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# Laboratory Update

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# May 2nd, 2018

## 1 Genomic Retrieval and BLAST Database Creation

Updated databases to include Strain level searches. Waiting on ISME Travel Grant Status (Mid-May)

BioRxiv: Resupply manuscript to MS ID 246553

Comments: Include data about functionality compared to other tools or show with an example dataset.

To-Do: Application for Mac, Windows, Linux using Tkinter in Python

Found Github Repository for [Something Similar](#)

## 2 Viral Contig Identification Study

Environments have been set-up and are ready to roll. The binner (MaxBin2) requires the raw reads to calculate abundances needed for binning. The CAMI data [website](#) contains dead links to retrieve reads. Will need to reach out to authors for data.

## 3 Identifying Virulence Factors in Phages

Have established baseline prevalence of virulence genes in phage genomes (See attached HTML). Focused on phages with more than 30 complete genomes in reference database (13 Genus types). Completed BLAST and HMM searches of Virulence factors against metagenomic contigs inferred from vHMM study.

### Next Steps

- Identify taxonomy of contigs with virulence factors
- Gather study metadata
- Compare metadata to significance of VFs

## 4 Creation of rpoB, HSP65, and 16S Databases

Data gathered from locations below, next steps are to make this into a virtualbox with instructions to allow for technician usage.

Downloading rpoB data from NCBI Nucleotide (Copy and Paste into Search Window)

1780 Sequences as of May 1st, 2018

May 2nd, 2018

```
((("Mycobacterium"[Organism] OR ("Mycobacterium"[Organism]  
OR Mycobacterium[All Fields]))) AND rpoB[Title]) AND  
(bacteria[filter] AND biomol_genomic[PROP] AND  
ddbj_embl_genbank[filter] AND ("500"[SLEN] : "5000"[SLEN]))
```

Downloading HSP65 data from NCBI Nucleotide (Copy and Paste into Search Window)

1710 Sequences as of May 1st, 2018

```
((("Mycobacterium"[Organism] OR ("Mycobacterium"[Organism]  
OR Mycobacterium[All Fields]))) AND hsp65[Title]) AND  
(bacteria[filter] AND biomol_genomic[PROP] AND  
ddbj_embl_genbank[filter] AND ("400"[SLEN] : "5000"[SLEN]))
```

Downloading [Silva-ARB Database](#): download SilvaSSUParctaxsilvatrunc.fasta.gz

See [Silva Release](#) information

## 5 Classifying predicted prophages as active or degraded

Concluded three types of genes indicate lysogenic life cycle (see below). Protein HMMs for these three types have been obtained through PFAM. Additional HMMs may need to be developed with sequenced viruses.

- Integrases  
Involved in phage insertion into host genome
- ParA - ParB - ParS  
Involved in extra chromosomal arrangement and replication
- Repressors  
Inhibits replication until stimulus

# May 11th, 2018

## 1 Genomic Retrieval and BLAST Database Creation

Updated databases to include Strain level searches. ISME Travel Grant Status: Abstract Accepted (Word on Travel Grant Unclear)

## 2 Identifying Virulence Factors in Phages

Methodology Questions:

Gene count or percentage of genes

### Virome Sampling Steps

- Identify taxonomy of contigs
- Predict genes and identify virulence factors
- Compare percentage in niche to baseline

## 3 Creation of rpoB, HSP65, and 16S Databases

SequenceServer is Awesome!

Data does comprise of identical reads with overlapping labels:

i.e. Mycobacterium massiliense strains containing the same sequence as M. abscessus