



# **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. \(github.com\)](https://github.com/rpetit3/spaTyper)

# 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/bph1-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] [--debug]

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	Type
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 \(github.com\)](https://github.com/jimmyliu1326/SsuisSero)

# 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 arguments:

- 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	JB122001449.fasta No Hits
3	



# Advanced Molecular Detection Southeast Region Bioinformatics

## Questions?

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