Progress Report

Siddharth Reed

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Last Week

- Wrote Literature Review
- Found genera/genomes for the 'mixed' networks (genera with CRISPR and Non-CRISPR genomes)
- Tested out HiDe, ran into error with lua

This Week

- Find the Non-CRISPR genera (genera where all known genomes do not have CRISPR)
- Email HiDe author about error, other HGT inference tool he wrote
- Investigate some other HGT inference tools in the mean time
- Start running all vs all diamond for some of the mixed genera I identified
- Pick tree building program
- Extract info from other CRISPR annotation set, gives info on subtype, counts, false counts `http://omics.informatics.indiana.edu/CRISPRone/`

Next Weel

- Have every all vs. all diamond run/running/scheduled
- Fix HiDe lua error OR identify another HGT inference method
- Review/reorganize genefamily, P/A matrix building scripts and write up specifically in docs