

Advanced Molecular Detection Southeast Region Bioinformatics

Outline



Updates



Agenda



LisSero



Meningotype



Questions

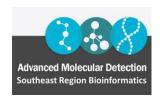
Updates – ABiL Trainings

ABiL in-person courses

- The ABiL in-person (advanced!) bioinformatics course will be held Tuesday Oct. 24th Friday Oct.
 27th 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)

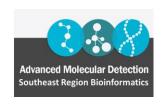
Agenda

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 (lmo1118, lmo0737, 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"

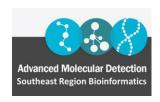
GitHub - MDU-PHL/LisSero: In silico serotype prediction for Listeria monocytogenes



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

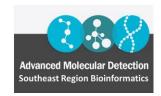
```
thsalikilakshmi@login1:/blue/bphl-florida/thsalikilakshmi/training/conda_envs
                                                                                 \times
(/blue/bphl-florida/thsalikilakshmi/training/conda envs/lissero) [thsalikilakshm ^
i@loginl conda envs]$ lissero --help
Usage: lissero [OPTIONS] FASTA...
 In silico serogroup prediction for L. monocytogenes. Alleles: lmoll18,
 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
                          Save log to a file instead of printing to stderr
 --logfile TEXT
  --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

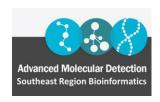
4	Α	В	С	D	Е	F	G	Н
1	ID	SEROTYPE	PRS	LMO0737	LMO1118	ORF2110	ORF2819	COMMENT
2	/blue/bphl-flo	1/2a, 3a	FULL	FULL	NONE	NONE	NONE	
3	/blue/bphl-flo	4b, 4d, 4e	FULL	NONE	NONE	FULL	FULL	



Output

The output consist of 8 columns:

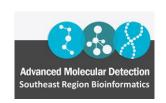
- ID: the full path to your file
- SEROTYPE: A predicted serotype if possible, otherwise Nontypable
- Five columns for each of the genes with either:
 - FULL: for a complete match to the gene in the database (as defined by the --min_cov and --min_id flags which default to at least 95% coverage and percent 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)

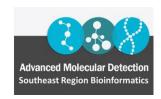
<u>GitHub - MDU-PHL/meningotype: In silico serotyping, finetyping and Bexsero antigen sequence typing of Neisseria</u> meningitidis



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

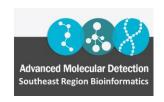
```
thsalikilakshmi@login1:/blue/bphl-florida/thsalikilakshmi/data/jbi
                                                                           ×
(/blue/bphl-florida/thsalikilakshmi/training/conda envs/meningotype) [thsalikila ^
kshmi@loginl jbi]$ meningotype --help
usage:
  meningotype [OPTIONS] <fastal> <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:
                  input FASTA files eg. fastal, fasta2, fasta3 ... fastaN
  FASTA
optional arguments:
  -h, --help
                  show this help message and exit
  --finetype
                  perform porA and fetA fine typing (default=off)
                  perform porB sequence typing (NEIS2020) (default=off)
  --porB
                  perform Bexsero antigen sequence typing (BAST) (default=off)
  --bast
  --mlst
                  perform MLST (default=off)
                  perform MLST, porA, fetA, porB, BAST typing (default=off)
  --all
```



Input

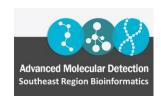
Takes fasta as input

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



Results

1	А	В	С	D	E	F	G	Н		J	K
1	SAMPLE_ID	SEROGRO	ctrA	MLST	PorA	FetA	PorB	fHbp	NHBA	NadA	BAST
2	JB122000642.fasta	С	ctrA	11	5-1,10-8	F3-6	NEIS2020_	130	20	0	-
3	JBI22000645.fasta	С	ctrA	11	5-1,10-8	F3-6	NEIS2020	130	20	0	-
4	JB122000669.fasta	С	ctrA	11	5-1,10-8	F3-6	NEIS2020	130	20	0	-
5	JB122000670.fasta	С	ctrA	11	5-1,10-8	F3-6	NEIS2020	130	20	0	-





Advanced Molecular Detection Southeast Region Bioinformatics

Questions?

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