

Mentors: David Beck & Mitch Pesesky | Rayna Tilley | Chemical Engineering (Beck Research Lab)

UW Benjamin Hall Interdisciplinary Research Building, 616 NE Northlake Pl, Seattle, WA 98105, United States

## Background

Antibiotic resistance is an increasing global threat, in many cases caused by specific antibiotic resistance genes. For some pathogens, these antibiotic resistance genes are usually present on plasmids- DNA elements, separate from the chromosome, that can be exchanged between bacteria. We are studying how plasmids can exchange specific genes with each other (becoming mosaic plasmids), potentially collecting several antibiotic resistance genes on a single plasmid.

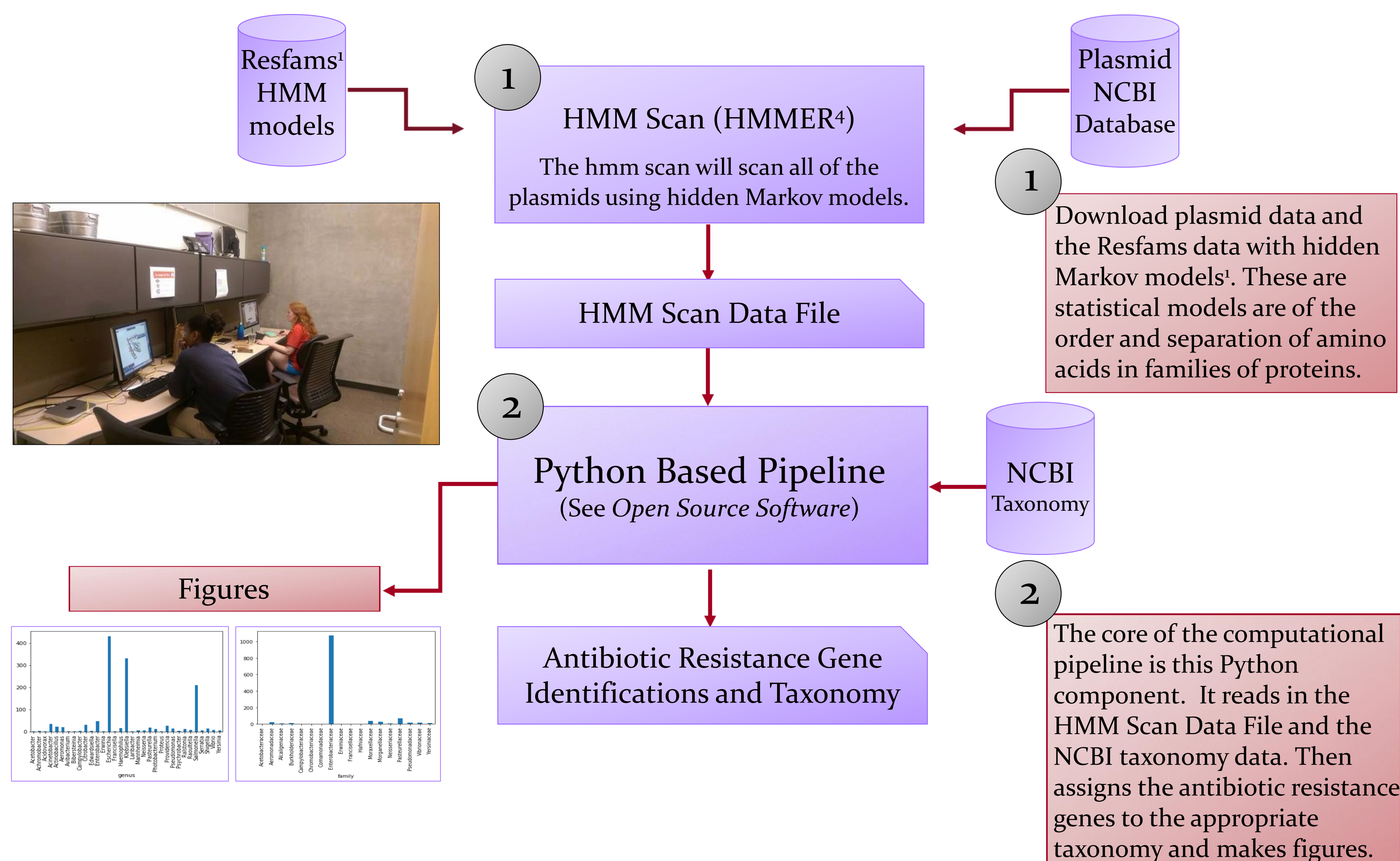
## Goals

- Create software to identify antibiotic resistance genes present in plasmid sequences using the Resfams antibiotic resistance gene hidden Markov model profiles.
- Validate the use of hidden Markov model profiles to detect antibiotic resistance genes in plasmids.
- Compare antibiotic resistance gene occurrence at different levels of taxonomy.

## Beck Research Lab Info

“The Beck Research Lab works on varied applications of computational biology and chemistry including biogeochemical cycling, human health, and the natural and built environments.”  
~Beck Research Lab

## Research and Implementation



## Conclusion

- Developed a high throughput screen for antibiotic resistance genes in a plasmid database using hidden Markov models.
- Hidden Markov models are effective for detecting antibiotic resistance genes.
- The Enterobacteriaceae family is enriched in the set of antibiotic resistance genes and plasmids possibly because they are human pathogens and they are under a lot of antibiotic pressure.

## Tools

Python, Biopython<sup>2</sup>, GitHub, Jupyter Notebooks<sup>3</sup>, Anaconda, Pandas, HMMER<sup>4</sup>, NumPy, Matplotlib

## Open Source Software



This QR scan will take you to the plasmid\_search repository in GitHub. You will be able to look at the Plasmid.ipynb file from Jupyter Notebook containing the code that produced these results..

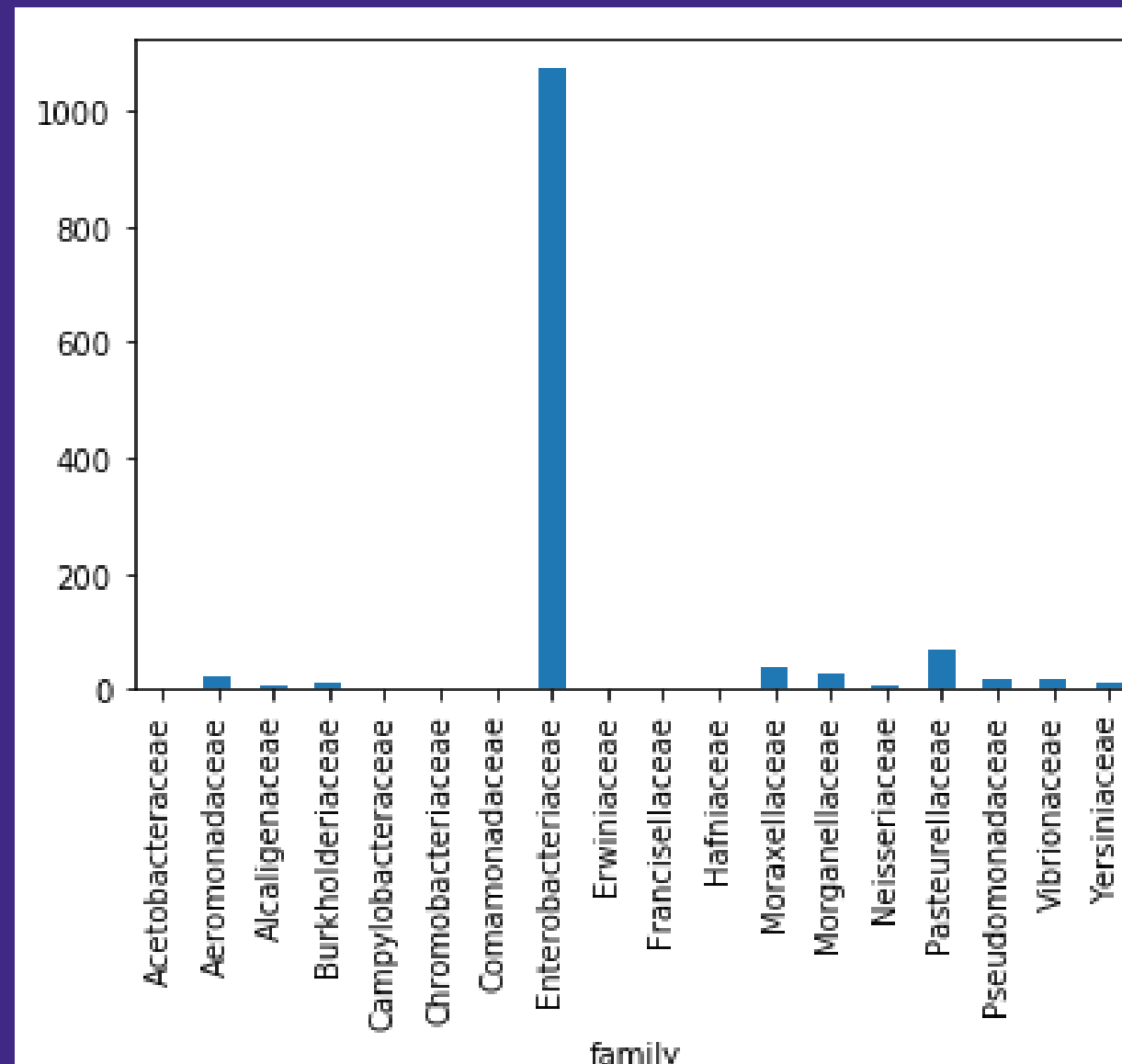
## References

1. Gibson *et al.* ISME Journal. 2014, doi:ISMEJ.2014.106.
2. Cock *et al.* Bioinformatics. 2009, 25, 1422-1423.
3. Kluyver *et al.* IOS Press. 2016, 10.3233/978-1-61499.
4. Eddy. PLoS Comp. Biol. 2011, 7:e1002195.

## Acknowledgments

I would like to thank my professor Dr. David Beck for being my mentor for the summer and for his guidance, and Dr. Mitch Pesesky for allowing me to participate and learn from his project. Thank you Women in Science and Engineering (WiSE) for giving me this wonderful opportunity.

Figure 1



## Results

Antibiotic resistance gene occurrence at different taxonomy levels are shown in Figures 1 & 2 for family and genus, respectively. In Figure 1, the Enterobacteriaceae family has a greater amount of antibiotic resistance genes than the other families. In Figure 2, *Escherichia*, *Enterobacter*, *Klebsiella*, *Shigella*, *Yersinia*, and *Salmonella* are all genera in the Enterobacteriaceae family, thus because they are so abundant it makes the outlier of the Enterobacteriaceae family more plausible.

Figure 2

