BLUE FUTURES PATHWAYS
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Learning Activity: Exploring eDNA

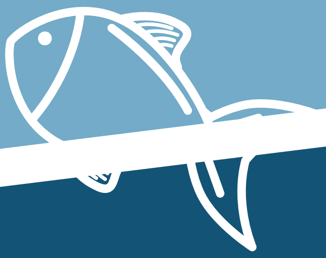
eDNA Case Study

eDNA and Fish Species

Environmental (e)DNA is the study of free DNA left behind in the environment by organisms. By analyzing eDNA, species living in or passing through an environment, from microorganisms to large animals, can be detected. This is helpful for researchers, as the presence and abundance estimate of organisms can be tracked without the need to capture and handle them, and even rare or seclusive species rarely found in conventional surveys can be detected.

Measuring eDNA in different parts of the ocean can help us answer all types of research questions, from looking at pathogens and parasites of wild salmon around open net farms to assessing shifts in biological communities relating to human disturbances (e.g. agricultural runoff, mining).

In the following case study, you will be examining how eDNA can be used to look at different species in areas off the B.C. coast.



How can we use eDNA to look at different Fish Species?

Researchers collected eDNA samples from the ocean surrounding Canada's coast, including the waters off of British Columbia and the Arctic Ocean. The researchers are interested in determining what type of salmon species are present in the water. This kind of information is important when determining which areas should be considered as potential Marine Protected Areas.

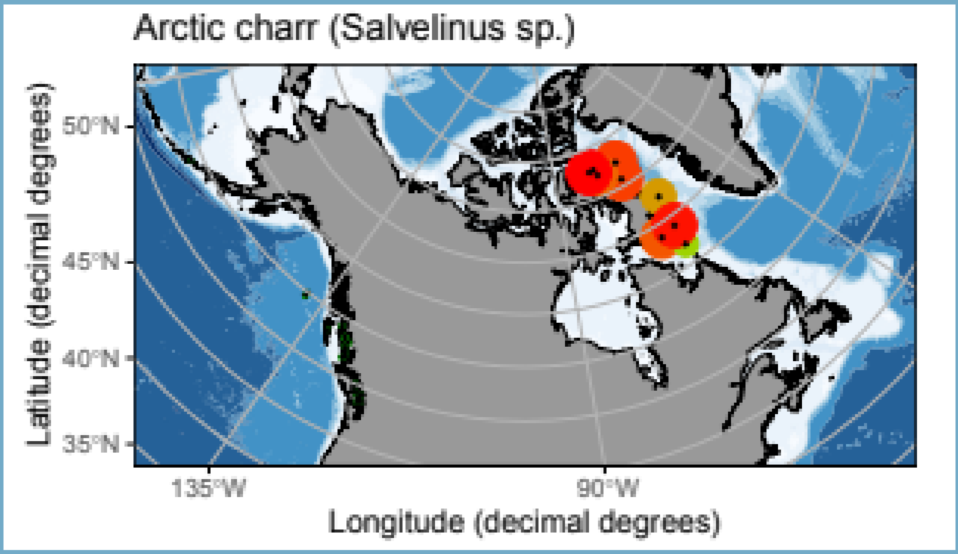
You are an eDNA data analyst who has been provided with maps based on the data that the researchers gathered. Your task is to analyze the maps, write a short summary of what the maps are indicating and make inferences on the different fish species within the family Salmonidae.

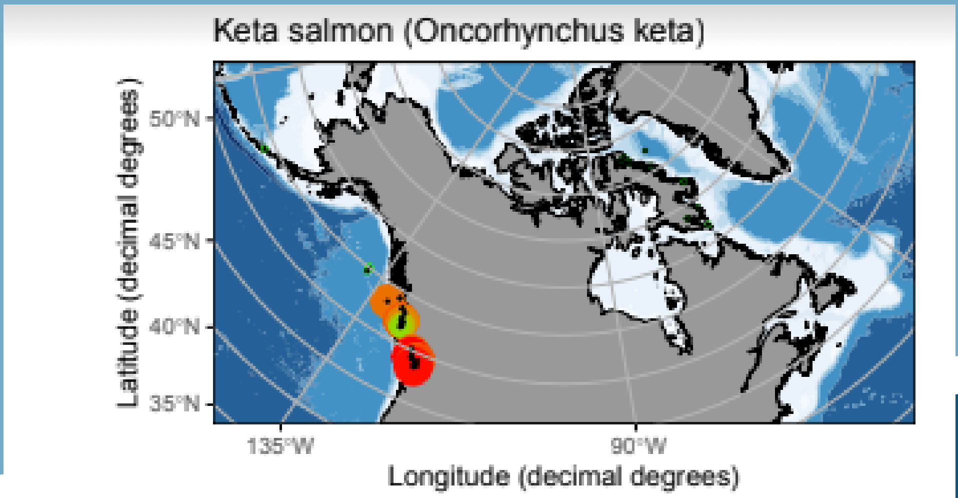
Before you dive into the data, answer the following questions

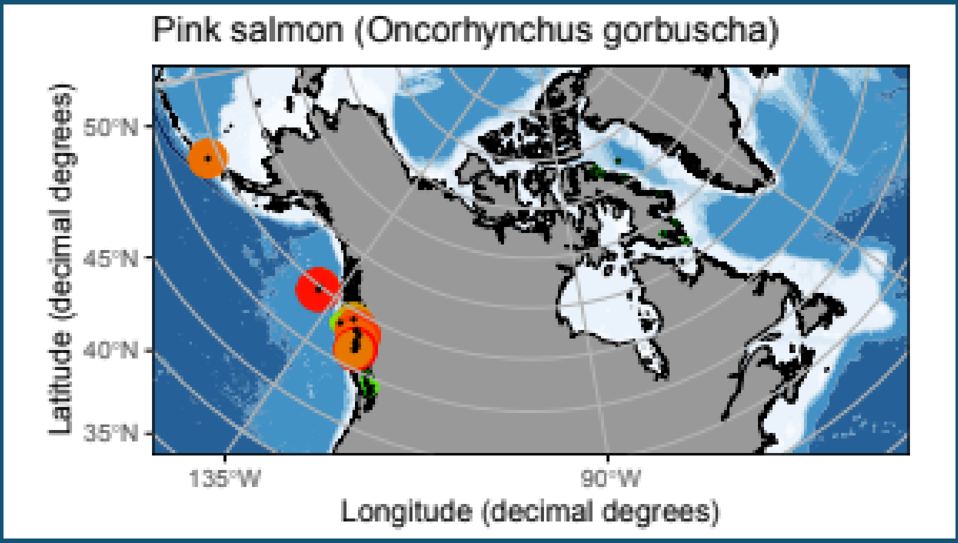
1. What is eDNA?
2. What is a marine protected area and why is it important?
3. Would you expect there to be distinct populations of different species in separate areas?Why or why not? (This is your hypothesis).

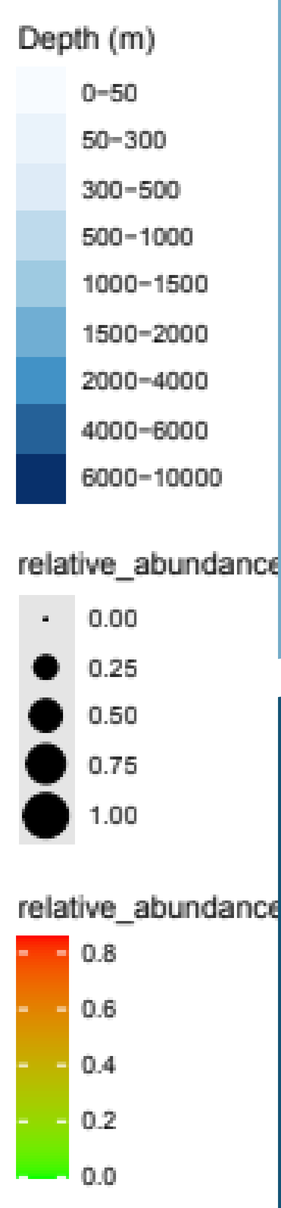
Let's look at the data

Looking at the maps, note what you see. How many different species are represented? Is there any overlap in location of species? Does there appear to be a higher relative abundance of eDNA related to one species over another?

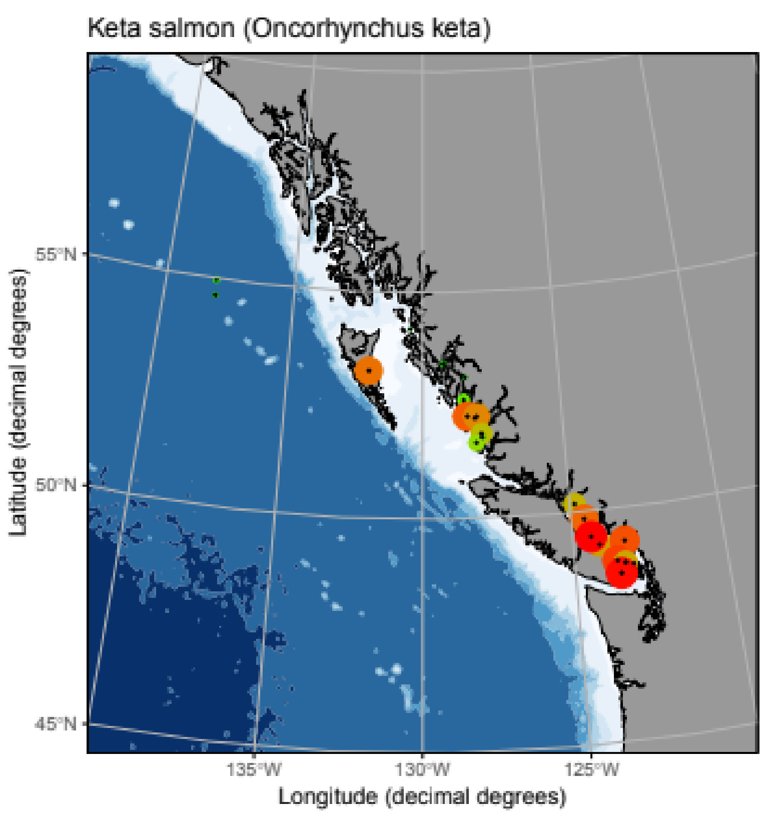

Arctic charr (Salvelinus sp.)

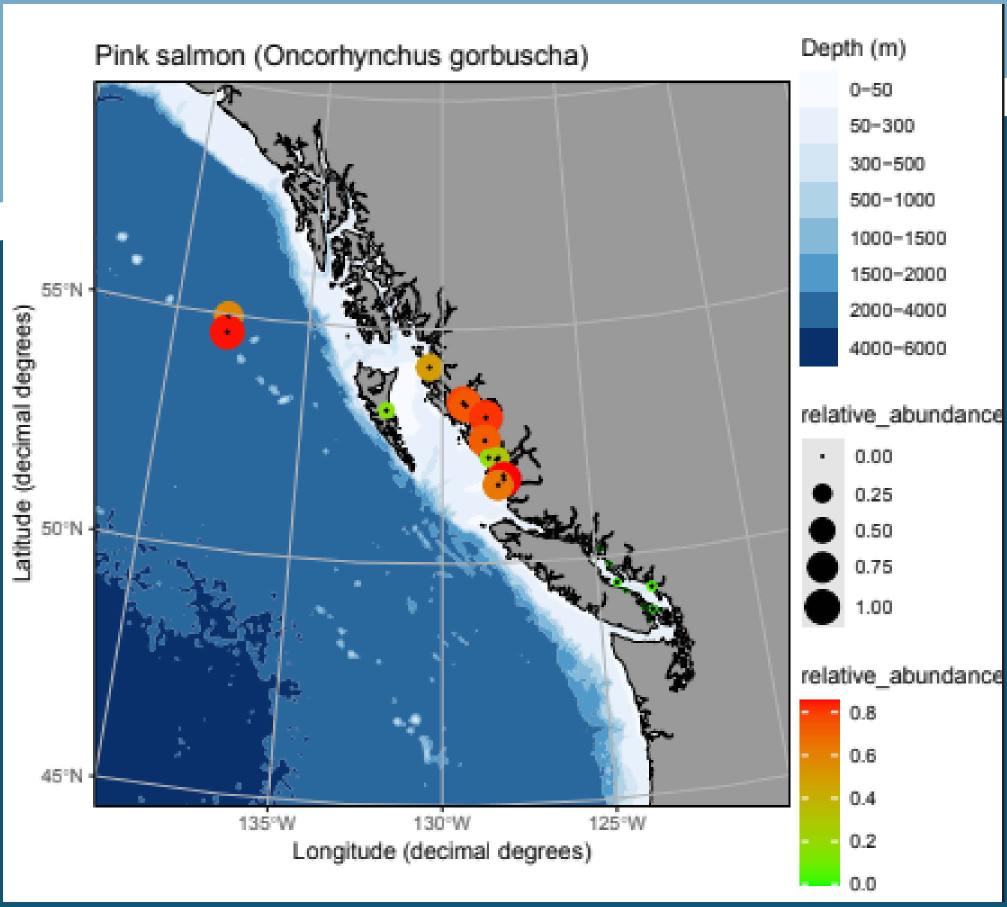

Keta salmon (Oncorhynchus keta)


Pink salmon (Oncorhynchus gorbuscha)



*Note: these two maps are zoomed in versions of the ones above.





Now that you have looked at the maps, explain what you discovered

1. What was the trend you found for fish abundance estimates? Did water depth play a role? Why do you think you found this?
2. How was eDNA useful in this study? What would researchers have had to do if they did not have access to eDNA?
3. What other information can we infer on the ecosystem based on knowing that there are these fish species present?
4. Given the data that we have, is this enough information to establish a Marine Protected Area? What other factors would we need to consider that is not shown here?

Extend your learning

If you are interested in conducting your own data analysis, you can use the raw data we have available to ask and answer your own questions. There is a large amount of data, so you will need to have some knowledge on how to do data analysis using excel, R-statistics, Matlab, or other data analysis software.

Answer key

Introductory questions:

1. eDNA stands for environmental DNA. It is the DNA of all the organisms found within an area and can be obtained from water, soil, or air samples.
2. Marine protected areas are areas of the ocean that have rules in place to regulate human disturbances. This includes activities such as fishing, tourism, etc. These areas are usually protected because they have biological or cultural significance. They are important as they can benefit a diversity of marine animals that can find sanctuary and recover within the area.
3. Different species can require different food and habitats. So it would make sense that with three different species would have three different distinct areas for population. You could correctly infer that this could be due to distinct environmental conditions between the Arctic Ocean, the Salish Sea and Northern Vancouver Island, migration or just the use of distinct river systems.

Discussion questions:

1. It is hard to determine a correlation between water depth and relative abundance of eDNA. Moreover, eDNA can only be used to estimate fish abundance and does not always reflect true abundance of a species. What can be determined is that there are three distinct populations. The maps also show the geographical range of the species among our sampling plan and that there doesn't appear to be overlap between the Arctic Charr and the two Salmon species.
2. eDNA was useful because it allowed the researchers to get an estimate of fish abundance without having to sample fish directly. The researchers would have had to capture fish and count them, which can be time consuming.
3. Knowing that these different fish species are in this area, then we start to know more about the habitat and know more about what other species are likely present (prey and predators of the species).
4. No, we don't have enough information to establish an MPA based on the data alone. This is a good starting point, but what we would want to know is the population, if there were other larger populations in other regions and other key species that were part of the ecosystem. It is also important to understand how those waters are being used from a human perspective, are the waters culturally significant? Who manages those waters? Are there marine industries within those waters? .