Fish eDNA

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Contents

Chapter 1

Our dataset

I was given the following dataset of fastq files which were generated by (1) collecting 18 water samples from rivers and lakes near oil-sands extraction site in the province of Alberta, Canada (see map below), (2) filtering the water samples, (3) extracting the DNA collected on the filer, and (4) sequencing the extracted DNA. For each sample collected, two different marker genes were used to amplify and sequence distinct DNA regions : the **12S** ribosomal RNA gene and the mitochondrial cytochrome oxidase subunit (**COI**).

Amplified regions details

Marker	Names	Forward primer sequence	Reverse primer sequence	Fragment size (bp)	Source
12S	MiFish-U	CCGGTAAAACTCGTGCCAGC	CATAGTGGGGTATCTAATCCCAGTTTG	277	[Miya et al. 2015](https://doi.org/10.1111/mec.14395)

Marker	Names	Forward primer sequence	Reverse primer sequence	Fragment size (bp)	Source
COI	COI-PS1	CGTATTTGGYGC[illegible]	CA[illegible]YATTCG	[illegible]158	DOI: %5B10.1098/rsos.150088](https://doi.org/10.1098/rsos.150088)