Azolla mtg 20230418

We have

-codiversification analysis, Azolla and Anabaena, based on the reseq data

-microbiome stuff (pacbio reads from the reference sequence run, using BugSeq, which is a black box)

-found 30 bins (taxa), but most seemingly very incomplete, including

-anabaena whole genome

-rhizobium nearly whole genome

-next step, extract 16S, make a phylogeny

-cookie-cutter paper

-they do the methods and results

-we complete the template with the intro/discussion

-FW would like to see the assembly, do some QC, some filtering, etc

-waiting on them for the Hi-C, annotations, RNAseq

TODO

-Carl – get samples to Libor

-Mick – extract 16S from the refseq data and make a phylogeny of that community

-Mick – check for co-diversification of the rhizobium as well as the anabaena

-Mick – metagenomes currently from the PacBio, try the Illumina (to quantify the abundance of rhizobium vs. nostoc – map the reads back to the pacbio assembly, fw skeptical that a hybrid assembly would contribute much). The refgenome is just pacbio – no illumina?

-Mick – get the raw data up on the Box

Papers

1. If chromosome-level azolla assembly, do a synteny WGD study with the Marsilea genome, etc.
2. Species delimitation of Azolla, incorporating the flow data, etc.
3. Co-diversification analyses, description of the community. HiC data will allow for the metagenomes to be binned better.
4. Cookie-cutter paper