had large impacts on the provision of key ecosystem services, such as food and income (5). There is a need for new bioinformatics and cyberinfrastructure that can predict these regime-shifts (6,7), and for identifying the drivers of such changes so that policies and technologies can be developed to help avoid them (should that be desired). Current methods for anticipating regime shifts perform poorly (8): either theoretical models of ecosystem dynamics are too abstract to provide useful operational forecasts, or data-driven approaches suffer from overfitting and cannot accurately forecast the emergence of novel conditions (i.e., those not seen in historical data on which models are trained).

In this project, a new approach to regime-shift prediction will be developed and designed for operational use. We will test this new approach in three ecosystem case-studies: coral, lake and mangrove ecosystems. This new bioinformatics cyberinfrastructure will consist of novel methods that combine scientific understanding of ecological dynamics (i.e., theoretical models) with the predictive power of machine learning. Specifically, this innovation in cyber infrastructure will target the use of **Universal Differential Equations** (9) to advance the machine learning of ecological dynamics. The predictive skill of this proposed innovation will be compared to other state-of-the-art approaches, and our goal is to significantly improve upon existing methods for predicting regime shifts in ecosystems. We will develop this new cyber infrastructure in close collaboration with the communities that this innovation will ultimately serve. Specifically, these stakeholders include environmental managers and conservation groups working in the three ecosystem case studies where we will deploy and test our predictive algorithms: lake systems in the USA that suffer from harmful algal blooms, tropical coral systems in the western Pacific that suffer from bleaching events driven by elevated ocean temperatures, and mangrove systems in Costa Rica that are impacted by multiple stressors such as hurricanes, coastal development and pollution.

Figure 1. Conceptual figure illustrating recent advances in Model enabled Machine Learning (MnML). For a given ecosystem, for example where there is a predator (a lynx) and a prey (a rabbit), mathematical theory for their interactions (A) can be used to augment training of a neural network (B) such that it can end up producing high accuracy predictions of population dynamics, even though only trained on a small amount of time-series data (C).

Nonlinear Ecological Dynamics and Current Practice
 Ecological dynamics are known to exhibit a wide range of behavior; from cycles to chaos (10,11), these population- and community-level dynamics emerge from the interactions of the many individuals that compose the system, including individuals within the same population as well as their predators, prey,

Proposals (15p)

PNAS

Identifying critical regions in small-world marine metapopulations

James R. Watson^{a,1,*}, David A. Siegel^{a,b}, Bruce E. Kendall^c, Satoshi Mitarai^d, Andrew Rassweiler^e, and Steven D. Gaines^f

^aEarth Research Institute, ^bDepartment of Geography, ^cStern School of Environmental Science and Management, and ^dMarine Science Institute, University of California, Santa Barbara, CA 93106; and ^eMarine Biophysics Unit, Okinawa Institute of Science and Technology, 1919-1 Tanchi Onna-son, Okinawa 904-0412, Japan

Edited by James Hemphill Brown, University of New Mexico, Albuquerque, NM, and approved September 13, 2011 (received for review July 14, 2011)

The precarious state of many nearshore marine ecosystems has prompted the use of marine protected areas as a tool for management and conservation. However, there remains substantial debate over their design and, in particular, how to best account for the spatial dynamics of nearshore marine species. Many commercially important nearshore marine species are sedentary as adults, with limited home ranges. It is as larvae that they disperse greater distances, traveling with ocean currents sometimes hundreds of kilometers. As a result, these species exist in spatially complex systems of connected subpopulations. Here, we explicitly account for the mutual dependence of subpopulations and approach protected area design in terms of network robustness. Our goal is to characterize the topology of nearshore metapopulation networks and their response to perturbation, and to identify critical subpopulations whose protection would reduce the risk for stock collapse. We define metapopulation networks using realistic estimates of larval dispersal generated from ocean circulation simulations and spatially explicit metapopulation models, and we then explore their robustness using node-removal simulation experiments. Nearshore metapopulations show small-world network properties, and we identify a set of highly connected hub subpopulations whose removal maximally disrupts the metapopulation network. Protecting these subpopulations reduces the risk for systemic failure and stock collapse. Our focus on catastrophe avoidance provides a unique perspective for spatial marine planning and the design of marine protected areas.

Many nearshore marine species are sedentary as adults, with home ranges on the order of 0.1–10 km (15). Longer distances are traveled as newly spawned larvae (15). During this stage, larvae advect primarily by means of ocean currents, potentially traveling distances orders of magnitude greater than those traveled as adults (i.e., ~100 km) (15–18). As a direct consequence of this larval dispersal stage, nearshore marine species exist in systems of interconnected subpopulations [3, 4]. Typically, larval connectivity has been estimated using simple statistics of ocean circulation and Euclidean distance (e.g., 3, 4, 19). This approach has been used extensively to gauge criteria for metapopulation persistence and in the design of protected areas (3, 4), but it ignores several important details (17, 18). For instance, theoretical studies have shown that heterogeneity, asymmetry, and temporal variability in larval connectivity patterns are key properties that affect the persistence of metapopulations (20–23). To a large degree, these properties are not captured by standard empirical methods and remain elusive in realistic settings.

To capture the complexity of larval connectivity patterns, we combine ocean circulation simulations with realistic metapopulation modeling. Over the past decade, simulation approaches to quantifying larval connectivity have grown in prominence and have been used to investigate the scales of larval dispersal (16–18, 24), the population genetic structure of nearshore species (25, 26), and processes affecting the composition of nearshore communities (27), to name a few examples. Here, our goal is to use ocean circulation simulations to explore how nearshore metapopulations respond to perturbation and to identify specific nearshore regions that are key to metapopulation robustness. We focus our attention on the dynamics of several commonly fished species in the Southern California Bight (Fig. 1): kelp bass (*Paralabrax clathratus*), kelp rockfish (*Sebastodes atrivittatus*), ocean whitefish (*Caulolatilus princeps*), red sea urchin (*Strongylocentrotus franciscanus*), opaleye (*Girella nigricans*), California halibut (*Pareques californicus*), and California sheephead (*Semicossyphus pulcher*), whose life history characteristics span a broad range. These species were used as part of a recent MPA planning program in the Southern California Region (9), and our methods use the numerical models developed for this process.

Patterns of larval connectivity for each study species are quantified in a two-step process. First, Lagrangian probability

connectivity | larval dispersal | protected area design | network theory | Lagrangian simulations

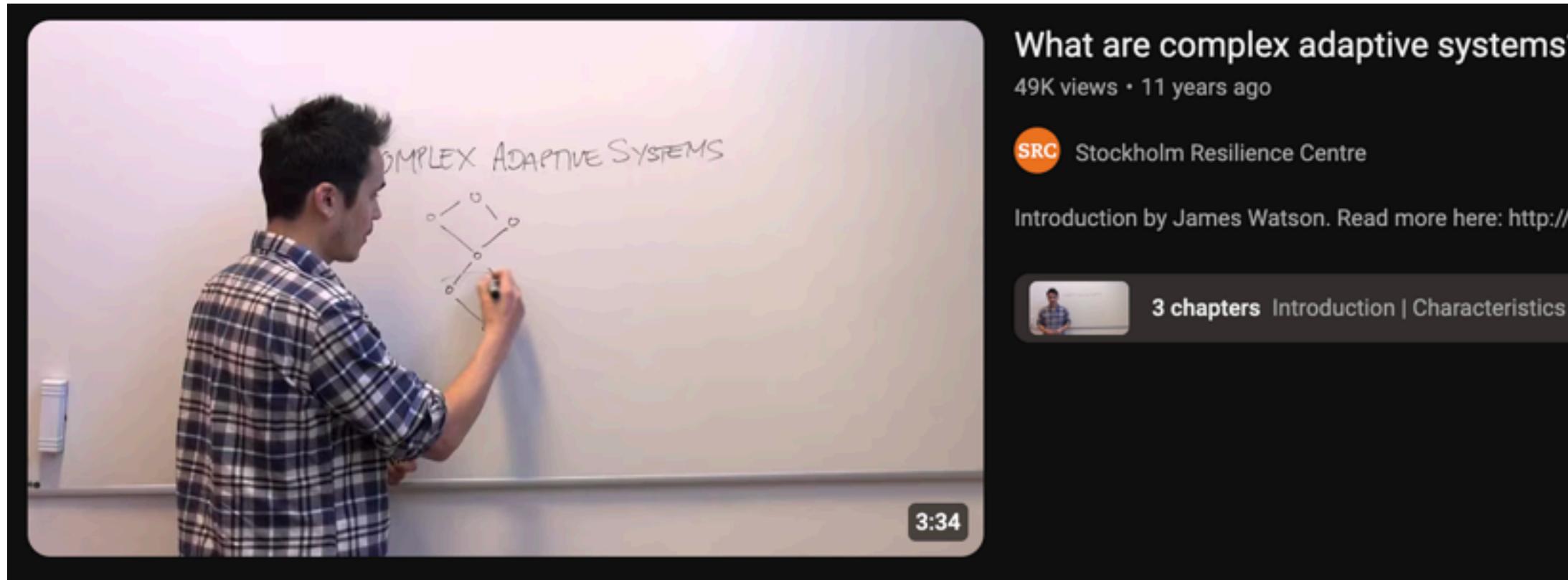
Nearshore marine ecosystems are some of the most productive and diverse environments on earth, maintaining a wide variety of organisms and providing essential food and services to the global population. Unfortunately, they are also under increasing stress from perturbations, such as oil spills, climate change, and overfishing, and are at risk for losing their productive output (1, 2). Mitigating the impacts of these perturbations is difficult because most nearshore marine species exist in a spatially complex system of connected subpopulations; stress placed at one location may detrimentally reduce stock levels at many others (3, 4). Quantifying patterns of connectivity is crucial to our ability to manage these systems effectively. For example, marine protected areas (MPAs) have emerged as an important tool for conservation and fisheries managers tasked with maintaining nearshore systems and accounting for the mutual demographic dependence of populations (3–9). Current approaches to their design center on either protecting essential habitats (5, 5, 9) or maximizing economic goals (10, 11). We provide an alternative and consider the design of MPAs as a problem of metapopulation network robustness, here defined as the ability of a system to withstand perturbation (12). Our goal is to account for patterns of connectivity and identify key regions whose protection from perturbation safeguards against systemic failure and stock collapse (12–14).

Author contributions: J.R.W., D.A.S., B.E.K., S.M., and S.D.G. designed research; J.R.W., S.M., and D.A.S. performed research; J.R.W. analyzed data; and J.R.W., D.A.S., B.E.K., S.M., A.R., and S.D.G. wrote the paper.
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 To whom correspondence should be addressed. E-mail: jwatson@princeton.edu.
 This article contains supporting information online at www.pnas.org/lookup/suppl/doi:10.1073/pnas.1111461108.
 DOI: 10.1073/pnas.1111461108

PNAS Early Edition | 1 of 7

Paper (10-30p)

Communicate



GroupSeries

Measuring and Managing the Complexity of Socio-Environmental Systems

James Watson

Assistant Professor, Oregon State University
email: jrwatson@coas.oregonstate.edu, web: jwatson.ceoas.oregonstate.edu/

Oregon State University THE PREDICTION LAB

0:10 / 56:57



Go Alpha Lo

Climate Water Project

How to restore the water cycle, and how that helps with hydrating the earth and soil, replenishing groundwater, restore rains in drought areas, lessen flooding, and slow down climate change.

By Alpha Lo · Over 4,000 subscribers

Lets talk about team research

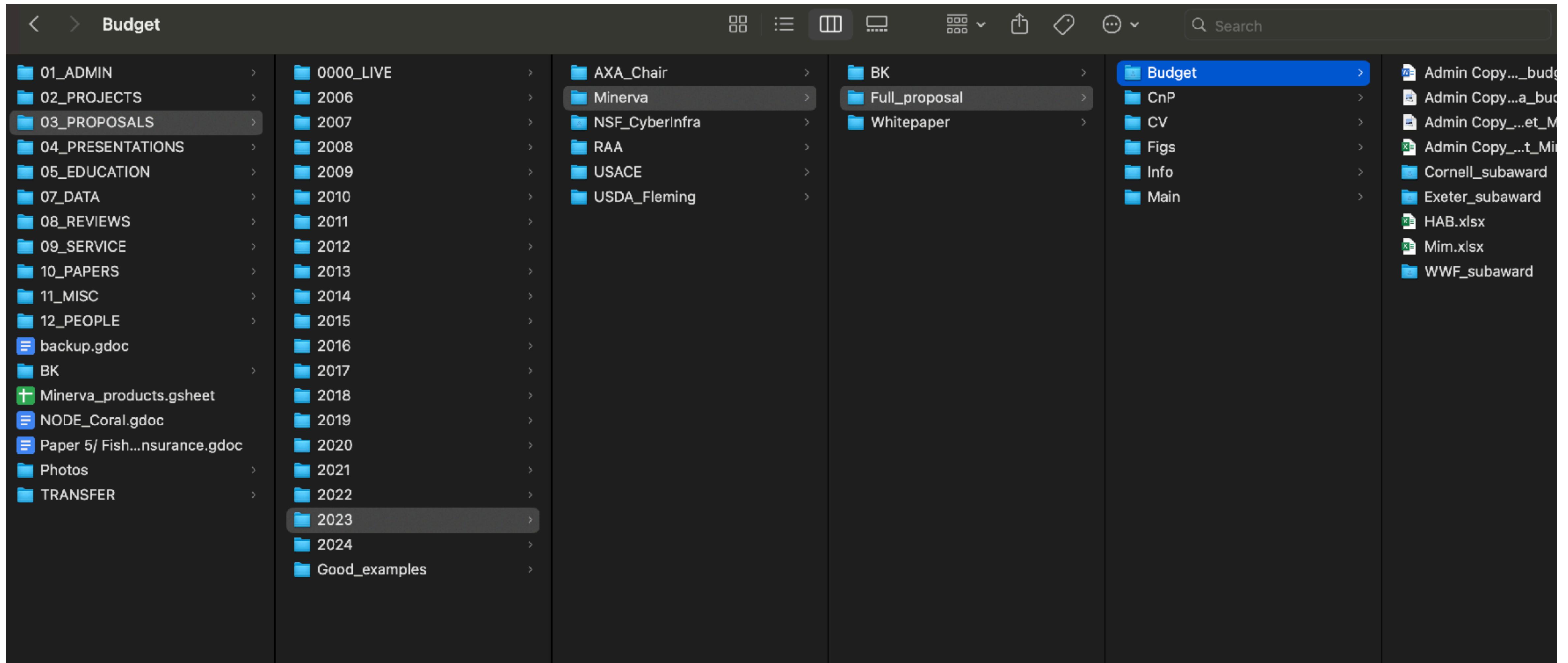
Digital Infrastructure

Lets talk about team research

Digital Infrastructure

- These are things I want you to explore in this class
- I want you to develop your own process for team research
- Here's what I do...

Epic folder organization



Clearly delineate roles

- Project leader
- Meeting note taker
- Who is doing what
- Set the collaboration norm (opt in vs opt out)



The Master Doc

- Record everything
- Especially your collaboration norm and policies
- Every meeting, notes should be taken
- Google doc is great. I am a big fan of the infinite one doc

Project Mim Master Doc

July 9, 2024 – Mim All Hands

Present

James, John W, Rebecca, Cassius

Meeting Agenda

Tech updates / show new front end to AI Articulator (John, Cassius)

Show new Pro Forma: Realistic Sales (sales team)

Discuss realistic pricing

Discuss AI Articulator only business plan

College Source and TES, and their degree planner: discuss business risk (how can we get these data?).... TES is really important.

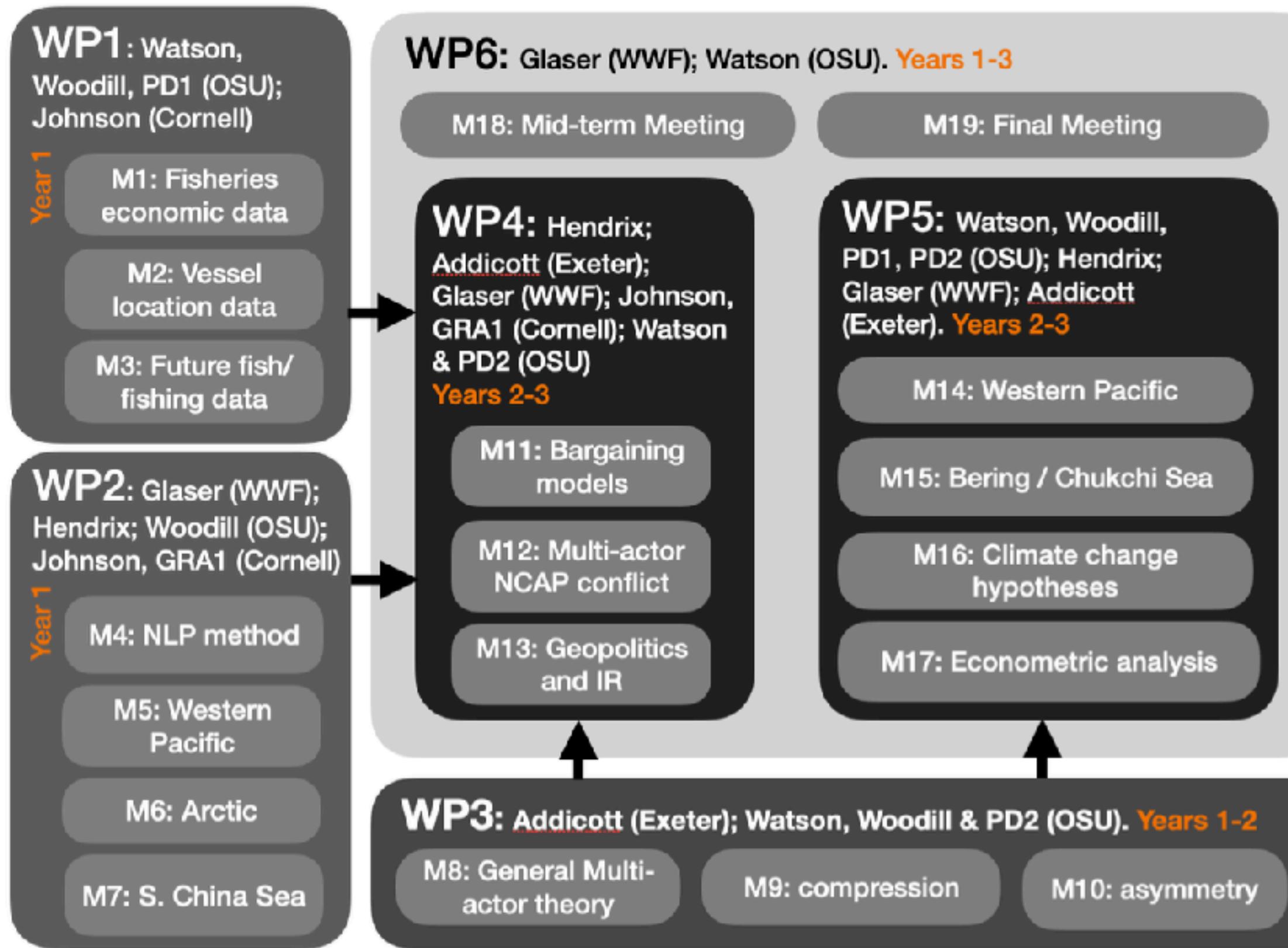
Can we make an equivalent database starting now... will soon be deep in time.

Or can we buy TES data for all use?

Can we train an AI on TES data (not use their data)?

Rebecca – other companies to research (~~Stellic~~)

You need a schedule



PROJECT SCHEDULE, MILESTONES, AND DELIVERABLES

Milestones and Schedule

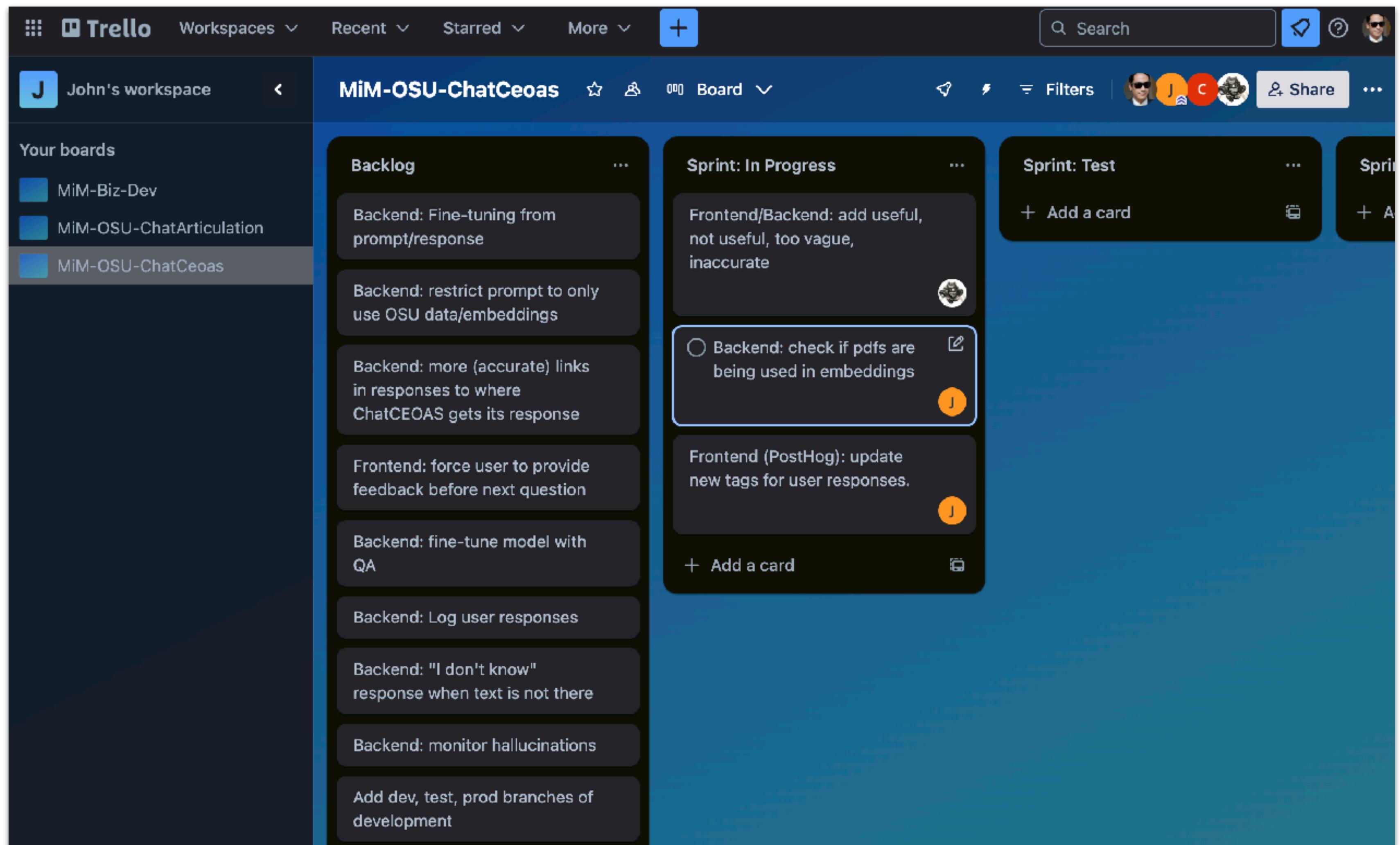
This project will be conducted over a 36-month period with all-hands meetings every year. The project schedule and milestones (M) includes:

Work package and Milestone	Month	1-6	6-12	12-18	18-24	24-30	30-36
Work package 1: Fisheries Economic, Oceanographic and Vessel Location Data							
M1: Fisheries economic data	x						
M2: Vessel location data	x						
M3: Future fish/fishing data	x	x					
Work package 2: Fisheries Conflict Databases							
M4: NLP conflict data method	x						
M5: Conflict data (Western Pc)	x	x					
M6: Conflict data (Bering Sea)	x	x					
M7: Conflict data (S. China Sea)	x	x					
Work package 3: Multi-actor Natural Capital Asset Pricing Theory							
M8: Multi-actor NCAP theory	x	x	x	x			
M9: Compression theory		x	x	x			
M10: Asymmetry theory			x	x	x		
Work package 4: Fisheries Conflict Theory							
M11: Bargaining modeling			x	x	x		
M12: multi-NCAP and conflict				x	x		
M13: Geopolitical context				x	x		
Work package 5: Case-study Application							
M14: Western Pacific NCAP			x	x	x		
M15: Bering Sea NCAP			x	x	x	x	
M16: Climate change hypotheses				x	x	x	
M17: Econometric analysis				x	x	x	
Work package 6: Stakeholder Interaction							
M18: Mid-term feedback			x				
M19: End-of project feedback							x

Figure 3. Organization chart for the project, describing the major work packages (WP), Milestones (M) and the project team members assigned to each work package (PD: post-doc; GRA: graduate student assistant).

You need project management

- A Kanban board
- A Trello board
- A spread sheet
- The master doc
- Some place to write down who is doing what, and when things are meant to be finished



Effective Communication

- Slack: only use for short messages (not important actionable)
- Emails: for important actionables.
- A weekly ceremony:
 - Monday Open
 - Friday Close
- State what you're going to do. What you accomplished. Radical honesty (in work) is important.



SCRUM

- Short sprints
- Periodic assessment

Integrated Development Environment (IDE)

- Scientific Code
 - R
 - Python
 - Matlab
 - Julia
 - C
 - Javascript
- Visual Studio
- Etc etc....

The screenshot shows the Posit website with a navigation bar at the top. Below the navigation, there are two main sections: "1: Install R" and "2: Install RStudio".

1: Install R
RStudio requires R 3.6.0+. Choose a version of R that matches your computer system.
R is not a Posit product. Please visit the R website below to download and install R. By doing so you accept the obligations and all liability associated with the R software and the R website.
[DOWNLOAD AND INSTALL](#)

2: Install RStudio
Meet the Visual Studio family

Visual Studio | The most comprehensive IDE for .NET and C++ developers on Windows. Fully packed with a sweet array of tools and features to elevate and enhance every stage of software development.
[Learn more →](#)
[Download Visual Studio](#)

Visual Studio Code | A standalone source code editor that runs on Windows, macOS, and Linux. The top pick for JavaScript and web developers, with extensions to support just about any programming language.
[Learn more →](#)
By using Visual Studio Code you agree to its [license](#) & [privacy statement](#)
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Wondering which tool is best for you? We can help.

LLMs and AI

ChatGPT

Give me some R code for modeling a lotka volterra predator prey system

Here's a clear and concise example of how to model the Lotka-Volterra predator-prey system using R:

Step-by-step approach:

Step 1: Define the differential equations.

Step 2: Use `deSolve` package to solve the system.

Step 3: Plot the results to visualize the predator-prey dynamics.

Here's the complete R code:

```
# Install and load required package
if (!require("deSolve")) install.packages("deSolve")
library(deSolve)

# Define the Lotka-Volterra model
lotka_volterra <- function(t, state, parameters) {
  with(as.list(c(state, parameters)), {
    ...
```

Ask anything

+ CPT-4.5

Rstudio IDE

flights-example.R

```
library(nycflights13) ## package containing flights dataset
library(lubridate)
library(dplyr)
library(ggplot2)

head(flights, n = 3)
daily <- flights %>%
  mutate(date = make_date(year, month, day)) %>%
  count(date) %>%
  mutate(wday = wday(date, label = TRUE))
head(daily, n = 3)
ggplot(daily, aes(wday, n)) +
  geom_boxplot(outlier.colour = "hotpink") +
  labs(x = "Weekday", y = "Flights",
       subtitle = "Number of 2013 New York Flights Each Weekday")
```

Environment History Connections Tutorial

Global Environment

daily 365 obs. of 3 variables

\$ date: Date[1:365], format: "2013-01-01" "2013-01-02" ...

\$ n : int [1:365] 842 943 914 915 720 832 933 899 902 ...

\$ wday: Ord.factor w/ 7 levels "Sun"<"Mon"<"Tue"<"...": 3 ...

Console Terminal Jobs

~/Documents/Flights/

A tibble: 3 x 19
 year month day dep_time sched_dep_time dep_delay arr_time sched_arr_time arr_delay carrier
 <int> <int> <int> <int> <dbl> <int> <int> <dbl> <chr>
1 2013 1 1 517 515 2 830 819 11 UA
2 2013 1 1 533 529 4 850 830 20 UA
3 2013 1 1 542 540 2 923 850 33 AA
... with 9 more variables: flight <int>, tailnum <chr>, origin <chr>, dest <chr>, air_time <dbl>,
distance <dbl>, hour <dbl>, minute <dbl>, time_hour <dttm>
> daily <- flights %>%
+ mutate(date = make_date(year, month, day)) %>%
+ count(date) %>%
+ mutate(wday = wday(date, label = TRUE))
> head(daily, n = 3)
A tibble: 3 x 3
 date n wday
 <date> <int> <ord>
1 2013-01-01 842 Tue
2 2013-01-02 943 Wed
3 2013-01-03 914 Thu
> ggplot(daily, aes(wday, n)) +
+ geom_boxplot(outlier.colour = "hotpink") +
+ labs(x = "Weekday", y = "Flights",
+ subtitle = "Number of 2013 New York Flights Each Weekday")

Number of 2013 New York Flights Each Weekday

Flights

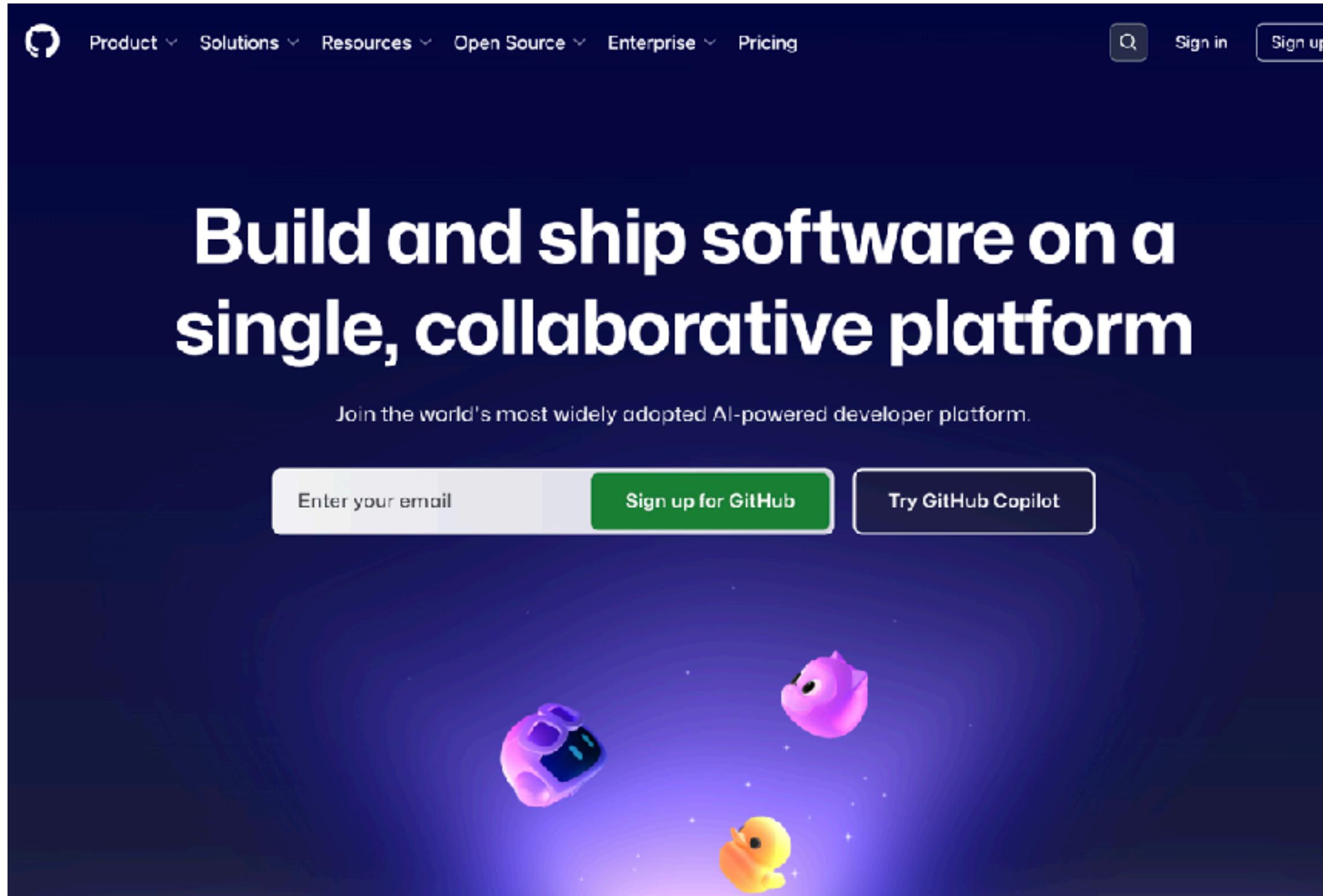
Weekday

Sun Mon Tue Wed Thu Fri Sat

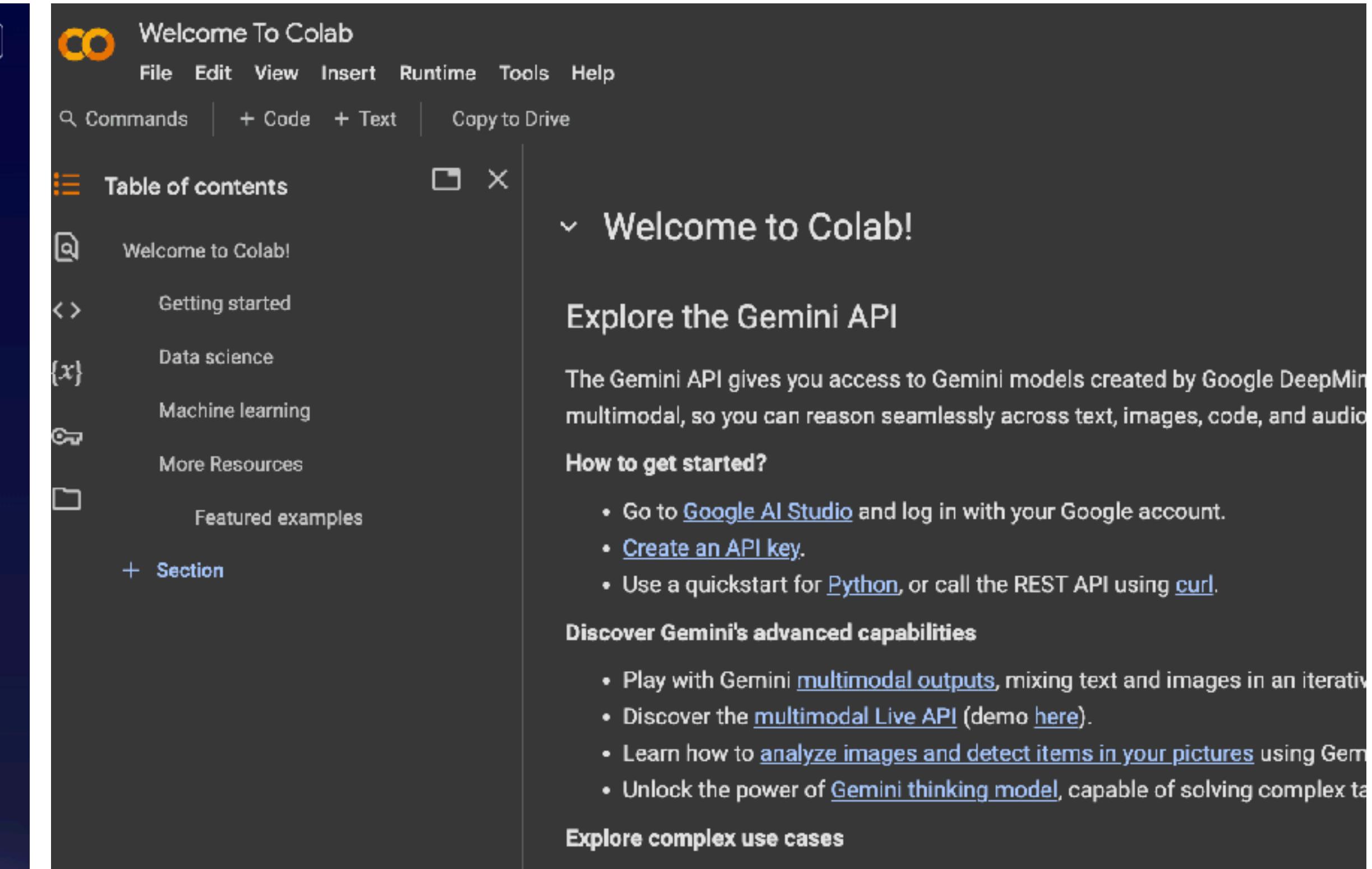
This is now the industry standard
Code either works or it doesn't

Version control and collaboration

Github



This is now the industry standard
Everyone uses Github for version control and collaboration



Google colab

Now over to you

- Setup your digital infrastructure
 - Drive folder (or similar)
 - Master doc
 - Trello board
 - Slack
 - Github repo
- Have your first meeting
 - ID meeting leader
 - Create an agenda (focus on brainstorming your project)
 - Take notes (in master doc; assign roles / jobs, schedule)
 - End with actions... updated Trello board

Week 2

Lecture 2 - Wednesday

- Setup your team's digital infrastructure
- Have your first team meetin
- Install R and Rstudio and make sure everyone has it working (15 mins)
- Make a GitHub repository for term project (10 mins)
- Co-write readme with your team. Learn how to push/pull/branches/merge (10 mins)

Week 2

Lab - Thursday

- Coding challenge: develop R code to simulate a Lotka-volterra predator-prey system. Use forward Euler integration, which is basically a for-loop, to simulate changes in the predator and prey populations over time. Save population time series as separate csv files. Then develop a separate R-script for plotting these time series. Save these plots as PNG figures. Create a GitHub repo for this coding challenge, and make the README.md, and embed these figures. Try to include a description of the equations that you just solved using R.
- practice using collaborative digital infrastructure (drive, core docs, schedule, meeting, roles and responsibilities, collaborative coding).
- co-developing a GitHub repo

