

IRIDA Integrated Rapid Infectious Disease Analysis Platform

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Genomics has become a critical part of Public Health Microbiology

But there are challenges:

- Data management, organization and access controls
- Validation and reproducibility of data analysis pipelines
- Computational infrastructure



S. enterica serovar Heidelberg PRJNA305824 ID 7

Samples

Line List

Analyses

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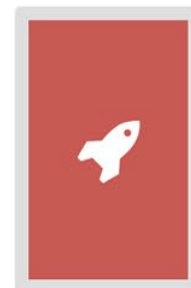
No samples selected

	Name	Organism	Project	Created On	Modified On
<input type="checkbox"/>	SRR3028741	Salmonella enterica subsp. enterica serovar Heidelberg	S. enterica serovar Heidelberg PRJNA305824	Mar 30, 2018 5:31 PM	May 25, 2018 2:27 PM
<input type="checkbox"/>	SRR3028776	Salmonella enterica subsp. enterica serovar Heidelberg	S. enterica serovar Heidelberg PRJNA305824	Mar 30, 2018 7:13 PM	May 25, 2018 2:11 PM
<input type="checkbox"/>	SRR3028774	Salmonella enterica subsp. enterica serovar Heidelberg	S. enterica serovar Heidelberg PRJNA305824	Mar 30, 2018 7:11 PM	Apr 13, 2018 10:21 AM

SNVPhyl Phylogenomics Pipeline

Pipeline Name	<input type="text" value="SNVPhyl_20190526"/>
Reference File	<input type="text" value="GCF_000293905.1_ASM29390v1_genomic.fna (S. enterica serovar Heidel ▾)"/> Upload New
Parameters	<input type="text" value="Default Parameters ▾"/> Customize
Description	<input type="text" value="Enter description of the analysis (Optional)"/>
Share Results with Projects	<input type="checkbox"/> S. enterica serovar Heidelberg PRJNA305824

Ready to Launch?



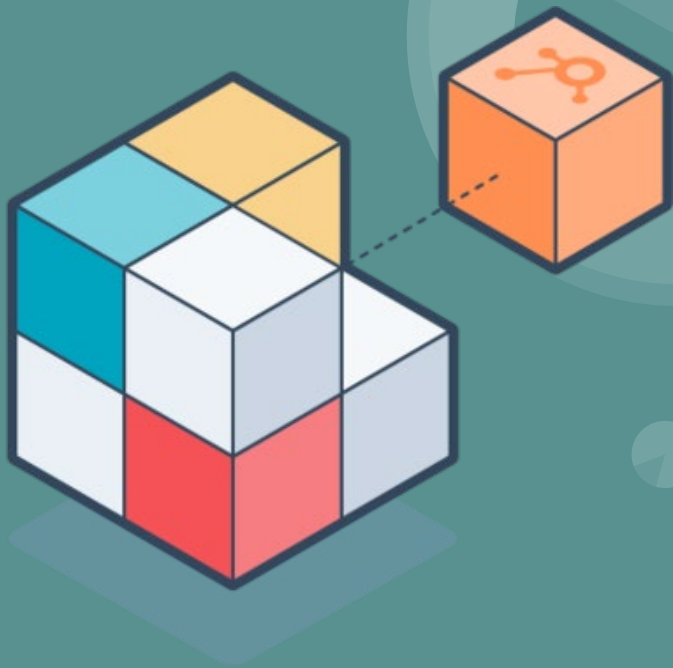
Files

S. enterica serovar Heidelberg PRJNA305824 / SRR3028741

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	<input type="text" value="SRR3028741_1.fastq"/>	349.3 MB File Size	25 May 2018 Date Created
	<input type="text" value="SRR3028741_2.fastq"/>	351.9 MB File Size	25 May 2018 Date Created

New Feature: Pipeline Plugins



Select a Pipeline

Your cart has no local samples selected. Select some samples from one of your [Projects](#) to run a pipeline.

Assembly and Annotation Pipeline

Generate an assembled and annotated genome from the reads within a sample using FLASH, SPAdes, and Prokka. Outputs analyzed and produced separately for each sample include: log files, assembly statistics, the contigs (all contigs, filtered contigs with repeats, filtered contigs without repeats), and annotations from Prokka.

Assembly and Annotation Collection Pipeline

The assembly and annotation collection pipeline provides the same results as the assembly and annotation pipeline, but all samples are analyzed together which allows you to download a single package for all samples submitted.

bio_hansel Pipeline

Rapidly subtype microbial genomes using single nucleotide variant (SNV) subtyping schemes (https://github.com/phac-nml/bio_hansel). Currently, only available for subtyping Salmonella Enteritidis and Salmonella Heidelberg genomes.

IslandViewer Genomic Island Prediction

IslandViewer is a computational tool that integrates four different genomic island prediction methods: IslandPick, IslandPath-DIMOB, SIGI-HMM, and Islander.

MentaLiST MLST Pipeline

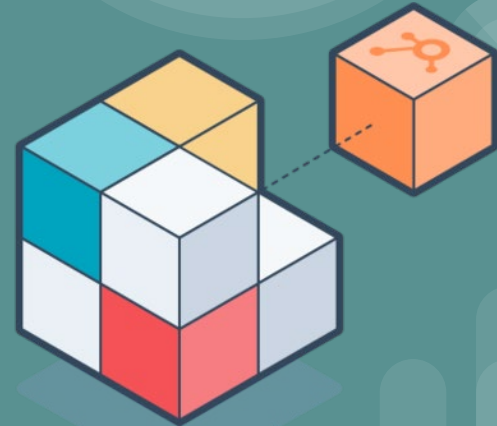
Genotype bacterial samples directly from reads, using an efficient k-mer based algorithm.

SNVPhyl Phylogenomics Pipeline

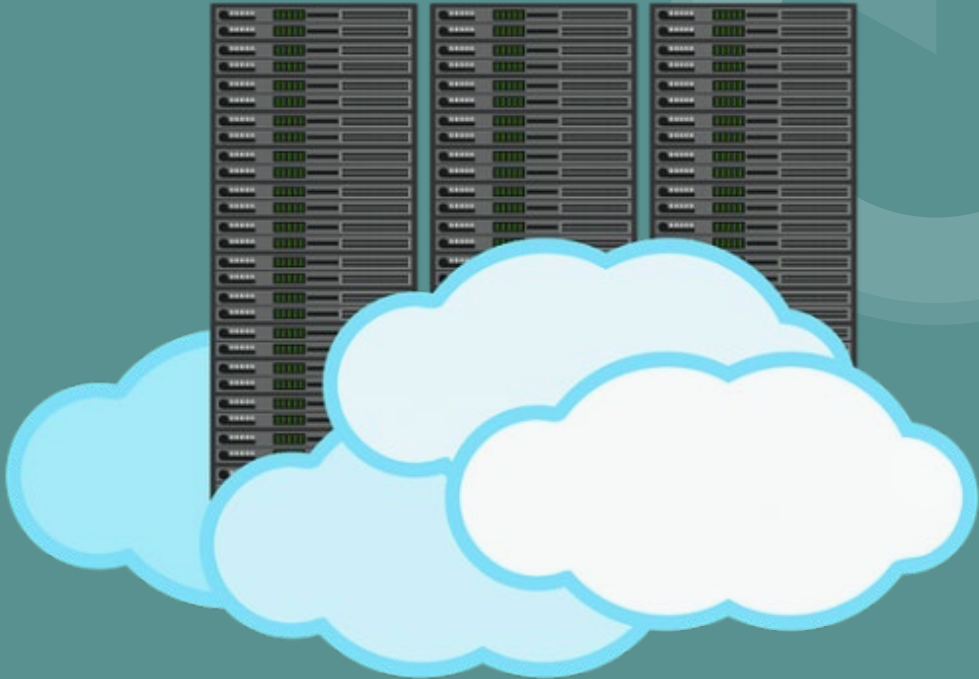
Generate a Whole Genome Phylogeny from a set of samples and a reference genome based on Single Nucleotide Polymorphisms (SNVs) using the SNVPhyl pipeline. This will provide a dendrogram as well as a table of all SNVs used and a SNV distance matrix between each sample.

New Feature: Pipeline Plugins

- Easier customization of IRIDA instances
- Allows each organization to focus on their own priorities
- Pipelines can be shared between IRIDA instances



Upcoming Feature: Cloud Deployment



Upcoming Feature: Cloud Deployment

- Deploy IRIDA to a cloud provider
- Minimal baseline resources, scales up as needed when analysis demands increase
- Lowers barrier to entry





Project Leaders

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Agence de la santé
publique du Canada

