Advanced Molecular Detection
Southeast Region Bioinformatics

Bactopia tools
10/30/2023

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

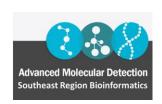- Also, just a reminder to email your requests to bphl-sebioinformatics@flhealth.gov

Agenda

November 13 – Bactopia Tools: Pbptyper and Prokka

November 27 – Bactopia Tools: rgi (resistance gene identifier) and Seqsero2

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

Mykrobe

- Antibiotic resistance prediction in minutes
- Currently supports *Mycobacterium tuberculosis, Staphylococcus aureus, Shigella sonnei, Salmonella typhi*
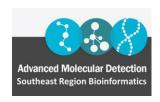
Mykrobe-tools/mykrobe: Antibiotic resistance prediction in minutes (github.com)
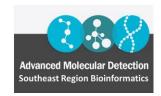
Installation

Can be installed through conda

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

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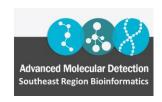Southeast Region Bioinformatics

Usage


```
(/blue/bph1-florida/thsalikilakshmi/training/conda_envs/mykrobe) [thsalikilakshmi@login6 assemblies]$ mykrobe --help
usage: mykrobe [-h] [--version] {predict,panels,variants,vars} ...


options:
  -h, --help             show this help message and exit
  --version              mykrobe version


[sub-commands]:
  {predict,panels,variants,vars}
    predict              Predict the sample's drug susceptibility
    panels               Add, update, or remove panels
    variants (vars)      build variant probes
```
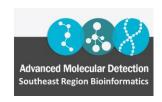
Input

$ mykrobe predict -S staph -s JBI22001448 -i JBI22001448_1.fastq.gz JBI22001448_2.fastq.gz -o mykrobe_out.csv
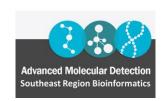
Results

1	sample,"drug","susceptibility","variants (dna_variant-AA_variant:ref_kmer_count:alt_kmer_count:conf) [use --format json for more info]","genes (prot_mut-ref_mut:percent_covg:depth) [use --	
2	JBI22001448,"Ciprofloxacin","S","","","v0.12.2","JBI22001448_1.fastq.gz;JBI22001448_2.fastq.gz","/blue/bphl-florida/thsalikilakshmi/training/conda_envs/mykrobe/lib/python3.10/site-packages/	
3	JBI22001448,"Clindamycin","R","","ermT:90:57","v0.12.2","JBI22001448_1.fastq.gz;JBI22001448_2.fastq.gz","/blue/bphl-florida/thsalikilakshmi/training/conda_envs/mykrobe/lib/python3.10/site-	
4	JBI22001448,"Erythromycin","R","","ermT:90:57","v0.12.2","JBI22001448_1.fastq.gz;JBI22001448_2.fastq.gz","/blue/bphl-florida/thsalikilakshmi/training/conda_envs/mykrobe/lib/python3.10/site-	
5	JBI22001448,"FusidicAcid","S","","","v0.12.2","JBI22001448_1.fastq.gz;JBI22001448_2.fastq.gz","/blue/bphl-florida/thsalikilakshmi/training/conda_envs/mykrobe/lib/python3.10/site-packages/my	
6	JBI22001448,"Gentamicin","R","","aacAaphD:100:66","v0.12.2","JBI22001448_1.fastq.gz;JBI22001448_2.fastq.gz","/blue/bphl-florida/thsalikilakshmi/training/conda_envs/mykrobe/lib/python3.10/	
7	JBI22001448,"Methicillin","S","","","v0.12.2","JBI22001448_1.fastq.gz;JBI22001448_2.fastq.gz","/blue/bphl-florida/thsalikilakshmi/training/conda_envs/mykrobe/lib/python3.10/site-packages/my	
8	JBI22001448,"Mupirocin","S","","","v0.12.2","JBI22001448_1.fastq.gz;JBI22001448_2.fastq.gz","/blue/bphl-florida/thsalikilakshmi/training/conda_envs/mykrobe/lib/python3.10/site-packages/myk	
9	JBI22001448,"Penicillin","R","","blaZ:90:48","v0.12.2","JBI22001448_1.fastq.gz;JBI22001448_2.fastq.gz","/blue/bphl-florida/thsalikilakshmi/training/conda_envs/mykrobe/lib/python3.10/site-pack	
10	JBI22001448,"Rifampicin","S","","","v0.12.2","JBI22001448_1.fastq.gz;JBI22001448_2.fastq.gz","/blue/bphl-florida/thsalikilakshmi/training/conda_envs/mykrobe/lib/python3.10/site-packages/my	
11	JBI22001448,"Tetracycline","S","","","v0.12.2","JBI22001448_1.fastq.gz;JBI22001448_2.fastq.gz","/blue/bphl-florida/thsalikilakshmi/training/conda_envs/mykrobe/lib/python3.10/site-packages/m	
12	JBI22001448,"Trimethoprim","S","","","v0.12.2","JBI22001448_1.fastq.gz;JBI22001448_2.fastq.gz","/blue/bphl-florida/thsalikilakshmi/training/conda_envs/mykrobe/lib/python3.10/site-packages/	
13	JBI22001448,"Vancomycin","S","","","v0.12.2","JBI22001448_1.fastq.gz;JBI22001448_2.fastq.gz","/blue/bphl-florida/thsalikilakshmi/training/conda_envs/mykrobe/lib/python3.10/site-packages/m	

Pasty

- A tool to identify the serogroup of *Pseudomonas aeruginosa* isolates
- Using an input assembly (uncompressed or g-zip compressed), the sequences are blasted against a set of O-antigens
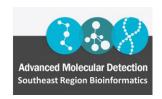- Serogroup is then predicted based on these results

rpetit3/pasty: A tool easily taken advantage of for in silico serogrouping of Pseudomonas aeruginosa isolates (github.com)
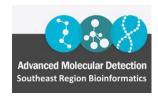
Installation

Can be installed through conda

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

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

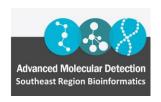conda install -c conda-forge -c bioconda pasty

Usage

```
(/blue/bphl-florida/thsalikilakshmi/training/conda_envs/pasty) [thsalikilakshmi@login6 conda_envs]$ pasty --help

Usage: pasty [OPTIONS]

A tool easily taken advantage of for in silico serogrouping of Pseudomonas aeruginosa isolates

╭─ Options ────────────────────────────────────────────────────────────────────────────────────────────╮
│
│   --version                    Show the version and exit.
│ * --assembly         TEXT      Input assembly in FASTA format (gzip is OK) [required]
│   --db               TEXT      Input database in uncompressed FASTA format                      .
│                               [default: /blue/bphl-florida/thsalikilakshmi/training/conda_envs/pasty/share/pasty-1.0.2/OSAdb.fasta]
│   --prefix           TEXT      Prefix to use for output files [default: basename of input]
│   --outdir           TEXT      Directory to save output files [default: ./]
│   --min_pident       INTEGER   Minimum percent identity to count a hit [default: 95]
│   --min_coverage     INTEGER   Minimum percent coverage to count a hit [default: 95]
│   --help                       Show this message and exit.
```

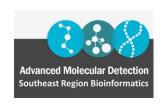# Input

Takes .fasta as input

$ pasty --assembly JBI22000866.fasta

Results (prefix.details.tsv)

This file provides the coverage and number of fragments for each of the serogroups

	sample	serogroup	coverage	fragments
1				
2	JBI22000866	O1	100	1
3	JBI22000866	O2	9.83	2
4	JBI22000866	O3	11.18	2
5	JBI22000866	O4	14.36	2
6	JBI22000866	O5	0	0
7	JBI22000866	O6	14.07	2
8	JBI22000866	O7	11.54	2
9	JBI22000866	O9	36.62	1
10	JBI22000866	O10	12.52	2
11	JBI22000866	O11	15.85	2
12	JBI22000866	O12	1.24	1
13	JBI22000866	O13	15.39	2
14	JBI22000866	WyzB	0	0

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Results (prefix.tsv)

This file will contain the final predicted serogroup based on highest coverage

sample	serogroup	coverage	fragments	comment
JBI22000866	O1	100	1	

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Questions?

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