



# **Advanced Molecular Detection**

## **Southeast Region Bioinformatics**

**AMRFinderPlus and Pha4ge's hAMRonization tool**

06/05/2023

# Outline



Updates – HPG & APHL



Agenda



Importance of AMR



AMRFinderPlus



Pha4ge's hAMRonization tool



Reading Output File Structure



Questions

# Updates - HPG

- Open OnDemand update/upgrade – scheduled for **June 10**
  - Additional features
  - OS improvements
  - Additional graphics updates
- Will not affect currently running jobs, but will affect active connections
  - You may need to reconnect
  - Most users should not need to make changes
  - Issues? Open a [support ticket](#)

# Updates - APHL

- Easy Genomics and Nextflow Training Application
  - [APHL Easy Genomics and Nextflow Training Application Survey \(surveymonkeys.com\)](https://surveymonkeys.com/s/1234567890)
  - Potentially one person per jurisdiction
  - In-person training in Arlington, VA - **August 14-16**
  - Applications are due by **June 15**
  - Must complete 8-10 hours of pre-work
  - Requires command line knowledge – proficient
- DataCamp subscription renewal/application
  - [DataCamp Membership Application 2023 Survey \(surveymonkeys.com\)](https://surveymonkeys.com/s/1234567890)

# Agenda

**June 12** – Outbreak/Cluster Report Training

**June 26** – Git & GitHub

## Future Trainings

- ONT & FL's Flisochar pipeline
- StaPH-B Toolkit Programs/Pipelines
- R Training Series
- Bactopia programs
- Dryad pipeline
- Generating R figures
- ...and more

# Importance of AMR

- Antimicrobial resistance genes accumulate in microorganisms – causing a large public health risk
  - Decrease in cure rates which in turn increases severity of diseases and increases potential for transmission
- ABRicate database concerns
  - ABRicate uses DNA matches vs AA matches
  - **Out of date!**
  - Use multiple databases to verify findings

# AMRFinderPlus

- [GitHub - AMRFinderPlus](#)
- “Plus” is for stress, heat, biocide, and virulence resistance genes for some organisms
  - [GitHub - AMRFinderPlus - Curated-organisms](#)
- AMRFinderPlus has an update command that allows you to update the database!
- We will use this command in the outbreak training next Office Hours call

# AMRFinderPlus – Installation and Usage

- Install AMRFinderPlus

```
$ conda create -yp /path/to/conda/envs/amfinderplus  
$ conda activate /path/to/conda/envs/amrfinderplus  
$ conda install -c bioconda ncbi-amrfinderplus
```

- Run AMRFinderPlus

```
$ amrfinder --help  
$ amrfinder --list_organisms  
$ amrfinder --organism Name Organism  
$ amrfinder --protein <protein_fasta>  
$ amrfinder --nucleotide <nucleotide_fasta>  
$ amrfinder --gff <annotation file>
```



# AMRFinderPlus – Other Commands

- Update/Download the latest version of the AMRFinder Database
  - **Note** – if running AMRFinderPlus the first time, this will need to be done. It should flag this as an error if it hasn't been done

```
$ amrfinder -u
```

- AMRFinder with --plus command for virulence, stress, and biocide genes

```
$ amrfinder --plus [options]
```

# AMRFinderPlus - Interpreting Results

- Output is a tab-delimited format (.tsv)
- The output will depend on the input file (i.e., protein, fasta, annotation)

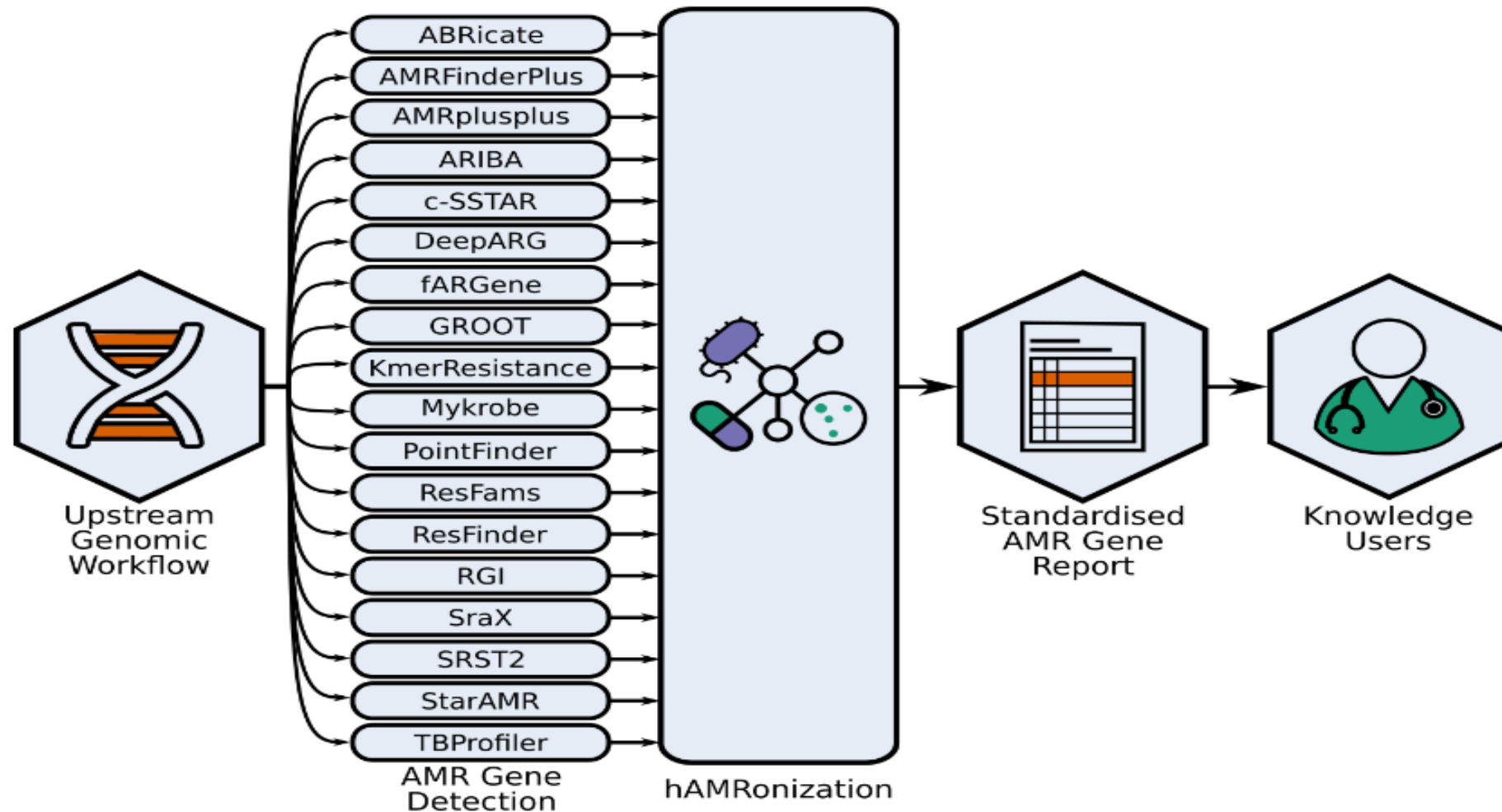
# AMRFinderPlus - Interpreting Results

- Protein identifier
- Contig ID
- Start codon
- Stop codon
- Gene symbol
- Sequence Name
- Scope
- Element Type
- Element Subtype
- Class
- Subclass
- Method
- Target length
- Reference Sequence length
- % Coverage
- % Identity
- Alignment length
- Accession of closest protein
- Name of closest protein
- HMM id
- HMM description

# Pha4ge's hAMRonization Tool

- Parse multiple AMR analysis reports into a common data structure
- hAMRonization repo contains the hAMRonization module and CLI parser tools that combine the outputs of 18 disparate antimicrobial resistance gene detection tools into a single unified format
- This is an implementation of the hAMRonization AMR detection specification scheme which supports gene presence/absence resistance and mutational resistance

# hAMRonization Workflow



# hAMRonization - Installation

- Install hAMRonization on your system

```
$ conda create -yp /path/to/conda/envs/hamronization  
$ conda activate /path/to/conda/envs/hamronization  
$ conda install -c bioconda hamronization
```

# hAMRonization - Usage

- Usage of hAMRonization tool

```
hamronize <tool> <options>
```

- Converts AMR gene detection tool outputs to hAMRonization specification format
- Options include:
  - -h, --help show the help message and exit
  - -v, --version show program's version number and exit
  - summarize provide paths to the reports you wish to summarize

# hAMRonization - Specific Tools

```
>hamronize abricate -h  
usage: hamronize abricate <options>
```

Applies hAMRonization specification to output from abricate (OUTPUT.tsv)

positional arguments:

report                      Path to tool report

optional arguments:

-h, --help                  show this help message and exit

--format FORMAT            Output format (tsv or json)

--output OUTPUT            Output location

--analysis\_software\_version ANALYSIS\_SOFTWARE\_VERSION

Input string containing the analysis\_software\_version for abricate

--reference\_database\_version REFERENCE\_DATABASE\_VERSION

Input string containing the reference\_database\_version for abricate





# hAMRonization - Interpreting Results & Demo

- Output is a tab-delimited format (.tsv)
- Output can either be a combination of 18 disparate antimicrobial resistance gene detection tools into a single unified format or summarized report of all the tools or you can even look at a single specific tool

# References

- [Home · ncbi/amr Wiki · GitHub](#)
- [GitHub - pha4ge/hAMRonization: Parse multiple Antimicrobial Resistance Analysis Reports into a common data structure](#)

# Time for Questions & Feedback

- Questions?
  - Do you need help with anything?
  - Requests for separate trainings?
- Feedback
  - What would you like to see?



# Advanced Molecular Detection Southeast Region Bioinformatics

## Questions?

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