**Advanced Molecular Detection**
**Southeast Region Bioinformatics**

**Bactopia tools**
10/16/2023

# Updates – ABiL Trainings

## ABiL in-person courses (Next week!)

- The ABiL in-person (advanced!) bioinformatics course will be held **Tuesday Oct. 24th - Friday Oct. 27th** at the Georgia Institute of Technology (GT)


## ABiL online courses

- If additional attendees decide to sign up later, that is not a problem, as the courses will still be available, and they can attend on a rolling basis under the contract
- If you did not receive the invitation for joining the courses, please let us know, we can help to get you enrolled

# Updates

- If your denied access to your HPG account, it might be due to reaffiliation of the accounts. In that case, please submit a help desk ticket to servicedesk@ufl.edu. They will send you a HPG account request form and this process may take from 2 to 15 days due to the volume of requests

- Also, just a reminder to email your requests to bphl-sebioinformatics@flhealth.gov

# Agenda

**October 30** – Bactopia Tools: Mykrobe and Pasty
**November 13** – Bactopia Tools: Pbptyper and Prokka

Future Trainings
- ONT & FL's Flisochar pipeline
- StaPH-B Toolkit Programs/Pipelines
- GISAID flagged SARS-CoV-2
- R Training Series
- Dryad pipeline
- …and more

# Mcroni

- A set of tools for analyzing sequence variation around the *mcr-1* gene (mobilized colistin resistance)

- mcroni takes a .fasta file and returns some summary information about the context of *mcr-1*. It also returns the expected local region for aligning the composite transposon

liampshaw/mcroni: Scripts for finding and processing promoter variants upstream of mcr-1 (github.com)

# Installation

Can be installed through conda

conda create –yp /blue/bphl-<state>/<user>/conda_envs/mcroni/
conda activate /blue/bphl-<state>/<user>/conda_envs/mcroni/
conda install –c conda-forge –c bioconda mcroni

# Background

- Snesrud et al. (2016) (PMID 27620479) proposed a model for the transposition of mcr-1 by ISApl1. A mobile composite transposon structure degraded over time

- Variation within this local genomic context of *mcr-1* therefore contains information on its evolutionary history. mcroni doesn't do anything complicated: it's just a convenient wrapper script for assessing this variation automatically (e.g., blasting for ISApl1, finding nearby plasmid replicons)
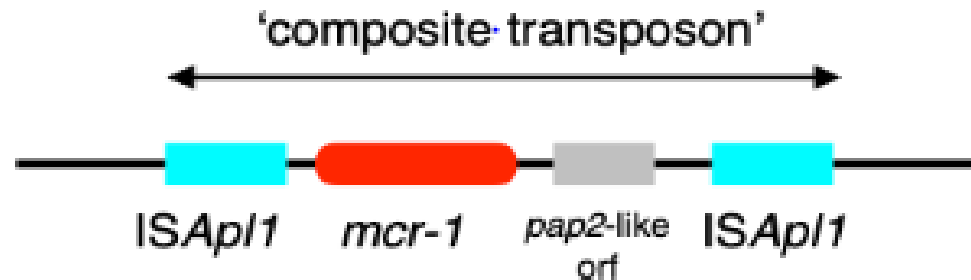
# Usage



```
(/blue/bphl-florida/thsalikilakshmi/training/conda_envs/mcroni) [thsalikilakshmi@login6 conda_envs]$ mcroni --help
usage: mcroni [-h] (--fasta FASTA | --filelist FILELIST) --output OUTPUT [-v] [--force | --append]


Analyse the local genomic context of mcr-1.


options:
  -h, --help           show this help message and exit
  --fasta FASTA        Fasta file
  --filelist FILELIST  Alternatively: a list of fasta files
  --output OUTPUT      Output prefix
  -v, --verbose        verbose output
  --force              Force overwriting of output files.
  --append             Append to existing output files.
```

# Input

Takes .fasta as input

```
$ mcroni --fasta /path/to/fasta/.fasta --output mcroni_out
```

# Results

| | A | B | C | D | E | F | G | H | I | J | K | L | M | N | O | P | Q | R | S | T |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | FILE | ISOLATE | MCR1.CONT | MCR1.STA | MCR1.STR | MCR1.VAF | PROMOTE | PLASMIDS | PLASMIDS | ISAPL1.UP | ISAPL1.UP | ISAPL1.UP | ISAPL1.UP | ISAPL1.DC | ISAPL1.DC | ISAPL1.DC | ISAPL1.DOWNSTREAM.INTERNAL.END | | | |
| 2 | /blue/bpl | JBI22000631 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | | | | |

# MOB_suite

- Software tools for clustering, reconstructing, and typing of plasmids from draft assemblies

- Plasmids are mobile genetic elements (MGE), which contribute to rapid evolution and adaption of bacteria to new niches through horizontal transmission of novel traits to different genetic backgrounds

- [phac-nml/mob-suite: MOB-suite: Software tools for clustering, reconstruction and typing of plasmids from draft assemblies (github.com)](github.com)

# MOB_tools

- MOB_init
  - Downloads databases from figshare, sketches the databases, and sets up the blast databases

- MOB_cluster
  - Creates plasmid similarity groups using fast genomic distance estimation using Mash
  - Plasmids are grouped into clusters using complete-linkage clustering and the cluster code accessions provided by the tool provide an approximation of operational taxonomic units OTU's

# MOB_tools

- MOB-typer
  - Provides in silico predictions of the replicon family, relaxase type, mate-pair formation type, and predicted transferability of the plasmid
  - Using a combination of biomarkers and MOB-cluster codes, it also provides an observed host-range of your plasmid based on its replicon, relaxase, and cluster assignment

- MOB-recon
  - This tool reconstructs individual plasmid sequences from draft genome assemblies using the clustered plasmid reference databases provided by MOB-cluster
  - It will also automatically provide the full typing information provided by MOB-typer

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# Installation

- Available as module on HPG

  module load mobsuite/3.1.0

- Can be installed through conda

  conda create -yp /blue/bphl-<state>/<user>/training/conda_envs/mob_suite/

  conda activate /blue/bphl-<state>/<user>/training/conda_envs/mob_suite/

  conda install -c conda-forge -c bioconda mob_suite

# Usage

```
[thsalikilakshmi@login6 assemblies]$ mob_typer
usage: mob_typer [-h] -i INFILE -o OUT_FILE [-g MGE_REPORT_FILE]
                 [-a ANALYSIS_DIR] [-n NUM_THREADS] [-s SAMPLE_ID] [-f] [-x]
                 [--min_rep_evalue MIN_REP_EVALUE]
                 [--min_mob_evalue MIN_MOB_EVALUE]
                 [--min_con_evalue MIN_CON_EVALUE] [--min_length MIN_LENGTH]
                 [--min_rep_ident MIN_REP_IDENT]
                 [--min_mob_ident MIN_MOB_IDENT]
                 [--min_con_ident MIN_CON_IDENT]
                 [--min_rpp_ident MIN_RPP_IDENT] [--min_rep_cov MIN_REP_COV]
                 [--min_mob_cov MIN_MOB_COV] [--min_con_cov MIN_CON_COV]
                 [--min_rpp_cov MIN_RPP_COV] [--min_rpp_evalue MIN_RPP_EVALUE]
                 [--min_overlap MIN_OVERLAP] [-k] [--debug]
                 [--plasmid_mash_db PLASMID_MASH_DB] [-m PLASMID_META]
                 [--plasmid_db_type PLASMID_DB_TYPE]
                 [--plasmid_replicons PLASMID_REPLICONS]
                 [--repetitive_mask REPETITIVE_MASK]
                 [--plasmid_mob PLASMID_MOB] [--plasmid_mpf PLASMID_MPF]
                 [--plasmid_orit PLASMID_ORIT] [-d DATABASE_DIRECTORY]
                 [--primary_cluster_dist PRIMARY_CLUSTER_DIST] [-V]
```

# Input

Takes .fasta as input

```
$ mob_typer --infile /path/to/fastas/.fasta --out_file mob_typer_results
```

# Results

| | sample_id | num_cont | size | gc | md5 | rep_type( | rep_type_ | relaxase_t | relaxase_ | mpf_type | mpf_type | orit_type( | orit_acces | predicted | mash_nea | mash_nei | mash_nei | primary_c | secondary | predicted | predicted | observe |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | | | | | | | | | | | | | | | | | | | | | | |
| 2 | JBI220006 | 187 | - | 57.21757 | 142cfc2c9 | IncI2,rep_ | KC845573, | MOBP | | NC_02252 | MPF_T | NC_01911 | - | - | conjugativ | - | | 1 | - | - | - | family | Enterobac | family |

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# Questions?

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