

PATRIC Bioinformatics Resource Center

Argonne National Lab

Lemont, Illinois

May 7–9, 2018



www.patricbrc.org





PATRIC User Registration

USERNAME**FIRST NAME****LAST NAME****EMAIL ADDRESS****ORGANIZATION****ORGANISMS****INTERESTS**[Register New User](#)

Workshop instructors

- ▶ Neal Conrad
- ▶ Marcus Nguyen
- ▶ Rebecca Wattam
- ▶ Jim Davis
- ▶ Maulik Shukla
- ▶ Bruce Parrello
- ▶ Ross Overbeek
- ▶ Janaka Edirisinghe

NIH/NIAID BRC Program

Provide publicly accessible database to:

- Store, update, integrate and display genome sequence data, annotation and associated data for human pathogens.
- Provide query, analysis and visualization of information with user friendly interfaces.
- Serve as public repository for NIAID-supported genome-scale programs.
- Collaborate on experimental research projects.

NIAID Bioinformatics Resource Centers

- ▶ PATRIC – bacteria
 - <https://patricbrc.org/>
- ▶ ViPR – viruses
 - <https://www.viprbrc.org>
- ▶ EuPathDB – eukaryotes
 - <https://eupathdb.org>
- ▶ Vectors – invertebrates
 - <https://www.vectorbase.org/>

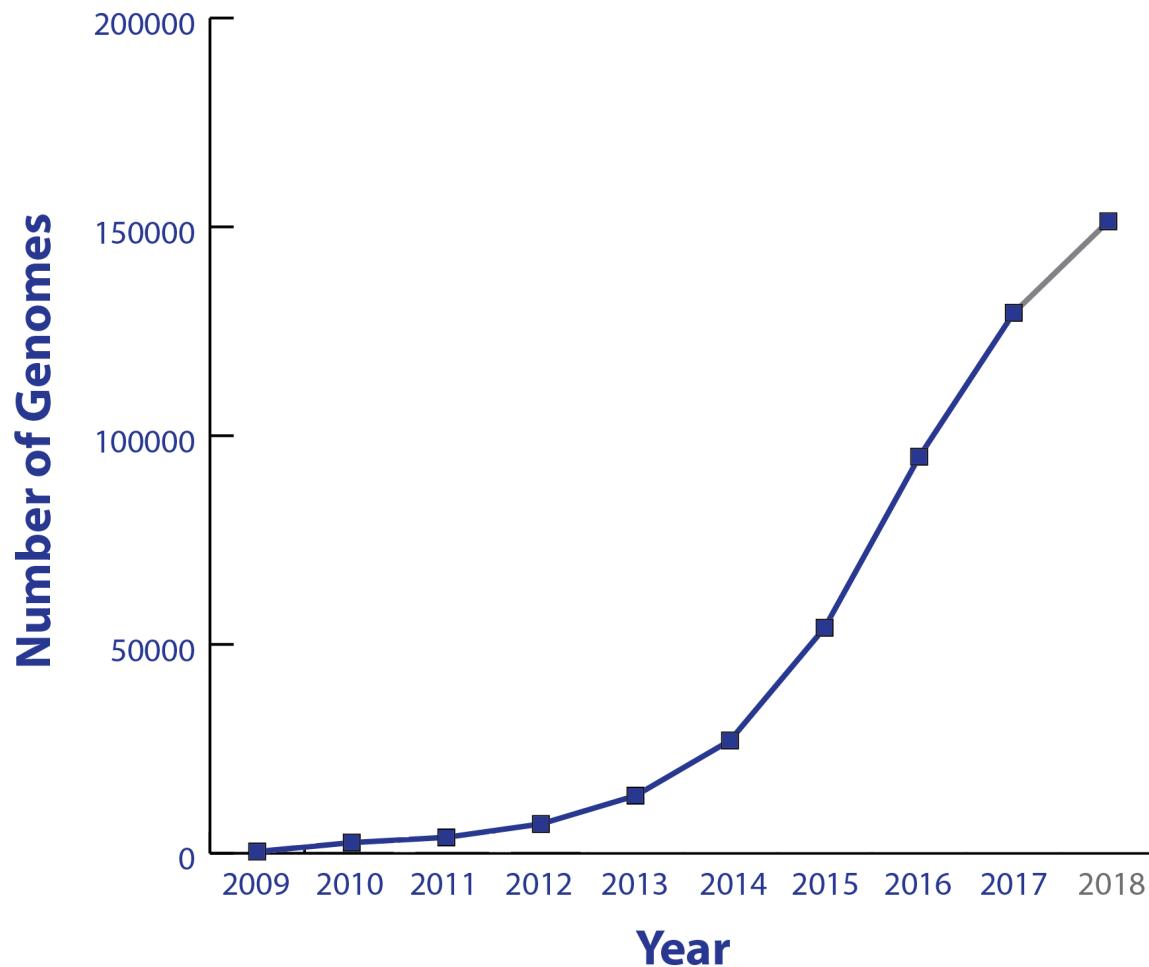


PATRIC (NIAID) Watchlist Genera

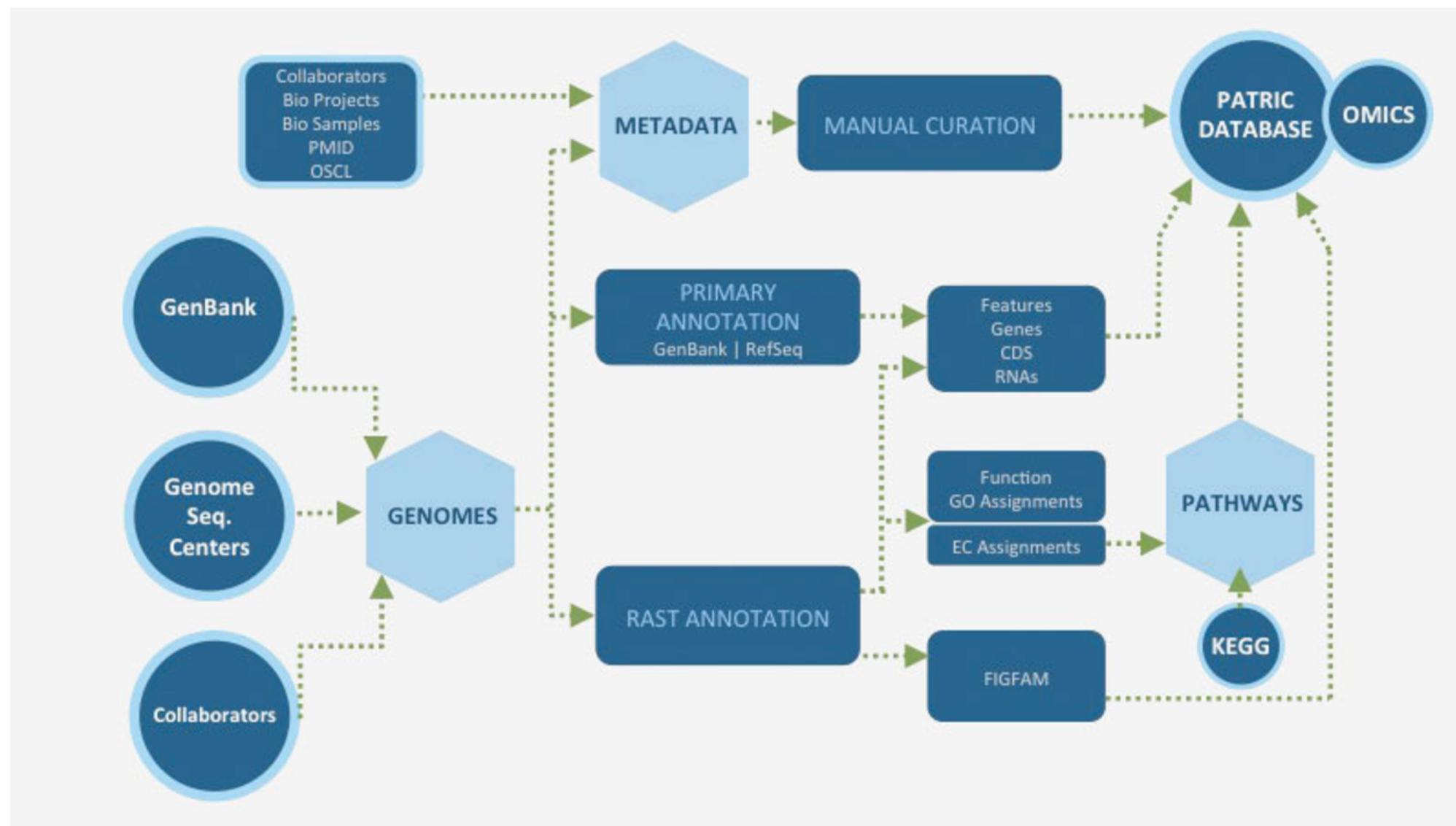
- ▶ *Bacillus*
- ▶ *Bartonella*
- ▶ *Borrelia*
- ▶ *Brucella*
- ▶ *Burkholderia*
- ▶ *Campylobacter*
- ▶ *Chlamydophila*
- ▶ *Clostridium*
- ▶ *Coxiella*
- ▶ *Ehrlichia*
- ▶ *Francisella*
- ▶ *Helicobacter*
- ▶ *Listeria*
- ▶ *Mycobacterium*
- ▶ *Rickettsia*
- ▶ *Salmonella*
- ▶ *Shigella*
- ▶ *Staphylococcus*
- ▶ *Streptococcus*
- ▶ *Vibrio*
- ▶ *Yersinia*

PATRIC has ALL Bacterial Genomes,
not just pathogens

How many genomes does PATRIC have?



PATRIC data processing



Uniform annotations across all genomes in PATRIC



SCIENTIFIC
REPORTS



PATRIC: A model organism database

RAST publications have more than 5,000 citations

annotating batches of genomes

Received
12 November 2014

Accepted
2 January 2015

Thomas Brettin^{1,2}, James J. Davis^{1,2}, Terry Disz³, Robert A. Edwards^{4,5}, Svetlana Gerdes^{1,3}, Gary J. Olsen⁶, Robert Olson^{2,4}, Ross Overbeek^{1,2}, Bruce Parrello^{1,3}, Gordon D. Pusch^{1,2}, Maulik Shukla⁷, James A. Thomason III⁸, Rick Stevens^{1,2,9}, Veronika Vonstein^{1,3}, Alice R. Wattam⁷ & Fangfang Xia^{2,4}

Some Unique PATRIC Features

► Comprehensive Data Collection

- Unified Database, including RefSeq, GenBank, other sources

► Uniform Annotation Across all Genomes

- RAST annotation, EC, GO, plus RefSeq annotations
- Uniform projection of Protein Families, AMR related genes and Virulence factors

► User Workspace for analysis of User data

- “Virtual Integration” your data in the context of all the public datasets

Protein family assignments enable analysis

The screenshot shows the front page of the journal "frontiers in Microbiology". The header features the journal logo with three colored cubes (blue, green, red) followed by the text "frontiers in Microbiology" and a "Systems Microbiology" tag. Below the header is a navigation bar with links for "SECTION", "ABOUT", "ARTICLES", "RESEARCH TOPICS", "FOR AUTHORS", "EDITORIAL BOARD", and "ARTICLE ALERTS". There are also social media icons for Twitter, Facebook, and RSS feed, along with a "ARTICLE ALERTS" button. A sidebar on the left indicates the user is viewing "Articles". A banner at the top right states "THIS ARTICLE IS PART OF THE RESEARCH TOPIC" and "Towards integrated metabolic and regulatory models of all microorganisms". The main content area displays a "METHODS ARTICLE" titled "PATtyFams: Protein Families for the Microbial Genomes in the PATRIC Database" from "Front. Microbiol.", 08 February 2016. The DOI is provided as <https://doi.org/10.3389/fmicb.2016.00118>. The author list includes James J. Davis^{1,2*}, Svetlana Gerdes^{2,3}, Gary J. Olsen⁴, Robert Olson^{1,5}, Gordon D. Pusch^{2,3}, Maulik Shukla^{1,2}, Veronika Vonstein^{2,3}, Alice R. Wattam⁶, and Hyunseung Yoo^{1,2}.

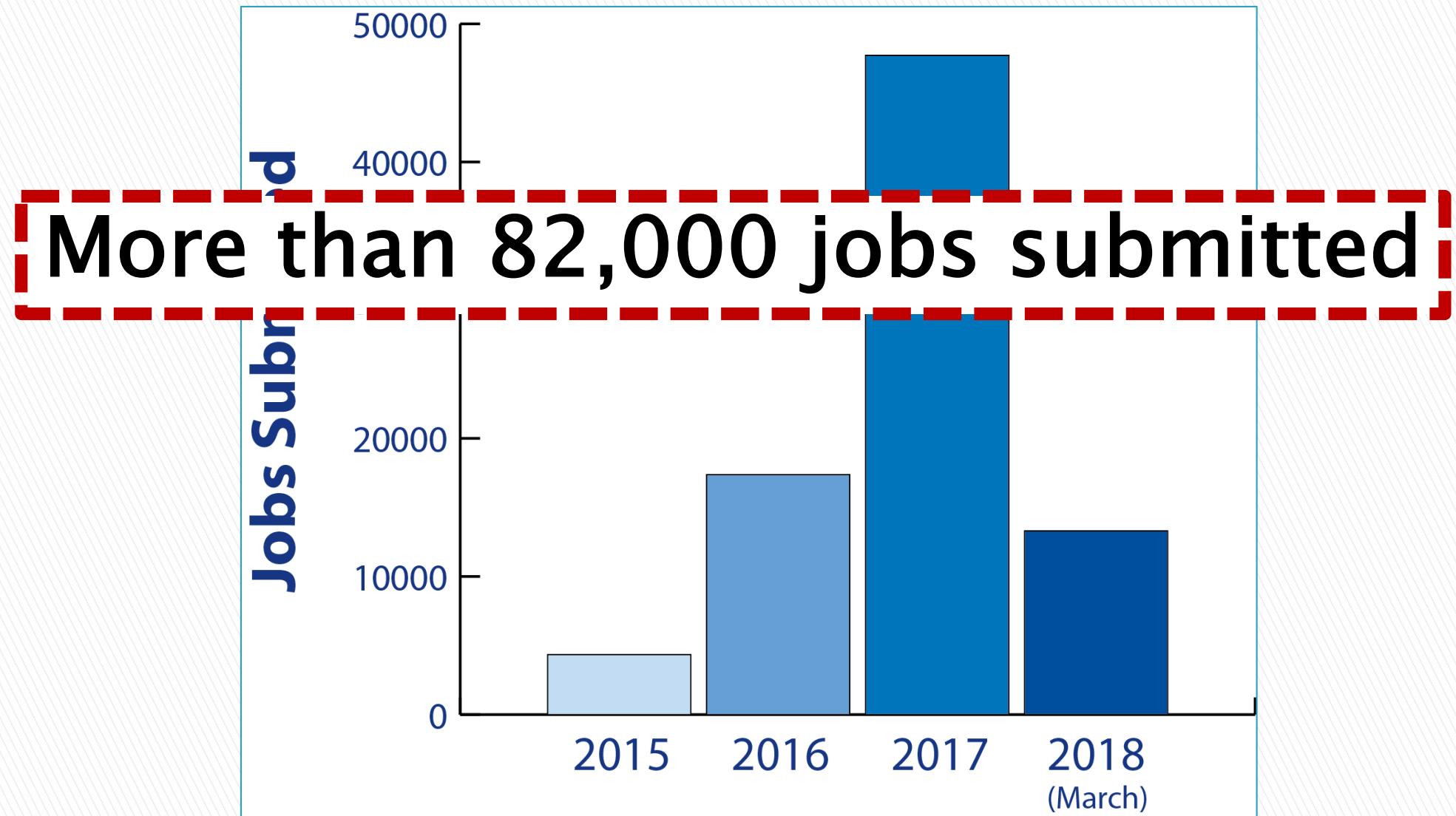
PATRIC Services

- ▶ Assembly – 2015
- ▶ Annotation – 2015
- ▶ Differential Expression – 2015

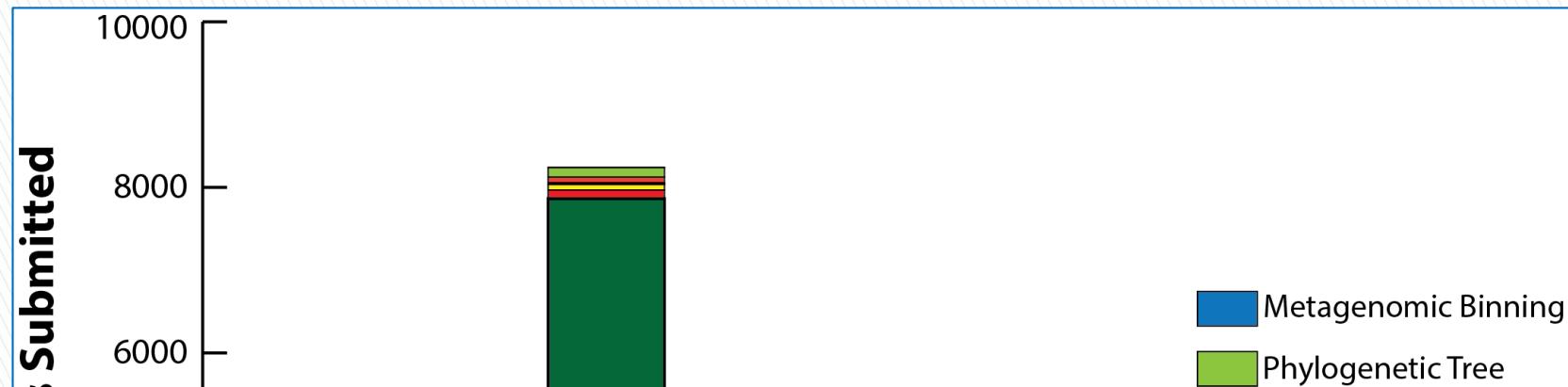
BYOD: Bring Your Own Data and analyze it in PATRIC

- ▶ Proteome Comparison – 2015
- ▶ RNA-Seq – 2015
- ▶ Transposon-Seq – 2017
- ▶ Variation – 2016

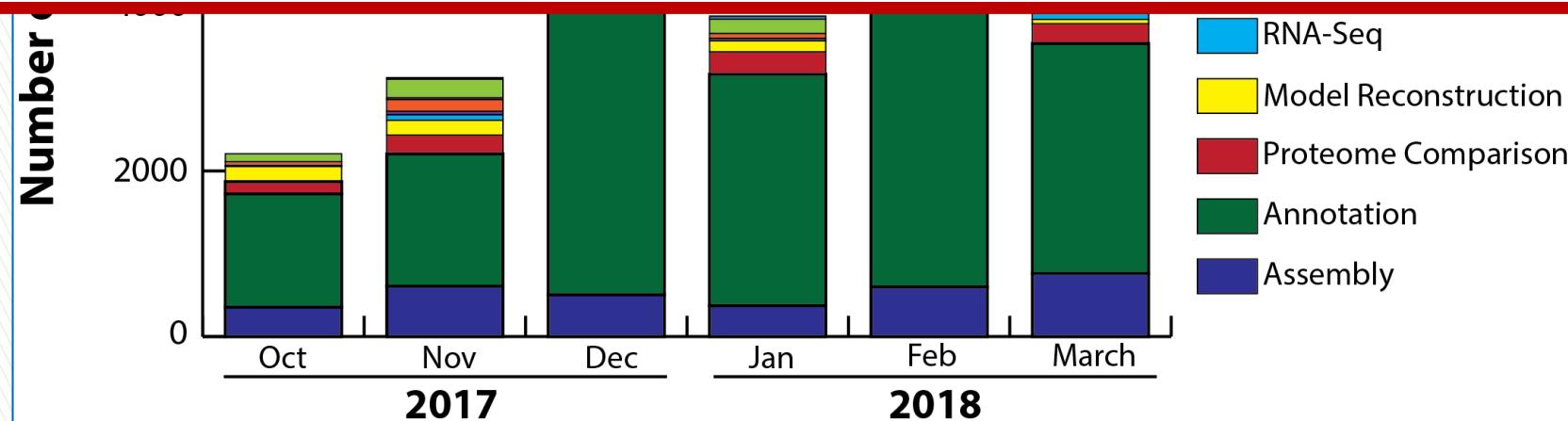
Does anybody use these services?



What services are they using most?



14,000 users returning in last 12 months



How can researchers find data of interest?



Where can one find metadata?

Locate in publications–
LABOR INTENSIVE

ARTICLES

Articles

Whole genome sequencing of meticillin-resistant *Staphylococcus aureus*

Makoto Kuroda, Toshiko Ohta, Ikuo Uchiyama, Tadashi Baba, Harumi Yuzawa, Ichizo Kobayashi, Longzhu Cui, Akio Oguchi, Ken-ichi Aoki, Yoshimi Nagai, JianQi Lian, Teruyo Ito, Mutsumi Kanamori, Hiroyuki Matsumaru, Atsushi Maruyama, Hiroyuki Murakami, Akira Hosoyama, Yoko Mizutani-Ui, Noriko K Takahashi, Toshihiko Sawano, Ryu-ichi Inoue, Chikara Kaito, Kazuhisa Sekimizu, Hideki Hirakawa, Satoru Kuhara, Susumu Goto, Junko Yabuzaki, Minoru Kanehisa, Atsushi Yamashita, Kenshiro Oshima, Keiko Furuya, Chie Yoshino, Tadayoshi Shiba, Masahira Hattori, Naotake Ogasawara, Hideo Hayashi, Keiichi Hiramatsu

Summary

Background *Staphylococcus aureus* is one of the major causes of community-acquired and hospital-acquired infections. It produces numerous toxins including superantigens that cause unique disease entities such as toxic-shock syndrome and staphylococcal scarlet fever, and has acquired resistance to practically all antibiotics. Whole genome analysis is a necessary step towards future development of countermeasures against this organism.

Methods Whole genome sequences of two related *S. aureus* strains (N315 and Mu50) were determined by shot-gun random sequencing. N315 is a meticillin-resistant *S. aureus* (MRSA) strain isolated in 1982, and Mu50 is an MRSA strain with vancomycin resistance isolated in 1997. The open reading frames were identified by use of GAMBLER and GLIMMER programs, and annotation of each was done with a BLAST homology search, motif analysis, and protein localisation prediction.

Findings The *Staphylococcus* genome was composed of a complex mixture of genes, many of which seem to have been acquired by lateral gene transfer. Most of the antibiotic resistance genes were carried either by plasmids or by mobile genetic elements including a unique resistance island. Three classes of new pathogenicity islands were identified in the genome: a toxic-shock-syndrome toxin island family, exotoxin islands, and enterotoxin islands. In the latter two pathogenicity islands, clusters of exotoxin and enterotoxin genes were found closely linked with other gene clusters encoding putative pathogenic factors. The analysis also identified 70 candidates for new virulence factors.

Interpretation The remarkable ability of *S. aureus* to acquire useful genes from various organisms was revealed through the observation of genome complexity and evidence of lateral gene transfer. Repeated duplication of genes encoding superantigens explains why *S. aureus* is capable of infecting humans of diverse genetic backgrounds, eliciting severe immune reactions. Investigation of many newly identified gene products, including the 70 putative

The entire genome sequences of *S. aureus* N315 and Mu50 have been

Another metadata location

NCBI Resources ▾ How To ▾

Nucleotide Nucleotide Advanced

GenBank ▾ Send to: ▾

Brucella ceti str. Cudo, whole genome shotgun sequencing project

GenBank: ACJD00000000.1

Genome Coverage: 6x
Sequencing Method: WGS and clone-based
Sequencing Technology: 454
Source available from: Thomas Ficht (tficht@cvm.tamu.edu)
The *Brucella ceti* Cudo strain was isolated from the aborted fetus of a bottlenose dolphin, *Tursiops truncatus*. *Brucella ceti* has been isolated from beached cetaceans found around the world.

What PATRIC does with that metadata

Genome View
Bacteria » Proteobacteria » Alphaproteobacteria » Rhizobiales » Brucellaceae » Brucella » Brucella ceti » **Brucella ceti str. Cudo**

Overview AMR Phenotypes Phylogeny Genome Browser Circular Viewer Sequences Features Specialty Genes Protein Families Pathways Sul

Brucella ceti str. Cudo

Length: 3389269bp, Chromosomes: 0, Plasmids: 0, Contigs: 7

Organism Info

Genome ID	595497.3
Genome Name	Brucella ceti str. Cudo
NCBI Taxon ID	595497
Genome Status	WGS
Strain	Cudo

Isolate Info

Isolation	bottlenose dolphin (<i>Tursiops truncatus</i>)
Source	
Isolation	isolated from a bottlenose dolphin (<i>Tursiops truncatus</i>)
Comments	

Host Info

Host Name	Bottlenose dolphin, <i>Tursiops truncatus</i>
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Sequence Info

Genomic Features

	PATRIC	RefSeq
CDS	3610	3154
tRNA	50	50
pseudogene	39	145
rRNA	7	9
misc_RNA	3	0
misc_binding	0	10

Protein Features

	PATRIC	RefSeq
Hypothetical proteins	787	864
Proteins with functional assignments	2823	2290
Proteins with EC number assignments	957	397
Proteins with GO assignments	928	1739
Proteins with Pathway assignments	752	220

Make the metadata searchable!

DATA ▾ WORKSPACES ▾ SERVICES ▾ HELP ▾ All Data Types ▾ bottlenose dolphin Q ? All terms ▾

Genomes (4)

Brucella ceti str. Cudo

Genome ID: 595497.3 | 7 Contigs

SEQUENCED: 3/23/09 (Virginia Bioinformatics Institute)

HOST: Bottlenose dolphin, *Tursiops truncatus*

Brucella ceti Cudo. Brucella ceti Cudo was isolated from a bottlenose dolphin (*Tursiops truncatus*). The genome sequence of this organism will provide interesting insights into the evolution of this species.

Brucella sp. F5/99

Genome ID: 437701.3 | 13 Contigs

SEQUENCED: 1/22/09 (Broad Institute)

Brucella sp. F5/99. Brucella sp. F5/99 was isolated from a bottlenose dolphin and will be used for comparative analysis with other Brucella species.

Brucella ceti strain CRO350

Genome ID: 120577.6 | 76 Contigs

SEQUENCED: 8/9/17 (Croatian Veterinary Institute, Zagreb)

COLLECTED: 6/27/15 HOST: *Tursiops truncatus*

Marine mammal brucellosis has been known for more than 20 years, but recent work suggests it is more widespread than originally thought. Brucella (B.) pinnipedialis has been isolated from pinnipeds, while *B. ceti* strains have been associated with cetaceans. Here we report a Brucella strain isolated from multiple lymph nodes of one bottlenose dolphin (*Tursiops truncatus*) during routine examination of dolphin carcasses found in the Croatian part of the northern Adriatic Sea during the summer of 2015. Classical bacteriological biotyping, PCR-based techniques (single, multiplex, PCR-RFLP) and 16S rRNA DNA sequencing were used to identify Brucella spp. Multiple-locus variable number tandem repeat analysis of 16 loci and multilocus sequence typing on 9 loci were used for genotyping and species determination. The combination of bacteriological, molecular and genotyping techniques identified our strain as ST27, previously identified as a human pathogen. This report provides, to our knowledge, the first evidence of ST27 in the Adriatic Sea and in bottlenose dolphins in particular as well as in European waters in general. The

Metadata filtering

PATRIC 3.5.10 ORGANISMS ▾ DATA ▾ WORKSPACES ▾ SERVICES ▾ HELP ▾ All Data Types Find a gene, genome, microarray Q ? All terms ▾ E

Taxon View
Bacteria » Firmicutes » Bacilli » Bacillales » Staphylococcaceae » **Staphylococcus** (11655 Genomes)

Overview Phylogeny Taxonomy Genomes AMR Phenotypes Sequences Features Specialty Genes Protein Families Pathways Subsystems Transcriptomic

Interactions

DOWNLOAD KEYWORDS

HIDE APPLY

Public	Genome Status	Reference Genome	Antimicrobial Resistance	Isolation Country	Host Name	Collection Year
true (11653)	WGS (10984)	Representative (41)	Resistant (2917)	United States (5105)	Human, <i>Homo sapiens</i> (7730)	2004 (1289)
false (2)	Plasmid (392)	Reference (2)	Susceptible (2859)	Netherlands (554)	<i>Bos taurus</i> (99)	2009 (879)
	Complete (279)		Intermediate (53)	Thailand (330)	Canine (94)	2012 (875)
				United Kingdom (321)	Pig, <i>Sus scrofa</i> (59)	2010 (792)
				Germany (306)	Pig, <i>Sus scrofa domesticus</i> (51)	2003 (699)
				Singapore (250)	Chicken, <i>Gallus gallus</i> (26)	2015 (622)

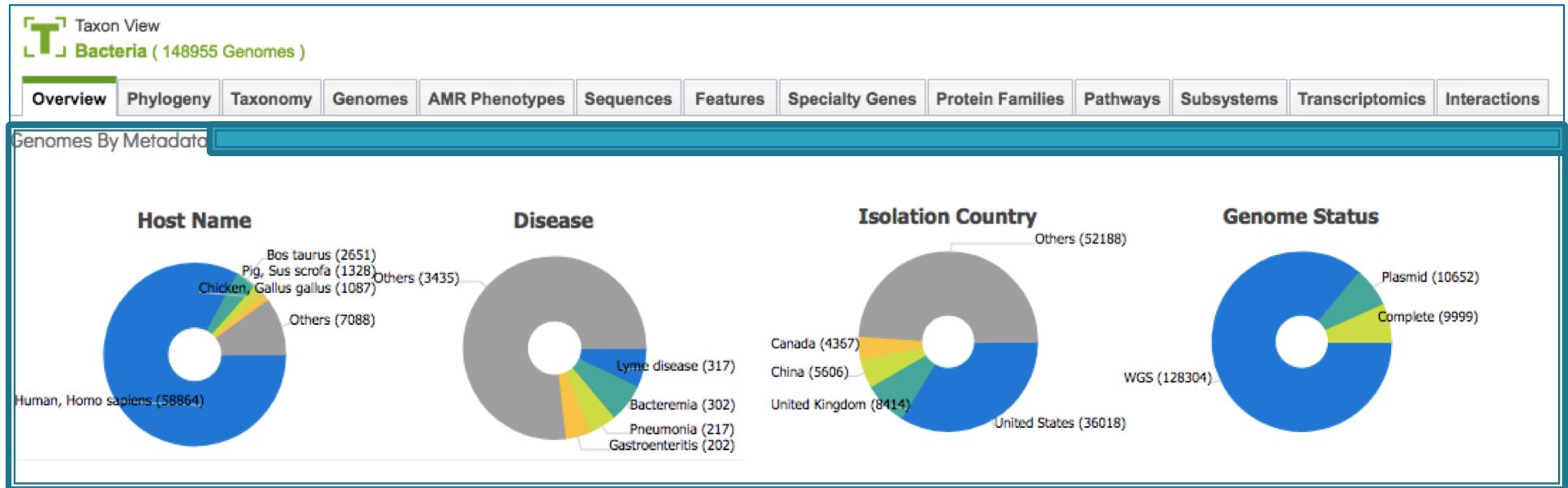
Metadata filtering

	Genome Name	Genome ID	Genome Status	Sequences	PATRIC CDS	Isolation Country	Host Name	Collection Year	Completion Date	Isolation Site
	Staphylococcus aureus P110256-141	1280.4912	WGS	401	3042	United States	Human, Homo sapiens	2010		Blood
	Staphylococcus aureus P110270-142	1280.4913	WGS	33	2596	United States	Human, Homo sapiens	2010		Blood
	Staphylococcus aureus P330170-177	1280.4993	WGS	59	2899	United States	Human, Homo sapiens	2011		Blood
	Staphylococcus aureus P330177-181	1280.4994	WGS	40	2504	United States	Human, Homo sapiens	2011		Blood
	Staphylococcus aureus P210439-24	1280.4954	WGS	59	2844	United States	Human, Homo sapiens	2011		Blood
	Staphylococcus aureus P210500-225	1280.4965	WGS	33	2784	United States	Human, Homo sapiens	2014		Blood
	Staphylococcus aureus P310372-198	1280.4970	WGS	29	2783	United States	Human, Homo sapiens	2011		Blood
	Staphylococcus aureus P310516-204	1280.4972	WGS	25	2676	United States	Human, Homo sapiens	2011		Blood
	Staphylococcus aureus P310516-223	1280.4974	WGS	25	2661	United States	Human, Homo sapiens	2011		Blood
	Staphylococcus aureus P310821-173	1280.4978	WGS	26	2683	United States	Human, Homo sapiens	2011		Blood
	Staphylococcus aureus P310906-176	1280.4982	WGS	29	2768	United States	Human, Homo sapiens	2011		Blood

Large scale summaries based on metadata – AMR



Large scale summaries based on metadata



How data is summarized at PATRIC: Consistencies across levels

[F] Feature View

Bacteria » Actinobacteria » Actinobacteria » Corynebacterales » Mycobacteriaceae » Mycobacterium » Mycobacterium tuberculosis » Mycobacterium tuberculosis H37Rv
fig|83332.12.peg.76 | Rv0067c | Transcriptional regulator, AcrR family

Overview Genome Browser Compare Region Viewer Transcriptomics Correlated Genes Interactions

Chart Table



keyword

|Log Ratio|: 1

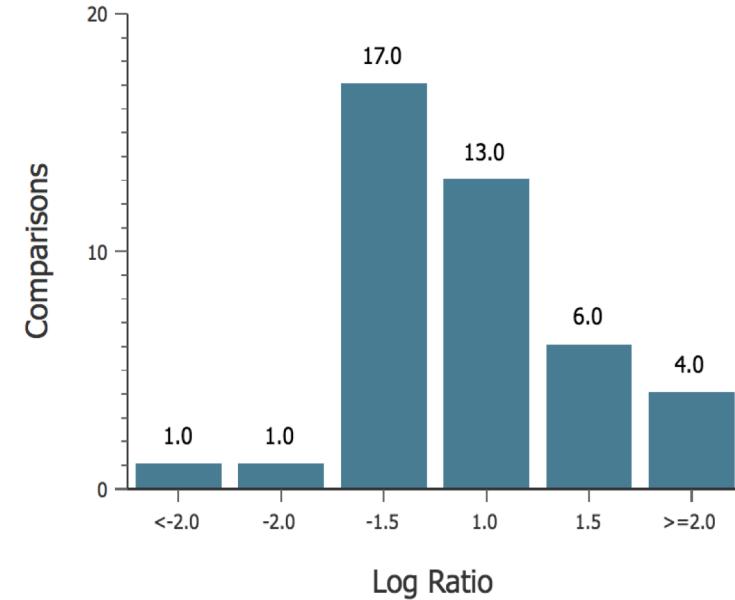
|Z-score|: 0

Filter

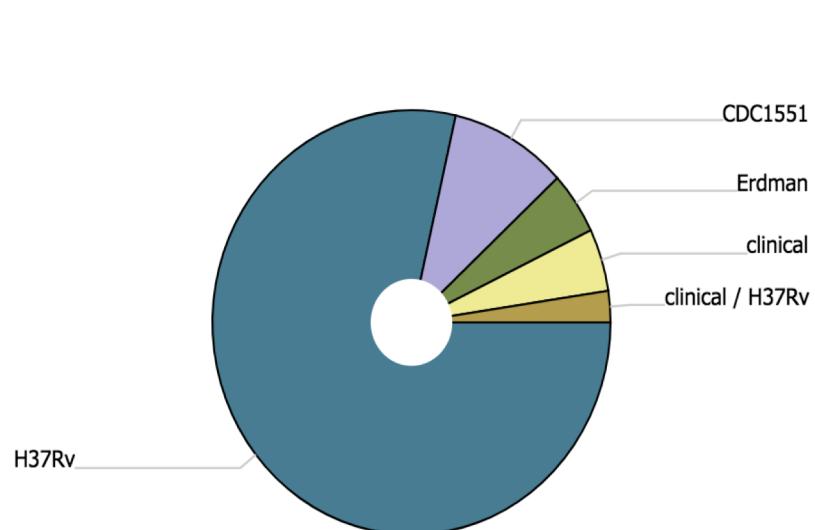
Reset Filter

Show All Comparisons

Log Ratio Z-score



Strain Gene Modification Experimental Condition



New Antimicrobial Data

PATRIC 3.3.10

ORGANISMS ▾ DATA ▾ WORKSPACES ▾ SERVICES ▾ HELP ▾

Data Types	Specialty Data Collections
Antibiotic Resistance	PATRIC Collaborations
Genomes	PATRIC DBPs
Genomic Features	NIAID Clinical Proteomics
Pathways	NIAID Genome Sequencing
Protein Families	NIAID Structural Genomics
Specialty Genes	NIAID Systems Biology
Transcriptomics	NIAID Functional Genomics

Download Data

FTP Server



Antimicrobial Resistance (AMR)

Antibiotics are a type of drugs used in the treatment and prevention of bacterial infections. Antimicrobial Resistance (AMR) refers to the ability of bacteria to resist the effects of antibiotics that are commonly used to treat them. Resistance arises through one of three ways: natural resistance in certain types of bacteria, genetic mutation, or by one species acquiring resistance from another. PATRIC provides a variety of data and analysis tools to help researchers study AMR and its genetic determinants. This includes AMR phenotype data for the bacterial genomes as well as genes and intergenic regions associated with AMR.

What do we mean by ...

Antibiotics:

Antibiotics are a type of antimicrobial drugs used in the treatment and prevention of bacterial infections. PATRIC provides basic information about commonly used antibiotics, including their chemical and physical properties, pharmacology, and mechanism of action. In addition, each antibiotic is linked to other relevant data available in PATRIC, such as AMR phenotypes for genomes, AMR genes, and AMR regions. Below are some examples:

- [amikacin](#)
- [ethambutol](#)
- [isoniazid](#)
- [rifampin](#)
- [streptomycin](#)

[View all antibiotics](#)

AMR Phenotypes:

AMR phenotypes refer to the resistance or susceptibility of a given organism to one or more antibiotics. PATRIC collects AMR phenotype data generated using antimicrobial susceptibility testing methods (AST) from published studies and collaborators. In addition, we also provide predicted AMR phenotypes using machine learning classifiers. See AMR phenotype data for select genera:

- [Mycobacterium](#)
- [Staphylococcus](#)
- [Streptococcus](#)
- [Acinetobacter](#)
- [Pseudomonas](#)

[View all AMR phenotype data](#)

AMR Genes:

AMR genes refer to the genes implicated in or associated with the resistance to one or more antibiotics. The resistance may result from

AMR Regions:

AMR regions refer to the small genomic regions implicated in or associated with the resistance to one or more antibiotics. The AMR

Today's schedule (May 7)

- ▶ 9:00 am Register for PATRIC Account, Overview
- ▶ 10:00 am Assemble a Genome in PATRIC and Data Upload
- ▶ 11:00 am Break
- ▶ 11:10 am Annotate a Genome in PATRIC Using RASTtk
- ▶ 12:00 pm Lunch
- ▶ 1:00 pm Similar Genome Finder
- ▶ 1:30 pm Build a Phylogenetic tree
- ▶ 2:15 pm Break
- ▶ 2:30 pm Comparative Genome Analysis
- ▶ 3:00 pm Proteome Comparison
- ▶ 3:30 pm Comparative Genomics (Proteins and Pathways)
- ▶ 4:30 pm Question and Answer session
- ▶ 5:00 pm Adjourn

Schedule (May 8)

- ▶ 9:00 am BLAST at PATRIC
- ▶ 9:30 am RNA-Seq Pipeline
- ▶ 10:00 am Break
- ▶ 10:15 am Expression Import Service
- ▶ 10:45 am Comparative Transcriptomics
- ▶ 12:00 pm Lunch
- ▶ 1:00 pm SNP and MNP Variation Service
- ▶ 2:00 pm Metagenomic binning service
- ▶ 3:00 pm Building a metabolic model
- ▶ 4:00 pm Question and Answer Session
- ▶ 5:00 pm Adjourn

Schedule (May 9)

- ▶ 9:00 am Command Line Interface
- ▶ 11:00 am Break
- ▶ 11:15 am Work with Private Data
- ▶ 12:00 pm Lunch
- ▶ 1:00 pm Work with Private Data
- ▶ 3:00 pm Question and Answer Session
- ▶ 4:00 pm Workshop concludes

Finding help after the workshop

Tutorials

Step-By-Step PDF Tutorials

Workshop Guide: Genome Assembly

This document provides step-by-step instructions for submitting an assembly job and examining the results in PATRIC.



Workshop Guide: Genome Annotation

This document provides step-by-step instructions for submitting an annotation job and examining the results in PATRIC.



Workshop Guide: Proteome Comparison

This document provides step-by-step instructions for doing a bi-directional BLASTP analysis comparing up to 10 genomes in PATRIC.



Workshop Guide: Protein Family Sorter

This document provides step-by-step instructions for analyzing the proteomes of genome(s) in PATRIC.



Workshop Guide: Genome Groups

This document provides step-by-step instructions for creating genome groups that will be used for downstream analysis.



Workshop Guide: Private Genome

This document demonstrates finding and examining data associated with a private genome that has been annotated in PATRIC.



Workshop Guide: RNA-Seq Data Submission

This document provides step-by-step instructions for submitting a RNA-Seq job and examining the results in PATRIC.



Workshop Guide: Expression Import

This document provides step-by-step instructions for loading expression data into PATRIC for downstream analysis.



Workshop Guide: Transcriptomics Page

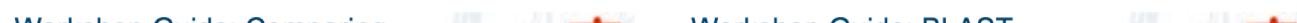
This document provides step-by-step instructions analyzing transcriptomic data that is available in PATRIC.



Workshop Guide: Overview



Workshop Guide: BLAST



Workshop Guide: Validation



[Search docs](#)

CONTENTS:

[Website Tutorials](#)[Genomics](#)[Transcriptomics](#)[Protein Tools](#)[Metabolomics](#)[Others](#)[Creating Genome Groups](#)[Examining Antimicrobial Resistance \(AMR\) data in PATRIC](#)[Reconstructing Genomes from Metagenomic Samples Using the RAST Binning Service \(RBS\)](#)[Using the PATRIC Metagenomic Binning Service](#)[Basic Steps](#)[Analyzing Your Metagenome Bins](#)[Developing PATRIC Code at Argonne](#)[The PATRIC Command Line Interface](#)

Using the PATRIC Metagenomic Binning Service

Basic Steps

1. Log in to the Patric web site with your Patric credentials.
2. Provide an input file.
3. Open the Binning Service
4. Run Binning
5. Examine Output

Log in to the PATRIC Website

See [Registration](#) for information on logging in to the PATRIC website. Once you are registered and logged in, you should see something like this:

The screenshot shows a web browser window for the PATRIC website (<https://www.patricbrc.org>). The page displays a workshop announcement titled "PATRIC WORKSHOP @ ARGONNE NATIONAL LABORATORY". The text describes a three-day workshop on November 14-16, 2017, at Argonne National Laboratory, featuring genome assembly, annotation, comparative analysis, variation, metabolic model construction, RNA-Seq analysis, Trn-seq analysis, and phylogenetic tree construction. A registration link is provided. To the right of the text is a photograph of a workshop room where several people are seated at desks with laptops, attending a presentation.

Provide Feedback

X

Assembly failed

Job number

Select file to attach (optional): No file chosen

Cancel

Submit

and Data Including an Antibiotics Database, AMR Phenotype Information, a Close Genome Finder Service, HPI/PPI Data and Visualization, a Compare Region Viewer, an ID-Mapping Tool, and Enhanced Global Search.

PATRIC March 2017 Data and Website Release: New Genomes In this release, PATRIC has added 3669 new genomes, bringing the total number of genomes in PATRIC to nearly 98,000. The full list of available bacterial genomes can be accessed from the Genomes Tab for all bacteria, and from the Genomes Data Landing Page. UniProt ID [...]

3/8/2017

PATRIC Workshop at GLBIO 2017 in Chicago, May 17, 2017

PATRIC will be hosting a 1/2-day workshop entitled “Assemble, Annotate and Analyze Your Own Genome using PATRIC, the All Bacterial Bioinformatics Resource Center,” at the Great Lakes Bioinformatics (GLBIO) Conference at the University of Illinois at Chicago on May 17, 2017 in Chicago, Illinois. The workshop will cover PATRIC’s analysis pipelines, which include genome assembly [...]

[Read More](#)

PATRIC

University of Chicago
5801 South Ellis Avenue
Chicago, IL 60637-5418

How to Cite PATRIC

If you use PATRIC web resources to assist in research publications or proposals please cite as:
[How to cite PATRIC](#)

Funding Statement

This project has been funded in whole or in part with Federal funds from the National Institute of Allergy and Infectious Diseases, National Institutes of Health, Department of Health and Human Services, under Contract No. HHSN272201400027C, awarded to RL Stevens

Citing PATRIC

If you use PATRIC web resources to assist in research publications or proposals please cite as:

Alice R. Wattam, James J. Davis, Rida Assaf, Sébastien Boisvert, Thomas Brettin, Christopher Bun, Neal Conrad, Emily M. Dietrich, Terry Disz, Joseph L. Gabbard, Svetlana Gerdes, Christopher S. Henry, Ronald W. Kenyon, Dustin Machi, Chunhong Mao, Eric K. Nordberg, Gary J. Olsen, Daniel E. Murphy-Olson, Robert Olson, Ross Overbeek, Bruce Parrello, Gordon D. Pusch, Maulik Shukla, Veronika Vonstein, Andrew Warren, Fangfang Xia, Hyunseung Yoo, Rick L. Stevens; **"Improvements to PATRIC, the all-bacterial Bioinformatics Database and Analysis Resource Center."** *Nucleic Acids Res* 2017; 45 (D1): D535-D542. doi: [10.1093/nar/gkw1017](https://doi.org/10.1093/nar/gkw1017) PMID: [27899627](https://pubmed.ncbi.nlm.nih.gov/27899627/)

Thanks for coming



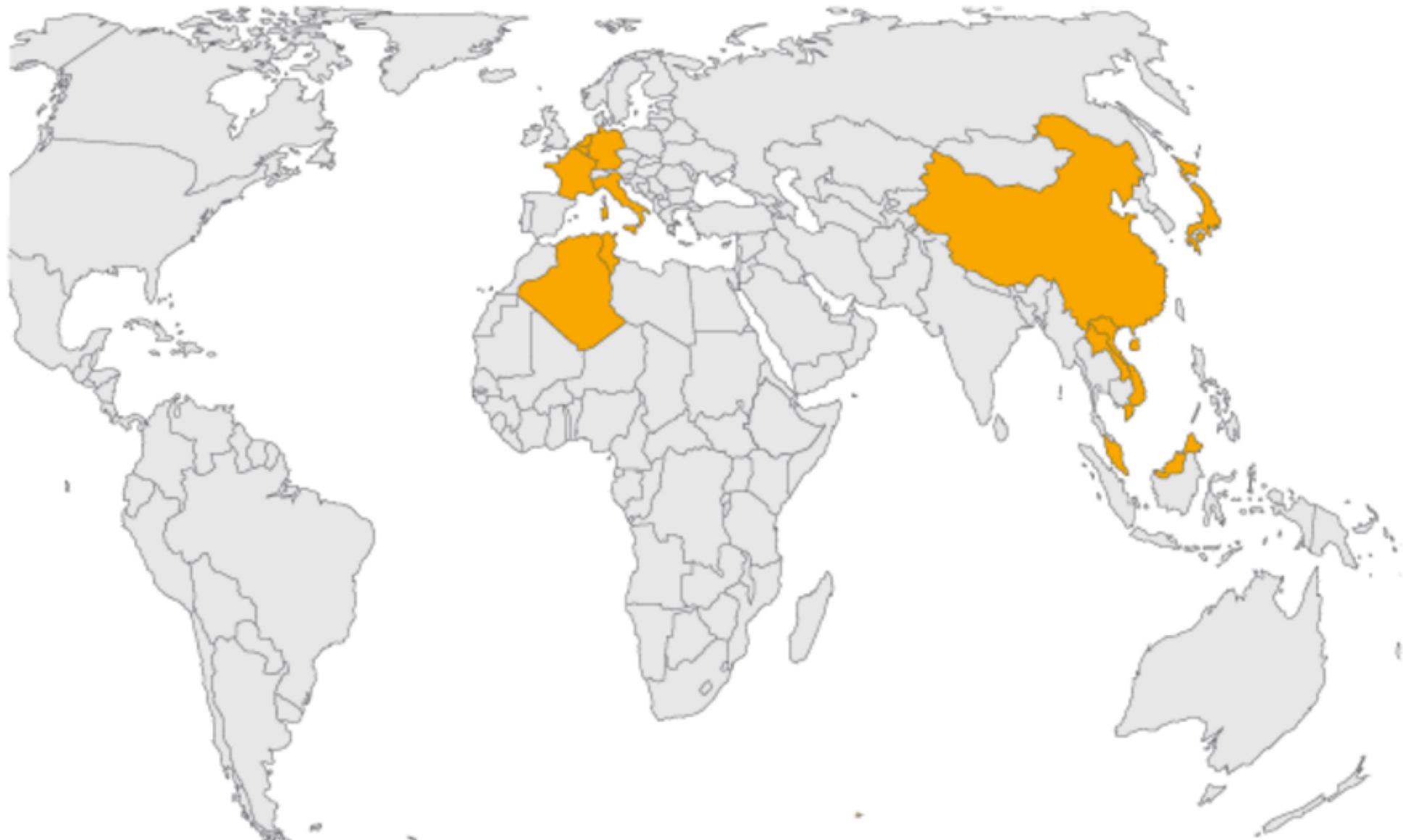
On to assembly....





Geographic distribution of the *mcr-1* gene (as of 1st March 2016)

A. Food animals



C. Humans



Skov and Monnet, Eurosurveillance, Volume 21, Issue 9, 03 March 2016

Countries shown in colour have reported at least one isolate with the *mcr-1* gene [1-30].