



# **Advanced Molecular Detection**

## **Southeast Region Bioinformatics**

# Outline



Updates



Agenda



LisSero



Meningotype



Questions

# Updates – ABiL Trainings

## ABiL in-person courses

- The ABiL in-person (advanced!) bioinformatics course will be held **Tuesday Oct. 24<sup>th</sup> - Friday Oct. 27<sup>th</sup>** at the Georgia Institute of Technology (GT)
- About 2 participants may attend from each state or jurisdiction
- Tanya has sent an email about the courses
- Email us ASAP if you're interested to guarantee a spot!

## 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 – Sanibel

- Sanibel pipeline has been developed and walkthrough will be done in an upcoming office hours
- A Nextflow pipeline to analyze NGS data in fastq format from bacterial genome (update from FLAQ\_AMR)

# Agenda

**October 16** – Bactopia Tools: Mcroni and MOB\_suite

**October 30** – Bactopia Tools: Mykrobe and Pasty

## Future Trainings

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

# LisSero

- *In silico* serogroup typing prediction for *Listeria monocytogenes*
- Detects the presence or absence of 5 genes (Imo1118, Imo0737, ORF2110, ORF2819 and Prs)
- The patterns obtained reflect the four main serotypes (1/2a, 1/2b, 1/2c, and 4b) obtained from food and human sources
- The patterns are not based on genes involved in somatic (O) or flagellar (H) biosynthesis, and are not specific to just one serotype, but rather to a group of serotypes
- If only Prs is detected, these isolates are often serotype 4a or 4c, though LisSero reports these as "Nontypable"

[GitHub - MDU-PHL/LisSero: In silico serotype prediction for Listeria monocytogenes](#)

# Installation

Can be installed through conda

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

# Usage

```
thsalikilakshmi@login1:/blue/bphl-florida/thsalikilakshmi/training/conda_envs
(/blue/bphl-florida/thsalikilakshmi/training/conda_envs/lissero) [thsalikilakshm
i@login1 conda_envs]$ lissero --help
Usage: lissero [OPTIONS] FASTA...

In silico serogroup prediction for L. monocytogenes. Alleles: lmo1118,
lmo0737, ORF2819, ORF2110, Prs

References:

* Doumith et al. Differentiation of the major Listeria monocytogenes
serovars by multiplex PCR. J Clin Microbiol, 2004; 42:8; 3819-22

Options:
  -h, --help                Show this message and exit.
  -s, --serotype_db TEXT    [default: /blue/bphl-florida/thsalikilakshmi/trainin
                             g/conda_envs/lissero/lib/python3.11/site-
                             packages/lissero/db]
  --min_id FLOAT            Minimum percent identity to accept a match. [0-100]
                             [default: 95.0]
  --min_cov FLOAT           Minimum coverage of the gene to accept a match.
                             [0-100] [default: 95.0]
  --debug
  --logfile TEXT            Save log to a file instead of printing to stderr
  --version                 Show Version Information
```





# Input

Takes .fasta as input

```
(/blue/bphl-florida/thsalikilakshmi/training/conda_envs/lissero) [thsalikilakshmi@login1 fastqs]$  
lissero /blue/bphl-  
florida/thsalikilakshmi/data/jbi/20230719_jax_230522_PLN_WAT_JD/assemblies/JBI23001288.fasta  
/blue/bphl-  
florida/thsalikilakshmi/data/jbi/20230719_jax_230522_PLN_WAT_JD/assemblies/JBI23001362.fasta >  
lissero_output
```

# Results

	A	B	C	D	E	F	G	H
1	ID	SEROTYPE	PRS	LMO0737	LMO1118	ORF2110	ORF2819	COMMENT
2	/blue/bphl-flo	1/2a, 3a	FULL	FULL	NONE	NONE	NONE	
3	/blue/bphl-flo	4b, 4d, 4e	FULL	NONE	NONE	FULL	FULL	

# Output

The output consist of 8 columns:

- ID: the full path to your file
- SEROTYPE: A predicted serotype if possible, otherwise Nontypable
- Five columns for each of the genes with either:
  - FULL: for a complete match to the gene in the database (as defined by the --min\_cov and --min\_id flags which default to at least 95% coverage and percent id)
  - NONE: when there is no match to the database
  - PARTIAL: where there are matches that fall below the --min\_cov and --min\_id thresholds
- COMMENTS: Which will try to explain a Nontypable results. Current cases are:
  - No Prs found: when there is no FULL match to the Prs gene is not likely to be a *Listeria monocytogenes*
    - Presence of all 5 genes, not a known serotype: when all 5 genes are present
- No combination of fully matched genes resulted in a known serotype: An unknown combination
  - In addition, it will say **Unusual 4b with Imo0737** when reporting 4b, 4d, 4e\* serotype

# Meningotype

- *In silico* typing of *Neisseria meningitidis* contigs
- Serotyping
- MLST
- Finetyping (*porA*, *fetA*, *porB*)
- Bexsero antigen sequence typing (BAST) (*fHbp*, *NHBA*, *NadA*, *PorA*)

[GitHub - MDU-PHL/meningotype: In silico serotyping, finetyping and Bexsero antigen sequence typing of \*Neisseria meningitidis\*](#)

# Installation

Can be installed through conda

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

# Usage

```
thsalikilakshmi@login1:/blue/bphl-florida/thsalikilakshmi/data/jbi
(/blue/bphl-florida/thsalikilakshmi/training/conda_envs/meningotype) [thsalikila
kshmi@login1 jbi]$ meningotype --help
usage:
  meningotype [OPTIONS] <fasta1> <fasta2> <fasta3> ... <fastaN>

In silico typing for Neisseria meningitidis
Default: Serotyping, MLST and ctrA PCR

PCR Serotyping Ref: Mothershed et al, J Clin Microbiol 2004; 42(1): 320-328
PorA and FetA typing Ref: Jolley et al, FEMS Microbiol Rev 2007; 31: 89-96
Bexsero antigen sequence typing (BAST) Ref: Brehony et al, Vaccine 2016; 34(39):
4690-4697
See also http://www.neisseria.org/nm/typing/

positional arguments:
  FASTA          input FASTA files eg. fasta1, fasta2, fasta3 ... fastaN

optional arguments:
  -h, --help          show this help message and exit
  --finetype          perform porA and fetA fine typing (default=off)
  --porB             perform porB sequence typing (NEIS2020) (default=off)
  --bast             perform Bexsero antigen sequence typing (BAST) (default=off)
  --mlst             perform MLST (default=off)
  --all             perform MLST, porA, fetA, porB, BAST typing (default=off)
```



# Input

Takes fasta as input

```
(/blue/bphl-florida/thsalikilakshmi/training/conda_envs/meningotype) [thsalikilakshmi@login1  
assemblies]$ meningotype --all JBI22000642.fasta JBI22000645.fasta JBI22000669.fasta  
JBI22000670.fasta > meningotype_output
```

# Results

	A	B	C	D	E	F	G	H	I	J	K
1	SAMPLE_ID	SEROGROUP	ctrA	MLST	PorA	FetA	PorB	fHbp	NHBA	NadA	BAST
2	JB122000642.fasta	C	ctrA	11	5-1,10-8	F3-6	NEIS2020_	130	20	0	-
3	JB122000645.fasta	C	ctrA	11	5-1,10-8	F3-6	NEIS2020_	130	20	0	-
4	JB122000669.fasta	C	ctrA	11	5-1,10-8	F3-6	NEIS2020_	130	20	0	-
5	JB122000670.fasta	C	ctrA	11	5-1,10-8	F3-6	NEIS2020_	130	20	0	-





# **Advanced Molecular Detection**

## **Southeast Region Bioinformatics**

# **Questions?**

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