High throughput Python pipeline to identify Horizontal Gene Transfer

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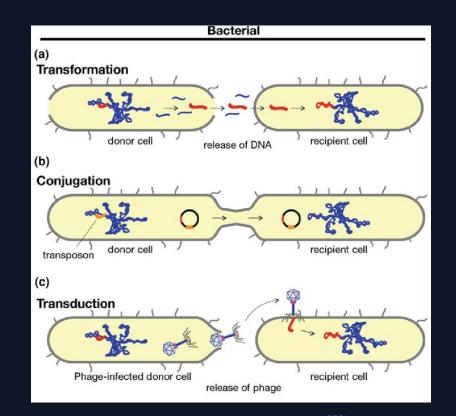
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### **Project Description**

 The purpose was to use BLAST to identify instances of horizontal gene transfer between bacteria and bacteriophages.



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Project Goals
The main goal of the project was to speed up the process.

 This goal was accomplished by locally downloading the database and using a tool based on the command line to query it.

Phage Query ID	Forward BLAST	Bacterial ID -	Reverse BLAST	Phage	
	*		,	Result ID	EA

## Project Timeframe

Start: September 2022End: March 2023



#### **Project Accomplishments**

 The major accomplishment of this project was making the analysis pipeline work faster with Diamond. • The original version of the pipeline was a long Python script that took about 5 minutes per query.

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#### Lessons Learned

- What went well? What could we have done differently?
  - Increased familiarity with working in HPC environment, using command line tools and bash commands.
  - -Should have asked for more help early and often.

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# Next Steps in Continuation of Research

- Filtered searches of nr database with diamond, to limit them by taxonomic groups.
- Analysis of the large list of pairs of bacteria and bacteriophages generated by the pipeline.

