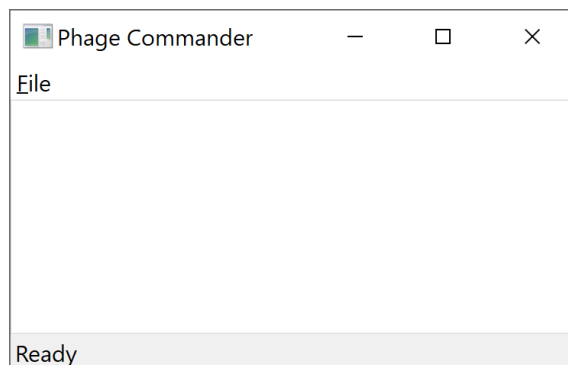# Introduction to Phage Commander

- **Phage Commander** is a software tool for sequencing phage genomes.

- Phage Commander runs a phage's DNA sequence through gene sequencing software tools and outputs a spreadsheet of potential genes. These tools include:
  - Glimmer, Genemark, Genemark HMM, Genemark S, Genemark S2, Genemark Heuristic, Prodigal, RAST, and Metagene

- Phage Commander's output can be exported as a spreadsheet.

- These slides describe how to use Phage Commander

- A draft paper describing Phage Commander in detail is here:
  https://www.biorxiv.org/content/10.1101/2020.11.11.378802v1

# Opening Phage Commander

**How to open Phage Commander:**

- Download Phage Commander from GitHub repository: **https://github.com/sarah-harris/PhageCommander**

- Run Phage Commander:
  - **Windows:** Navigate to phagecommander/bin. Click on the executable: phagecom-windows.exe
  - **Linux or Mac:** Open a shell. Navigate to phagecommander. Type py phagecom.py. If you need to install any of the supporting packages, first type: 'pip install .' (in the PhageCommander-master directory – the directory that contains setup.py)

- A small Phage Commander window will appear:

# Using Phage Commander

**How to use Phage Commander:**

- In the Phage Commander Window, click on the **File** menu, and select **New**.

- A Select Query Tools window will open (see next slide).
  - If using **GeneMark.hmm** you will need to select your phage's bacterial host from the drop down menu under **Species**
  - To use **RAST**, you will need to create a login and password at https://rast.nmpdr.org

- Press **Open** and select your phage's fasta file – you may use the example fasta file included in the GitHub repository: Patience.fasta

- Press **Query** to run Phage Commander. Phage Commander will now run the sequence through the selected sequencing tools – this may take several minutes.

- When Phage Commander completes, press **OK**

# Select Query Tools Window

# In the Event of an Error

- If Phage Commander runs successfully, you will see a window saying "**Done! Query Successful**"

- Press **OK** and you will see the Phage Commander output in the form of a spreadsheet (expand the window)

- If phage commander encounters an error, the error message will display which program is causing the error (e.g. Glimmer, Aragorn, GMS2, etc.)

- To work around this, re-run Phage Commander without including the program causing the error

**Total Calls column Is the number of programs identifying a gene**

**"GM" is the genes identified by GeneMark**

**"HMM" is the genes identified by GeneMark.hmm**

**"Heuristic" is the genes identified by GeneMark Heuristic**



**Each row is a gene**

# Exporting Phage Commander Results

- To export as excel spreadsheet, select:
  - **File → Export → Excel**

- To export as GenBank (.gb) format file, select:
  - **File → Export → GenBank**
  - Make sure number in "Calls" box is maximum (should usually be 8)
  - Make sure "Less than or equal to" circle is filled
  - Press "Save as" and enter desired filename
  - Press "Export"

# Exporting Phage Commander results in .gb format



**Make sure this number is the maximum**

**Press "Save as" and enter desired filename**

**Select "Less than or equal to"**

**Press "Export"**