Introduction

SeqSero is a pipeline for *Salmonella* serotype determination from raw sequencing reads or genome assemblies. A web app is available at www.denglab.info/SeqSero

Dependencies

SeqSero depends on:

1. Python 2.7 and Biopython 1.65 (http://biopython.org/wiki/Download)
2. Burrows-Wheeler Aligner (http://sourceforge.net/projects/bio-bwa/files/)
3. Samtools (http://sourceforge.net/projects/samtools/files/samtools/)
4. NCBI BLAST (ftp://ftp.ncbi.nlm.nih.gov/blast/executables/LATEST/)
5. SRA Toolkit (http://www.ncbi.nlm.nih.gov/Traces/sra/sra.cgi?cmd=show&f=software&m=software&s=software)

Make sure all the executables are added to your search path. SeqSero also uses the *in silico* PCR program (isPcr) written by Jim Kent (http://hgwdev.cse.ucsc.edu/~kent/exe/linux/), which is supplied by the SeqSero package.

Executing the code

Usage: SeqSero.py

-m <int> (input data type, '1' for interleaved paired-end reads , '2' for separated paired-end reads, '3' for

single reads, '4' for genome assembly)

-i <file> (/path/to/input/file)

-b <string> (algorithms for bwa mapping; 'mem' for mem, 'sam' for samse/sampe; default=sam;

optional)

Output

Upon executing the command, a directory named "SeqSero_result_<time_you_run_SeqSero>" will be created. Your result will be stored in "Seqsero_result.txt" in that directory.