1. Dependencies
   1. Make both YAML and step by step installations in MD
   2. Remove hutlab load as a requirement
   3. Add in PhyloPhlAn, MEGAHIT, and Mash in addition to the current requirements
   4. Make sure import statements in python scripts still work
   5. Make checkm and phylophlan databases environmental variables and check for them
2. Pull the checkm script that does the per-MAG abundance from SAM files
3. Switch PhyloPhlAn and Checkm2 from separate script to integrated script with single call for each for each sample
4. Create --remove-intermediate-files flag
5. Create --no-placement flag that stops the workflow after checkm2
6. Cleaned up code with less repetition

Tests

1. Test --skip-contig flag that skips contig generation