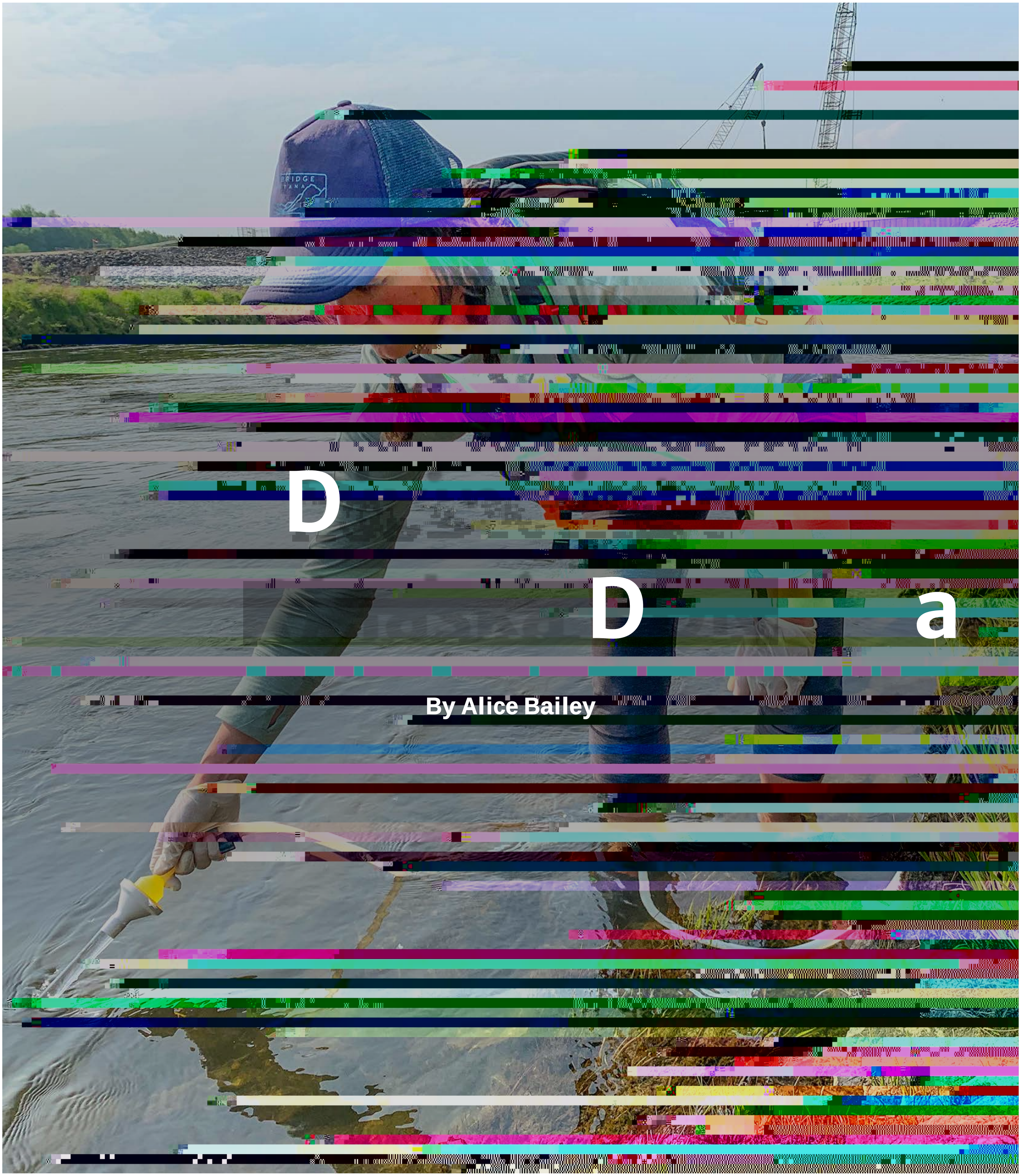
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By Alice Bailey

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All along the salmon migration route from the Bering Sea, technicians at research sites collect the particles with filtering devices that function like water vacuum cleaners. As water is sucked up through a hose, everything floating in it is trapped on a small, round filter.

The filters are carefully packaged and sent to UAF's Ichthyology and Evolution Lab in Fairbanks, where Harings and her team are waiting to extract information from what looks like a circle of brown pond scum.

The scum in fact contains valuable information about who is in the river.

"We are extracting environmental DNA, which is DNA that exists in the water from any kind of organism that's there, including plants and animals," Harings said. "In this case, we are targeting Chinook and chum salmon DNA."

Last spring, Harings carefully processed filters from five diGerent locations in the Yukon River drainage system. She worked with undergraduate Kristen Reece, who is in UAF's

The goal is to test a cost-effective way to help estimate the number of adult salmon arriving at spawning areas, known as escapement. The complex mixture of DNA extracted from the filters will be put into a sequencing machine. Genomics technology, or bioinformatics,

“With this project, we have the opportunity to have a better understanding of escapement

called bioinformatics — is rapidly evolving, allowing for faster and more affordable access to genetic information.

“Nowadays, all kinds of things are possible. We can cheaply and easily access volumes of data that, 40 years ago, would have taken the work of an entire government agency,” said Andrés López, an associate professor at the College of Fisheries and Ocean Sciences and the Curator of Ichthyology and Aquatics at the UA Museum of the North. As director of the Ichthyology and Evolution Lab, he also advises Harings on her environmental DNA study of Chinook and chum salmon.

A DNA molecule, which looks like a twisted ladder (double helix), is composed of two strands of millions, sometimes billions, of chemical compounds called nucleotides.

Genes are specific sequences of the nucleotides. The order and composition of genes determines how an organism grows, develops and reproduces. The study of these genes is known as genomics.

In the lab, researchers use machines to break cells open and extract the DNA molecules. Heat is applied until the two strands of the double helix unravel, then scientists duplicate the sequences they are interested in studying.

“Once DNA is isolated, you have two options: to dive into one aspect of an organism, or to look at an ecosystem more broadly,” explained López.

More data is being generated every day — which continually broadens the types of questions that scientists can ask.

“In biology, you are going to have a hard time finding any sort of question that is not helped by access to genetic data,” said López. Harings’ salmon project is just one example.

CFOS faculty and students are working within three general realms of genomics: population genetics, evolutionary genetics and environmental DNA analysis.

Using population genetics, scientists look at tissue samples to see what individuals of a single species are doing in a certain place, how they got there and the extent to which they interbreed with one another across their range.

Graduate student Sydney Almgren is looking at the genetic diversity of Pacific herring in the eastern Bering Sea. Herring are caught as bycatch in the pollock trawl fishery, and her project will help managers to know if diGerent spawning populations are genetically distinct.

With an evolutionary genetics approach, scientists recreate the entire sequence of an organism's DNA to understand how species evolved. The art of genome assembly is like piecing together a puzzle, and public databases help fill in the missing pieces.

"We are starting to use genomics to get at the real ability of species to survive and flourish, or not, in their environment, how they have adapted over millions of years and how quickly they can change," said CFOS assistant professor . "If they can't adapt, they have to move or die."

Glass is creating a genomic database of key species in Alaska.

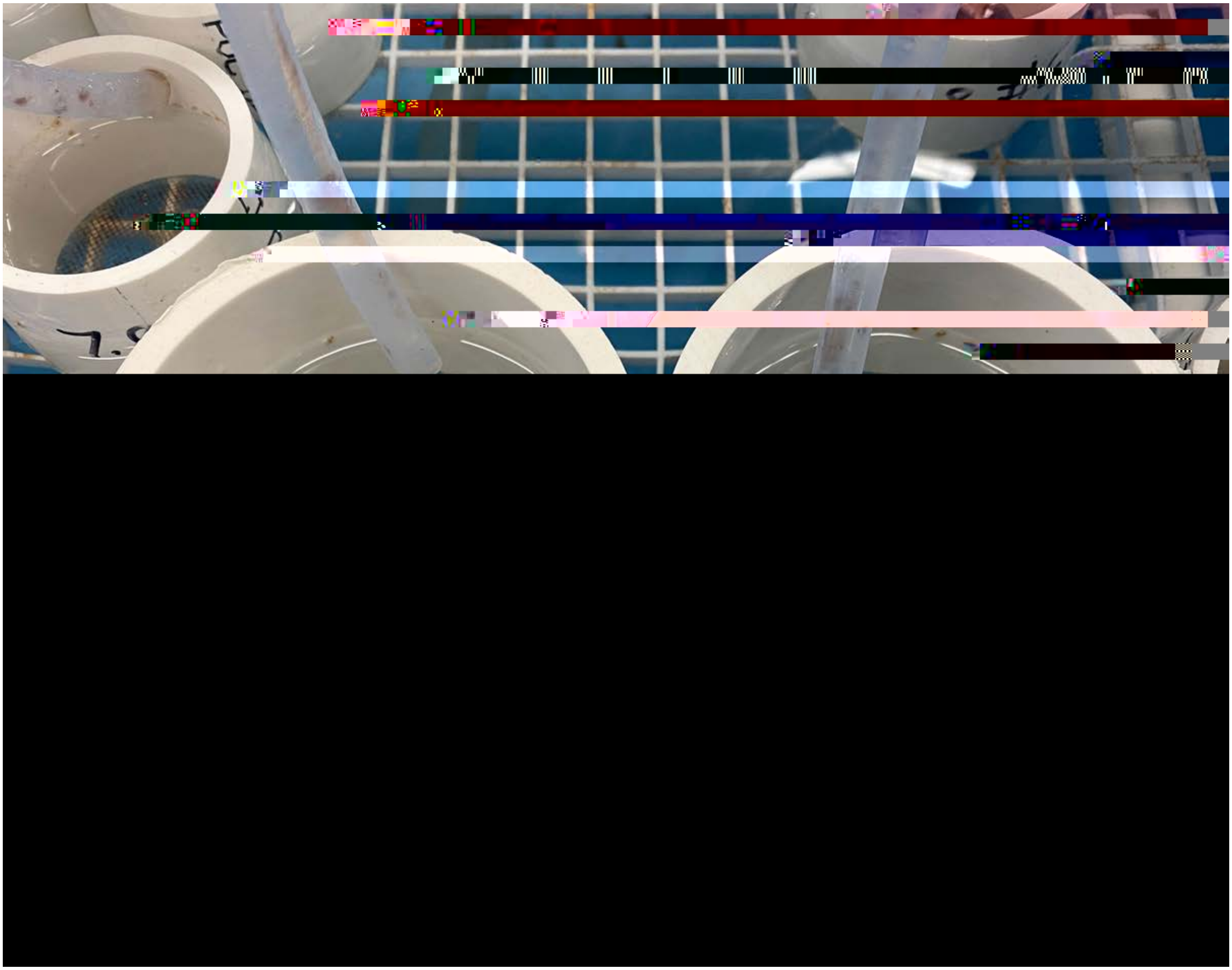
metabarcoding allows scientists to rapidly characterize biodiversity by analyzing genetic sequences and matching them to a database.

The method is also helping understand the marine phase of salmon lives.

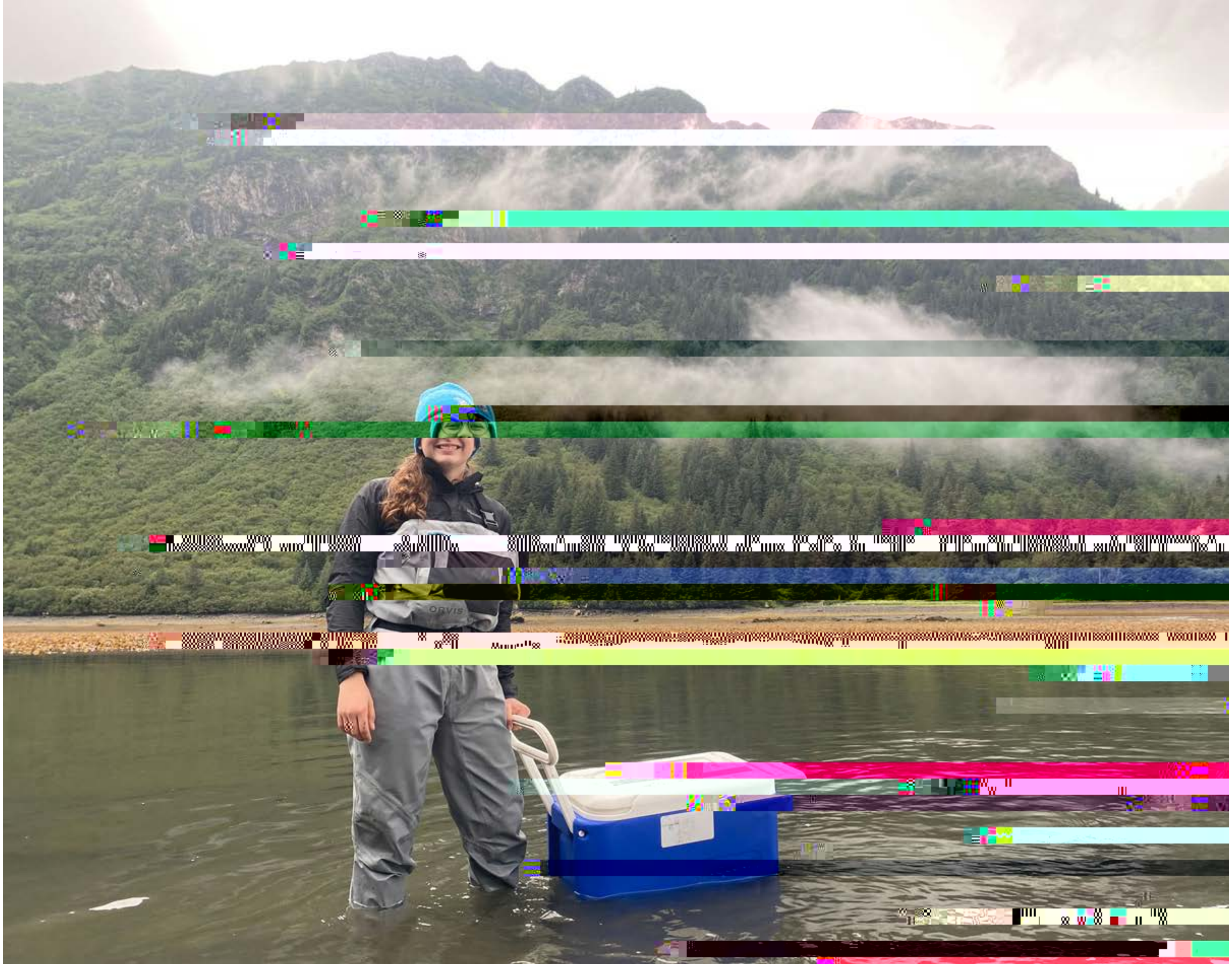
“This year’s winter surveys successfully used eDNA to identify the presence of salmon and their potential predators on the high seas,” said CFOS professor Megan McPhee, who is based in Juneau. “It promises to be an important tool in the study of salmon ocean ecology.”

While there is not yet a genomics degree at UAF, genomics courses are oGered across diGerent units. CFOS faculty said skills learned for DNA analysis are applicable across the sciences and are highly desired by employers.

“The natural path is to start building those skills,” said López. “Even if someone doesn’t want to be in the field handling stinky fish, they could become a superstar by analyzing data on the computer.”



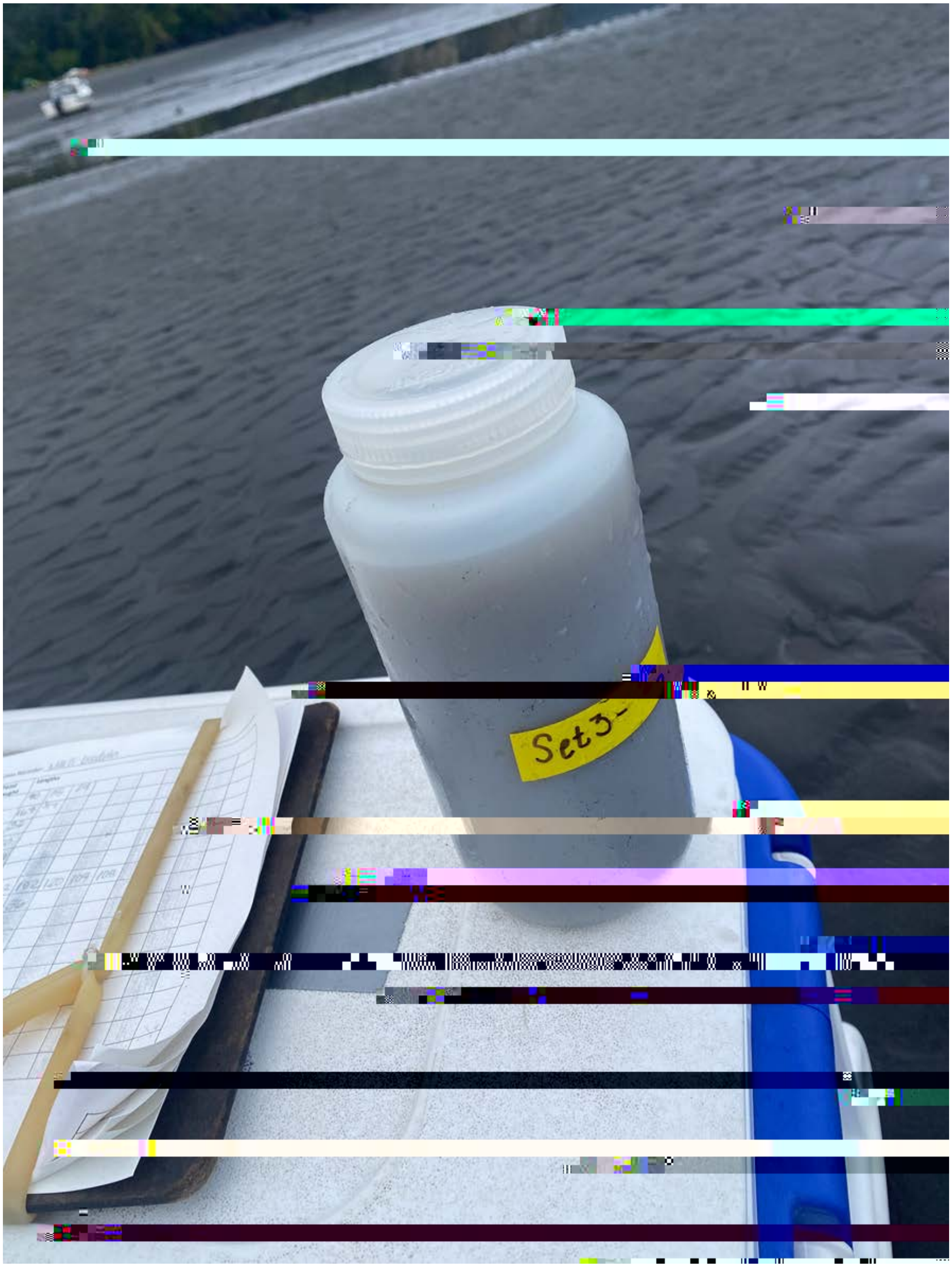
CFOS graduate student Shelby Bacus is working with assistant professor



Glass’ graduate student Maris Goodwin is using eDNA to study how w

diGerent sites, by comparing DNA found in the water and sediment with creatures she catches with a seine net, such as flatfish and salmonids.

“My project addresses the need to develop rapid, accurate and cost-e g cient tools to monitor potential ecosystem shifts caused by a warming climate,” said Maris.



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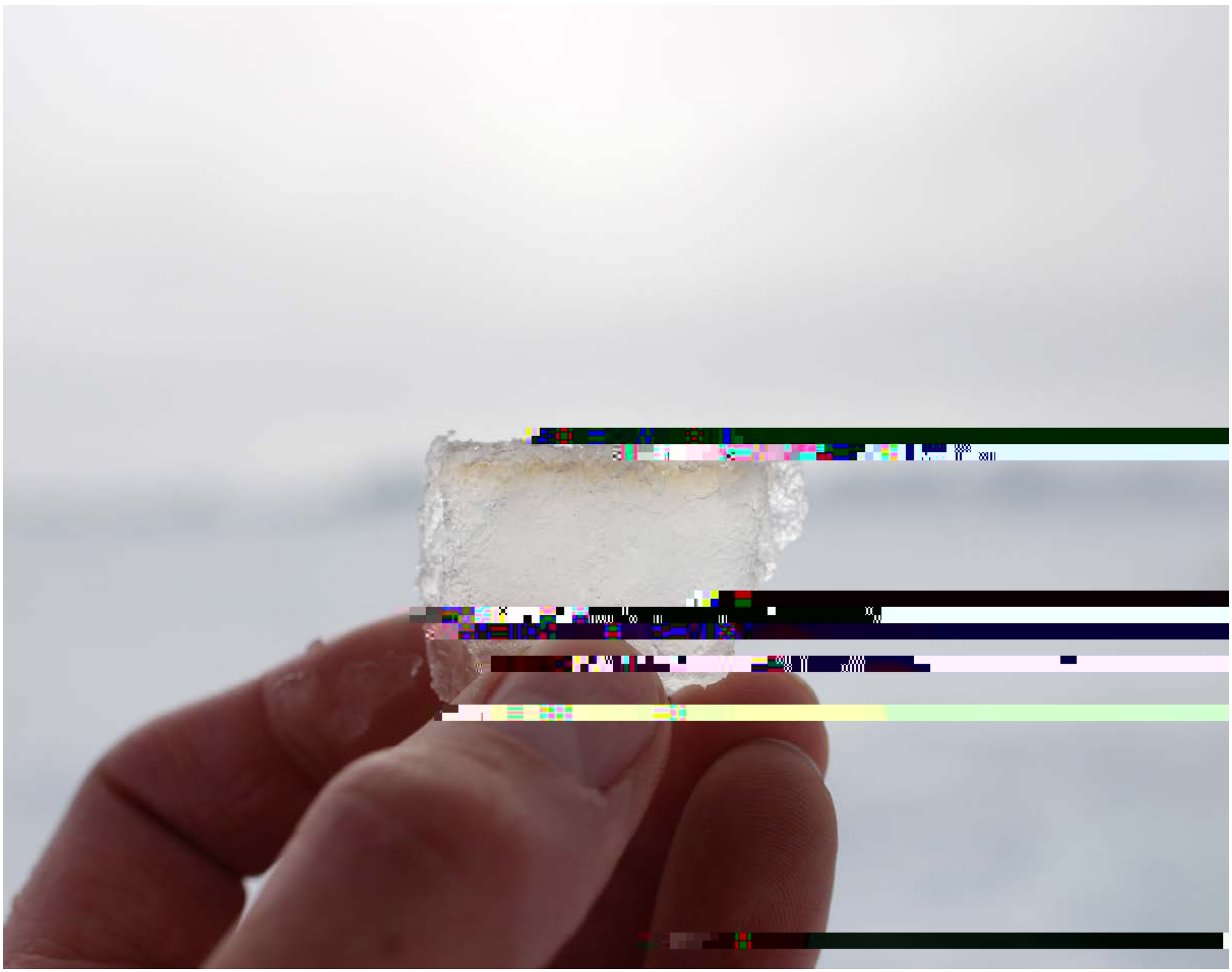
CFOS assistant professor Gwenn Hennon's lab, where several UAF

Despite their tiny size, phytoplankton are important because they make up most of the biomass in the oceans. They also do about half of the carbon fixation and oxygen production on the planet. So it's safe to say that changes to these microbes have a ripple eGect up the food chain.



Sea ice freezes with tiny cavities that are habitat for these phytoplankton, which provide a substantial amount of oxygen to the ocean and food for the zooplankton that Arctic cod and other animals eat.

Hennon’s graduate student Kyle Dilliplaine is interested in how increased light levels (caused by decreases in snow cover) and crude oil contamination affect diatoms, a large type of algae, living in Arctic sea ice. He exposes diatoms and other phytoplankton collected in ice cores to different conditions in Hennon’s lab. Through a process called transcriptome sequencing, he hopes to create an index of how organisms react to light and oil.

“There will be some species that are unaffected, and perhaps even prefer, certain conditions, whereas others will be negatively impacted,” he said.