

Advanced Molecular Detection Southeast Region Bioinformatics

Outline



Agenda



Notes



Spatyper



Ssuissero



Questions

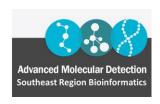
Agenda

January 22 – Bactopia Pipeline

February 5 – Sanibel Pipeline

Future Trainings

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



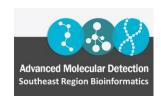
Notes

- Thanks everyone for responding to AMD Southeast Region Annual Needs Assessment Survey
- If any staff members require new HPG user training, please feel free to email us

Spatyper

- Computational method for finding spa types in Staphylococcus aureus
- Staphylococcal protein A (SpA) is a multifunctional, highly conserved virulence factor of *Staphylococcus* aureus
- Spa typing is a molecular typing method that is used to identify different strains of S. aureus.
- It is an important tool for the control and prevention of S. aureus spread around healthcare settings
- By identifying the most prevalent spa types, epidemiological surveys and nosocomial infection control policies can be developed
- Prints spa type to stdout egenomics letter combination and then the ridom spa type
- If multiple pcr products are found it will print spa types for each product
- It downloads sparepeats.fasta and spatypes.txt from the ridom server to repository directory if files not provided or already in directory

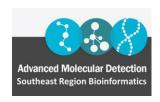
rpetit3/spaTyper: Computational method for finding spa types. (github.com)



Installation

Can be installed through conda

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



Usage

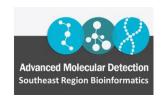
```
(/blue/bphl-florida/thsalikilakshmi/training/conda envs/spatyper) [thsalikilakshmi@login5 assemblies]$ spaTyper --help
usage: spaTyper [-h] [-r REPEAT FILE] [-o REPEAT ORDER FILE] [-d FOLDER] [-f FASTA [FASTA ...]] [-g GLOB] [-e] [--output OUTPUT] [--version] [--debu
spaTyper.py: Get spa types
Version: 0.3.3
License: GPLv3
USAGE: python spaTyper.py -f fasta file.fasta
Prints spa type to stdout
It will download sparepeats.fasta and spatypes.txt to repository directory
if files not provided or already in directory. It can be loaded as a python
module. Python 3 version only.
options:
  -h, --help
                       show this help message and exit
  -r REPEAT FILE, --repeat file REPEAT FILE
                        List of spa repeats (http://spa.ridom.de/dynamic/sparepeats.fasta)
  -o REPEAT ORDER FILE, --repeat order file REPEAT ORDER FILE
                       List spa types and order of repeats (http://spa.ridom.de/dynamic/spatypes.txt)
  -d FOLDER, --folder FOLDER
                        Folder to save downloaded files from Ridom/Spa server
  -f FASTA [FASTA ...], --fasta FASTA [FASTA ...]
                        List of one or more fasta files.
```



Input

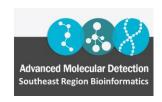
Takes fasta files as input

\$ spaTyper -f JBI22001448.fasta > spaTyper_results



Results

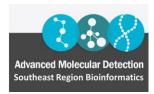
1	Sequence name	Repeats	Туре
2	4 length=203738 depth=1.23x	08-16-02-25-34-25	t1451
3		•	



Ssuissero

- Rapid Streptococcus suis serotyping on Nanopore Sequencing Data
- This pipeline is designed to rapidly infer Streptococcus suis serotype from Oxford Nanopore data by first assembling a draft genome using Flye followed by genome polishing with racon and medaka
- The processed assembly is subsequently queried against the Cps Blast Database to determine isolate serotype
- An additional variant calling step is employed to resolve serotype 2 and 1/2, as well as 1 and 14

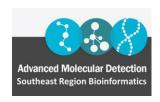
jimmyliu1326/SsuisSero: Rapid Streptococcus suis Serotyping on Nanopore Sequencing Data (github.com)



Installation

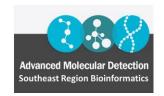
Can be installed through conda

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



Usage

```
(/blue/bphl-florida/thsalikilakshmi/training/conda_envs/ssuissero) [thsalikilakshmi@login5 assemblies]$ SsuisSero.sh --help
Usage: /blue/bphl-florida/thsalikilakshmi/training/conda envs/ssuissero/bin/SsuisSero.sh
Required arguements:
-i input file
-o path to output directory
-s sample name
-x input type [fasta or fastq]
Optional arguments:
-h|--help
          display help message
-t|--threads number of threads [Default: 4]
```



Input

Accepts fasta or fastq files as input

\$ SsuisSero.sh -i JBI22001449.fasta -x fasta -s JBI22001449.fasta -o ssuissero_results



Results

1	Sample_Name Serotype
2	JBI22001449.fasta No Hits
2	



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Questions?

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