

AURORA

A woman wearing a blue baseball cap with a logo, a green long-sleeved shirt, and dark pants is standing in a river. She is using a yellow pipette to collect water samples. She has a backpack and is wearing gloves. In the background, there are construction cranes and a bridge under construction.

Diving into Alaska's DNA

By Alice Bailey

Above: Maggie Harings uses a portable filtration device in June 2022 to collect salmon DNA in the Chena River near the Chena River Lakes Flood Control Project's Moose Creek Dam. Photo by Erik Schoen.

Graduate student Maggie Harings is after tiny particles suspended in the Chena River.

She can't see them, but she knows they exist. She also knows they carry valuable information about Chinook and chum salmon, those important but declining energy sources for people, animals and Interior Alaska's ecosystems.

Each summer, the salmon swim up the Yukon River, take a right turn at the Tanana River and then take a left on the Chena before passing Fairbanks. As they swim through town, they slough off microscopic tissues and cells, just as humans do as they move through the world.

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.

Helping detect spawners

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

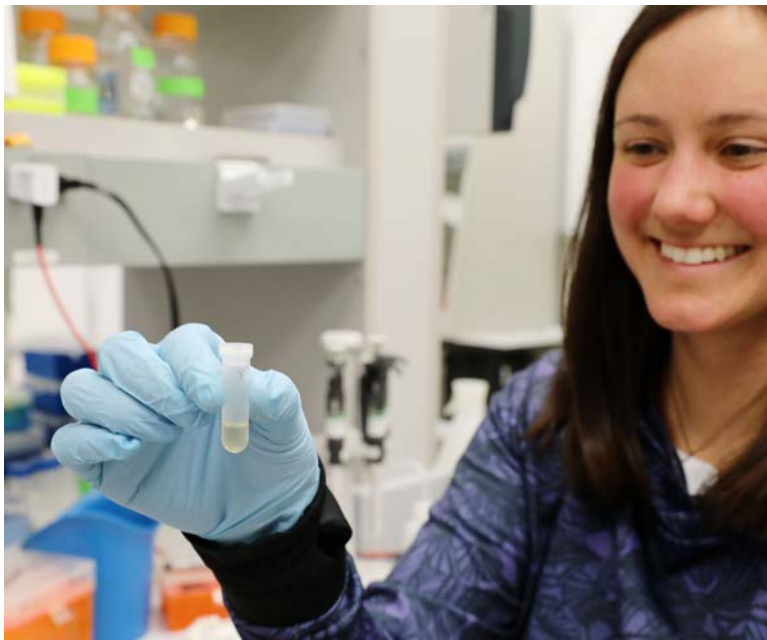
"We are extracting environmental DNA, which is DNA that exists in the water from any kind of organism that's there, including plants and animals," Harings said. "In this case, we are targeting Chinook and chum salmon DNA."

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

Biomedical Learning and Student Training program.

In the basement of the University of Alaska Museum of the North, Harings and Reece isolated the DNA from other stuff caught on the filters through a series of steps that included rinsing and chemical reactions. They used a fancy dropper called a pipette to move the solution into tiny bottles and spun it all to remove unwanted material from the DNA solution.





Top: Kristen Reece carefully transfers a reagent into a tube during the DNA isolation process in the Ichthyology and Evolution Laboratory at the University of Alaska Museum of the North in summer 2022. Bottom: In the same lab, Maggie Harings holds a tube containing salmon DNA collected from one of five Yukon River tributaries. Photos by Alice Bailey.

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, determines how much Chinook and chum DNA is in each sample. That information is used to estimate the concentration of each species swimming by weirs and counting towers.

This data could help fill in gaps when counting fish is impossible during periods of high water — a problem that is happening more frequently as the climate changes.

“With this project, we have the opportunity to have a better understanding of escapement patterns and abundance, which directly impacts a vital food source for the subsistence community,” said Reece.

Reece and Harings collaborate with CFOS alum **Allison Matter '12, '17**, who is assisting with eDNA filtration as an Alaska Department of Fish and Game biologist.

“Projects like this give us the opportunity to see how a new technique might work without compromising data, while building relationships within the scientific community,” Matter said.

A long way from fruit flies

A hundred years ago, scientists used fruit flies to figure out core principles of genetics, long before people understood the structure and workings of DNA.

Every cell in an organism contains a complete set of the species genome (genes passed from parents to offspring), which is why researchers only need a tiny piece of an organism’s tissue to understand its genetic make-up. The technology used to acquire, store and analyze DNA — a field

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

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

“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.

Genomics branches out

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 different 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 **Jessica Glass '15**. “If they can't adapt, they have to move or die.”

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

“We need more efforts to coordinate eDNA sampling efforts across the North Pacific, like an atlas for marine species, where you can publicly access data and see where it’s collected to not duplicate efforts,” she said.



Emily Reynolds, Karen Grosskreutz and Lindsey Stadler use beach seines in April 2022 to collect DNA from invertebrates, fishes, seabirds and marine mammals to understand biodiversity in Kachemak Bay. Photo courtesy of Jessica Glass.

The third type of genomics research at CFOS, eDNA analysis, is like a cousin of more traditional genomics, in which genetic evidence can be used as a detector of whether or not a species is present at a certain location. This method, used by Harings in her salmon research, is becoming increasingly cost-effective and portable.

“With one water sample, we can target marine mammals, birds, invertebrates and fishes at the same time,” explained Glass.

Metagenomics, or metabarcoding, is a type of eDNA analysis that looks at the collection of genomes found in the environment. Similar to scanning a barcode at a grocery store, eDNA

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.

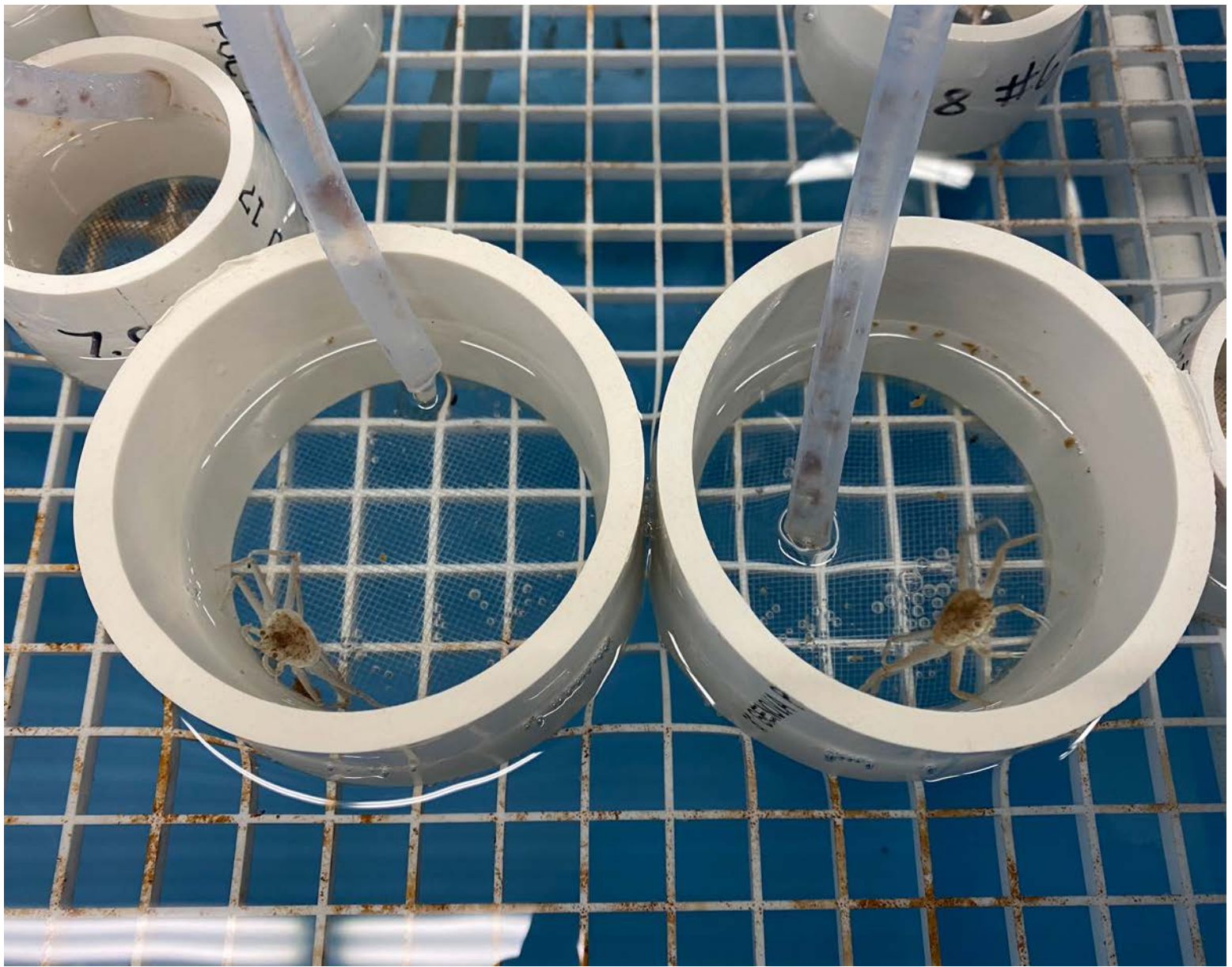
“This year’s winter surveys successfully used eDNA to identify the presence of salmon and their potential predators on the high seas,” said CFOS professor Megan McPhee, who is based in Juneau. “It promises to be an important tool in the study of salmon ocean ecology.”

Students explore and build skills

While there is not yet a genomics degree at UAF, genomics courses are offered across different 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.”

In addition to classes, here are some other genomics projects that UAF students are working on:



Juvenile crabs collected from the ocean are placed in separate treatments at the NOAA laboratory in Kodiak in August 2022. Shelby Bacus collects samples to calculate gene expressions every 60 days. Photo by Shelby Bacus.

Shelby Bacus

CFOS graduate student Shelby Bacus is working with assistant professor Amanda Kelly to study the health of Kodiak Tanner crabs, which are often sold commercially as snow crabs. Bacus has 600 crabs in the

Kodiak lab. She exposes them to different treatments then performs analyses on samples of them at UAF. Specifically, she is looking for gene expressions of proteins that develop when fish experience heat shock.

Bacus is interested in how these gene expressions change as the ocean becomes warmer and more acidic.

“Understanding how crab populations fluctuate under the influence of climate change will allow us to better manage the Tanner crab fishery in Alaska and associated ecosystems,” said Bacus.



Shelby Bacus deploys a benthic sled near Kodiak to collect juvenile crabs living on the seafloor in August 2022. Photo by Emily Ryznar.



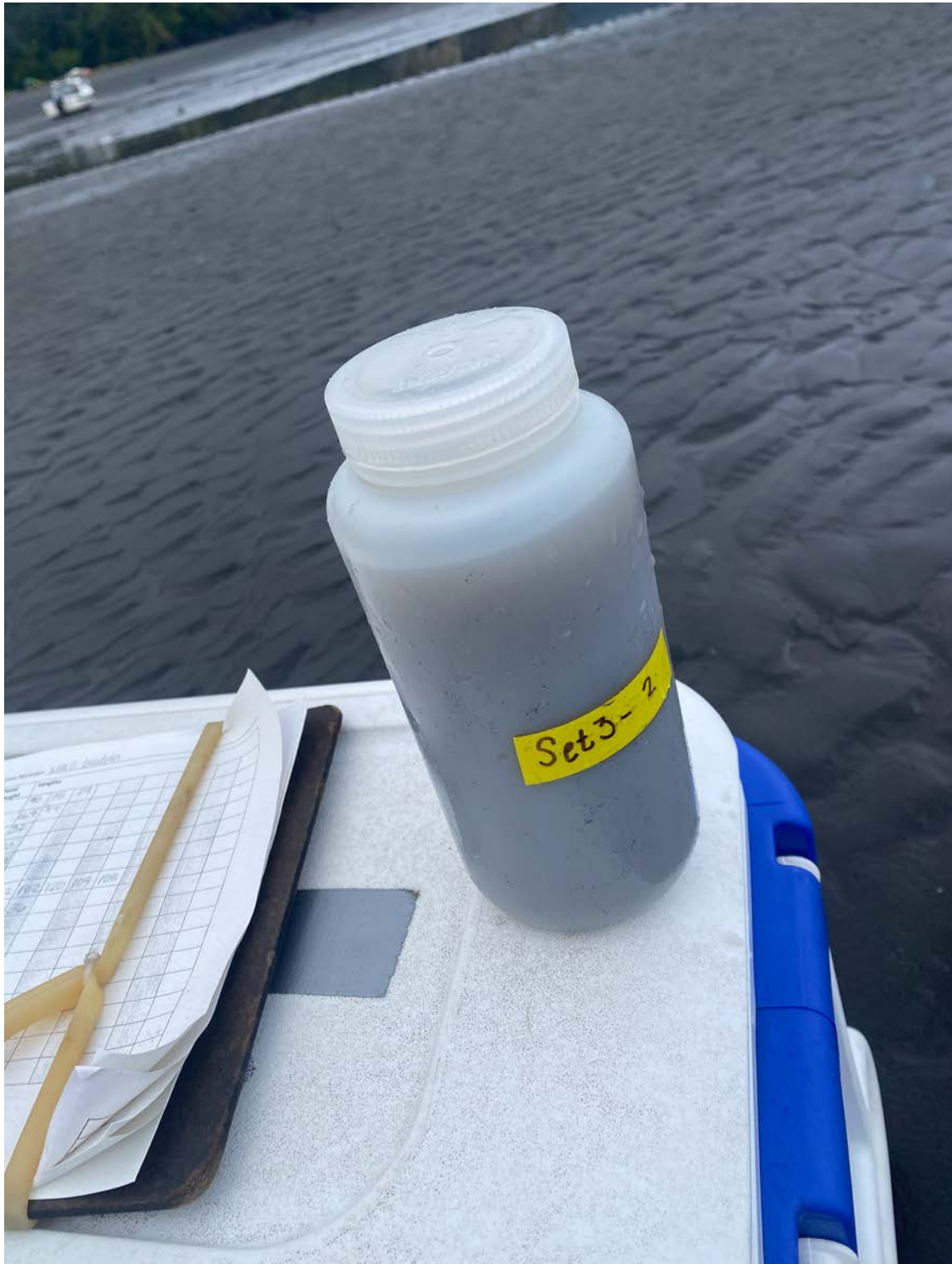
Maris Goodwin wades in Kachemak Bay with a cooler containing water samples in August 2022. The samples are on ice to prevent eDNA degradation. Photo by Emily Reynolds.

Maris Goodwin

Glass' graduate student Maris Goodwin is using eDNA to study how coastal ecosystems in the Gulf of Alaska are affected by environmental conditions such as glacial melt. She is measuring biodiversity at

different 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-efficient tools to monitor potential ecosystem shifts caused by a warming climate,” said Maris.



A one-liter water sample, collected near a beach seine site, sits on a cooler on Kachemak Bay in August 2022. The eDNA in the sample will be compared with fish and other organisms

caught in nets. Photo by Maris Goodwin.



Kyle Dilliplaine '17 collects samples of sea ice near the geographic North Pole as part of the U.S. Arctic Geotraces project in 2015. Photo courtesy of the U.S. Coast Guard.

Kyle Dilliplaine

CFOS assistant professor Gwenn Hennon's lab, where several UAF students conduct genetic research, focuses on phytoplankton and their interactions with other marine microbes.

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 effect up the food chain.

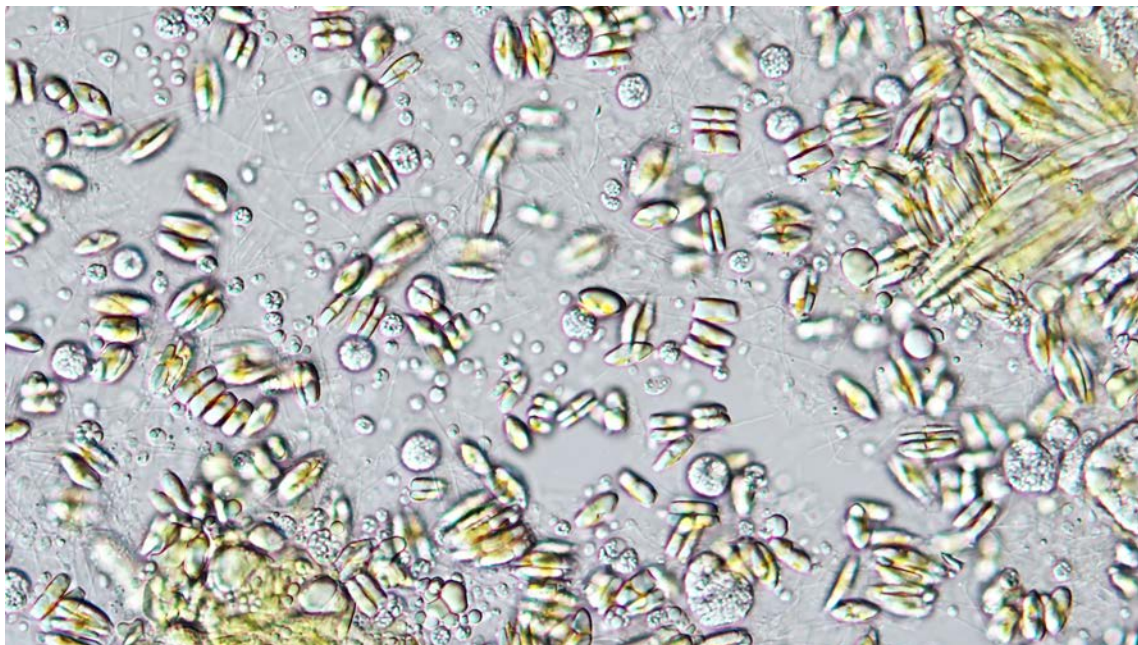


Kyle Dilliplaine holds a sample of sea ice in April 2022. The ice is porous and provides habitat for algae that are essential to the Arctic ecosystem. The algae convert inorganic carbon into biomass through photosynthesis. Photo by Kyle Dilliplaine.

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.



Viewed at 400 times magnification, a mixed culture of sea-ice diatoms and marine fungi collected near Utqiagvik are maintained in the Phytoplankton Laboratory. Photo by Kyle Dilliaine.



In the Genomics Core Lab at UAF's West Ridge Research Building, Jake Cohen extracts DNA from a 0.2 micron filter after several liters of seawater passed through it. The extracted DNA was then amplified for sequencing and analysis. UAF photo by JR Ancheta.

Jake Cohen

Hennon's graduate student Jake Cohen is using genomics to study how the microbial community structure of the Gulf of Alaska changed in

response to the marine heat wave of 2019 and how (or if) it has recovered.

Part of the process is cataloging prokaryotes (bacteria and other organisms whose cells lack a nucleus) and eukaryotes (more complex organisms, including phytoplankton, whose cells have nuclei). To do so, he uses a genomics process called amplicon sequencing. Machines at UAF's Genomics Core Lab amplify and copy genes of interest and then sequence them. Cohen compares these sequences to known databases of microbes, in order to see what types of bacteria and phytoplankton are present in the water.

Bacteria serve as recyclers of the ocean, breaking down dead organic matter so it can be returned to nutrients for phytoplankton.

“Bacteria are hard to tell apart by looking under a microscope, but they can have really different things that are doing in the water. In order to understand how the ecosystem is working, you need to have a more detailed look,” Hennon said.



Plates hold genomic DNA from seawater samples in the UAF Genomics Core Lab. Certain gene regions in the DNA will be amplified using the polymerase chain reaction technique, allowing

*researchers to catalog the prokaryotic and eukaryotic communities in the samples. UAF photo
by JR Ancheta.*





[Aurora home](#)