**1/31/2020 Meeting with Adam, Andy, Christian**

**Questions to ask:**

Is it reasonable to have the lakes as sites in order to have replication at the site level? And then use the sampling sites within each lake as repeat visits on the lake?

Can you explain how the multiple testing works? Microscopy, PCR, SEM, and Gene Sequencing? All of them tested with microscopy, negative microscopy results -> PCR testing?

Focus on microscope

Microscope + -> PCR used to confirm what they see in the microscope, if negative in PCR then

+ + -- invaded

+ inconclusive – at risk, more sampling relative to other water bodies

Will we have access to more data? From other sites? Other seasons?

I read an article (Holser, BOR, 2009) that stated that there used to be/maybe still is a non-zero probability of misidentification of the species? But that the Bureau of Reclamation developed and employed improved microscopic methods (cross-polarized light source), improved PCR, and improved sample collection to mediate the issues.

Specific research questions:

eDNA criticism – false positive rate

what is the false negative rate?

Identify water bodies which have mixed results + and – at microscope level (over time?)

How does detection probability compare to eDNA, what’s the false negative rate for both methods?

Given that, how many samples do we need to collect?

Invite BOR to be a partner via Github?

We’re developing this for real world applications.