

# PATRIC Bioinformatics Resource Center

Argonne National Lab

Lemont, Illinois

May 7–9, 2018



[www.patricbrc.org](http://www.patricbrc.org)





Search



## 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/>

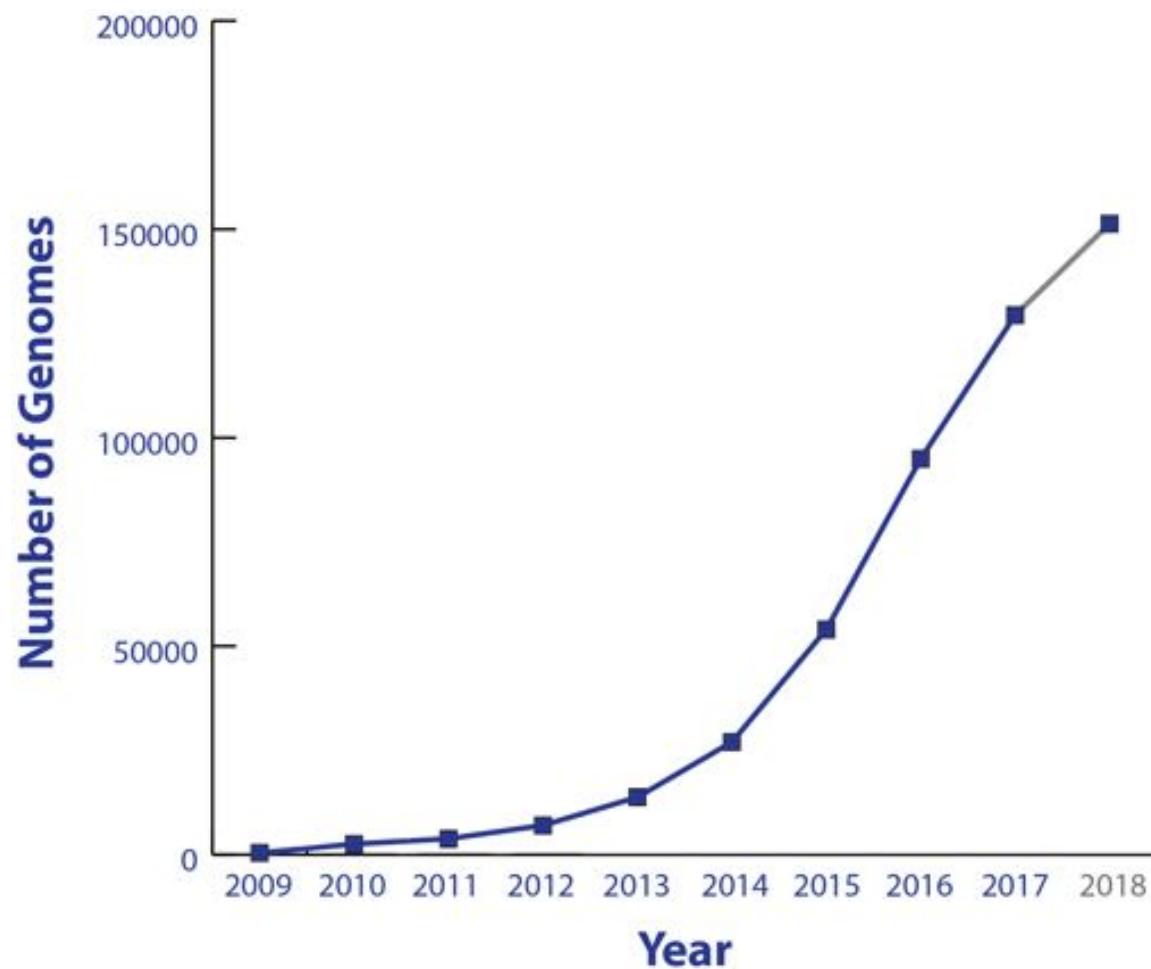


# PATRIC (NIAID) Watchlist Genera

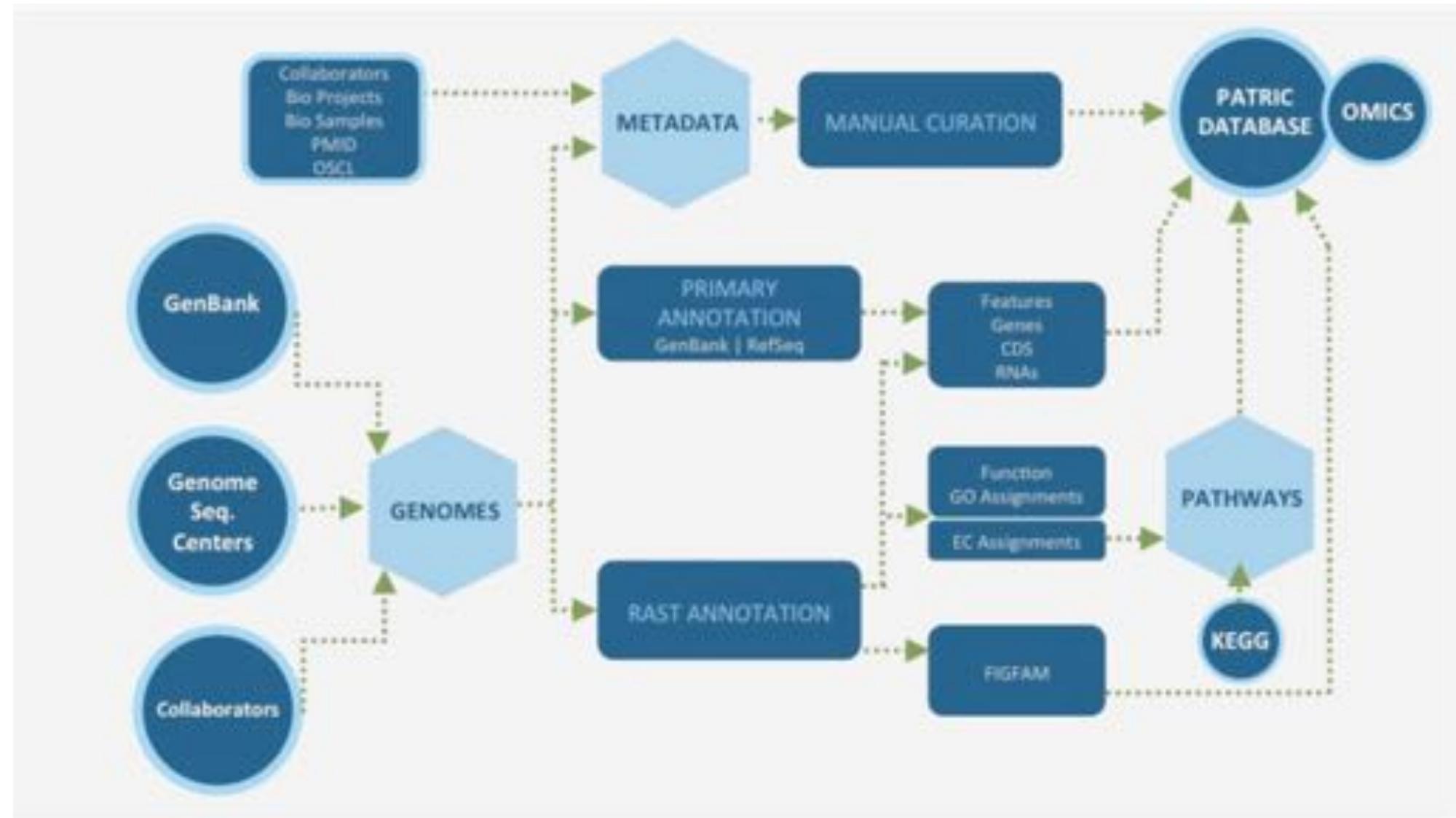
- ▶ *Bacillus*
- ▶ *Bartonella*
- ▶ *Borrelia*
- ▶ *Brucella*
- ▶ *Burkholderia*
- ▶ *Campylobacter*
- ▶ *Chlamydophila*
- ▶ *Clostridium*
- ▶ *Coxiella*
- ▶ *Ehrlichia*
- ▶ *Francisella*
- ▶ *Helicobacter*
- ▶ *Listeria*
- ▶ *Mycobacterium*
- ▶ *Rickettsia*
- ▶ *Salmonella*
- ▶ *Shigella*
- ▶ *Staphylococcus*
- ▶ *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 genome-scale resource for annotation of bacteria and archaea

## RAST publications have more than 5,000 citations

Annotating batches of genomes

Received  
12 November 2014

Accepted  
2 January 2015

Thomas Brettin<sup>1,2</sup>, James J. Davis<sup>1,2</sup>, Terry Disz<sup>3</sup>, Robert A. Edwards<sup>4,5</sup>, Svetlana Gerdes<sup>1,2</sup>, Gary J. Olsen<sup>6</sup>, Robert Olson<sup>2,4</sup>, Ross Overbeek<sup>1,2</sup>, Bruce Porrelo<sup>1,2</sup>, Gordon D. Pusch<sup>1,2</sup>, Maulik Shukla<sup>7</sup>, James A. Thomason III<sup>8</sup>, Rick Stevens<sup>1,2,9</sup>, Veronika Vonstein<sup>1,2</sup>, Alice R. Wattam<sup>7</sup> & Fangfang Xia<sup>2,4</sup>

# 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 includes the journal logo, the word "frontiers", and the subtitle "in Microbiology | Systems Microbiology". Below the header is a navigation bar with links for "SECTION", "ABOUT", "ARTICLES", "RESEARCH TOPICS", "FOR AUTHORS", "EDITORIAL BOARD", and "ARTICLE ALERTS". A social media icon bar is also present. The main content area features a red banner indicating the article is part of a research topic titled "Towards integrated metabolic and regulatory models of all microbial genomes". The article title is "PATtyFams: Protein Families for the Microbial Genomes in the PATRIC Database", categorized as a "METHODS ARTICLE". The date is "Front. Microbiol., 08 February 2016" and the DOI is "https://doi.org/10.3389/fmicb.2016.00118". The authors listed are James J. Davis<sup>1,2\*</sup>, Svetlana Gerdes<sup>2,3</sup>, Gary J. Olsen<sup>4</sup>, Robert Olson<sup>1,5</sup>, Gordon D. Pusch<sup>2,3</sup>, Maulik Shukla<sup>1,2</sup>, Veronika Vonstein<sup>2,3</sup>, Alice R. Wattam<sup>6</sup> and Hyunseung Yoo<sup>1,2</sup>.

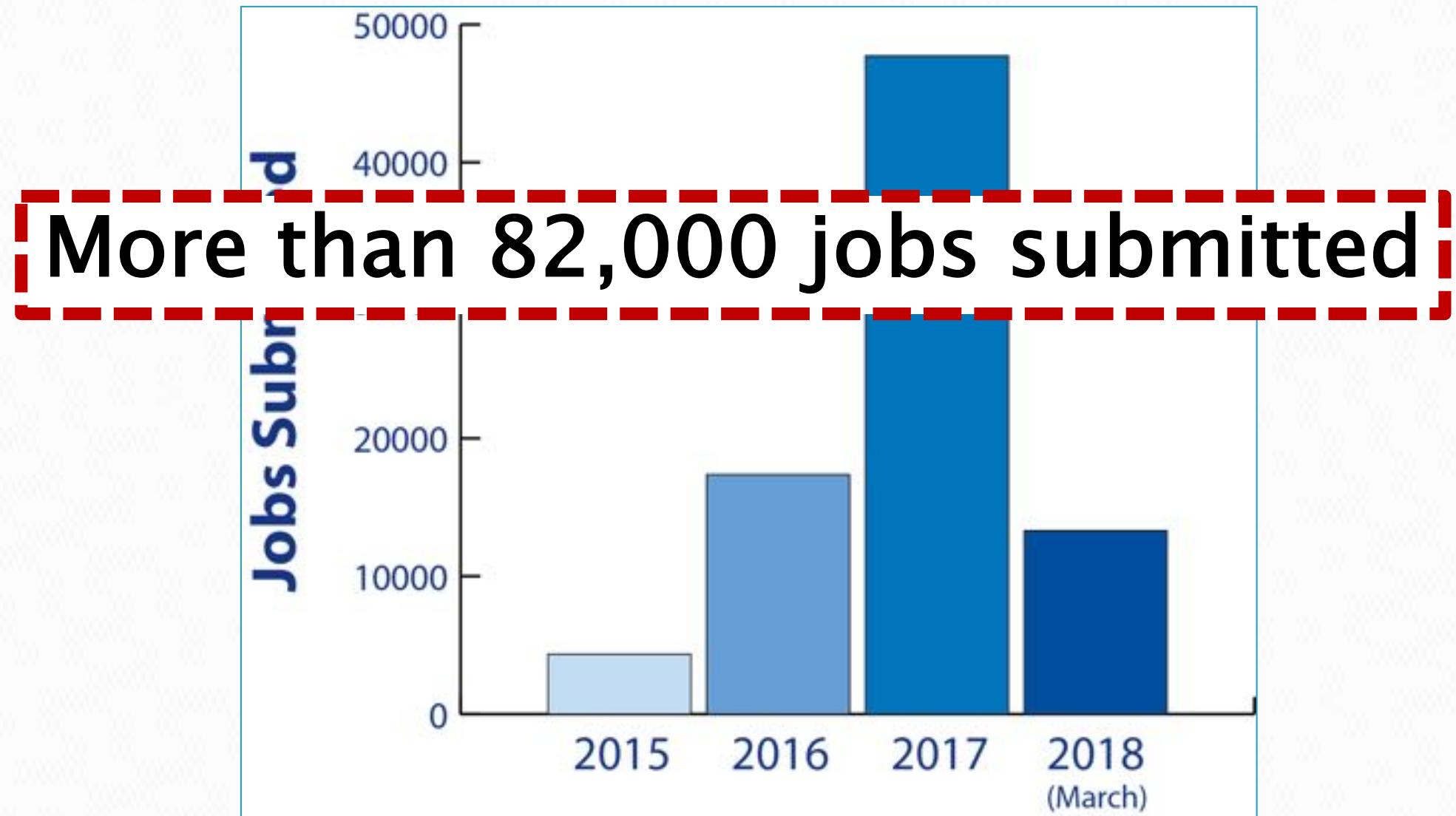
# PATRIC Services

- ▶ 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

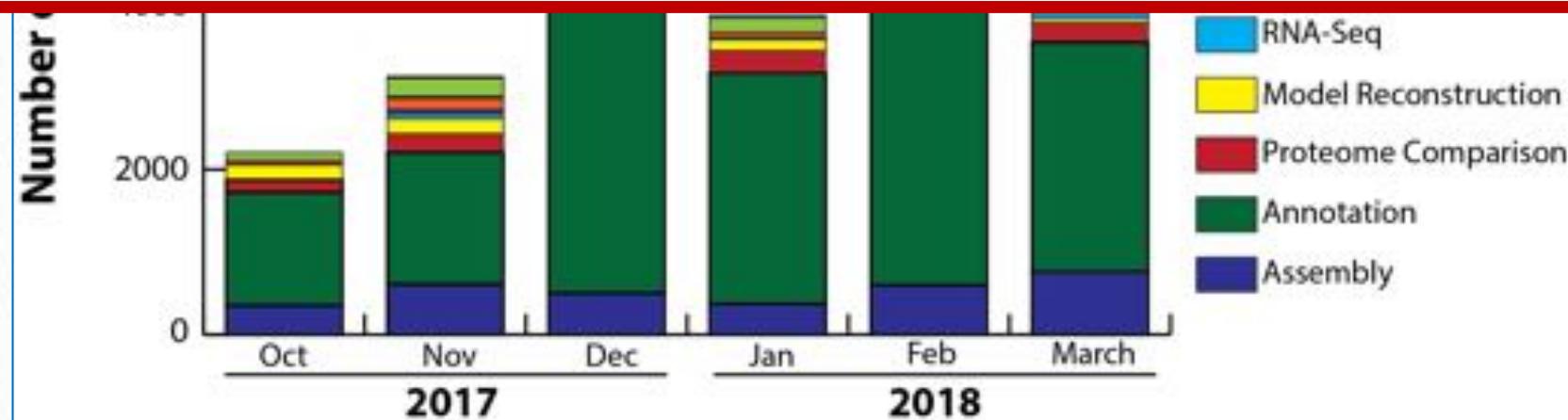
## Does anybody use these services?



## 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, Masahiro Hattori, Naotake Ogasawara, Hideo Hayashi, Kelichi 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 Sub

**Brucella ceti str. Cudo**

Length: 3389269bp, Chromosomes: 0, Plasmids: 6, Contigs: 7

Genomic Features

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

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	

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	926	1739
Proteins with Pathway assignments	752	220

Host Info

Host Name	Bottlenose dolphin, <i>Tursiops truncatus</i>
-----------	---

Sequence Info

# 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: 120577.8 | 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.*) *pinnipedalis* 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 3.6.10 ORGANISMS DATA WORKSPACES SERVICES HELP All Data Types Find a gene, genome, microarray, All terms

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> (59)	2009 (879)
	Complete (279)		Intermediate (53)	Thailand (330)	Canine (94)	2012 (875)
				United Kingdom (321)	Pig, <i>Sus scrofa</i> (58)	2010 (792)
				Germany (306)	Pig, <i>Sus scrofa domesticus</i> (51)	2003 (899)
				Finland (240)	Chimpanzee, <i>Pan troglodytes</i> (340)	2014 (879)

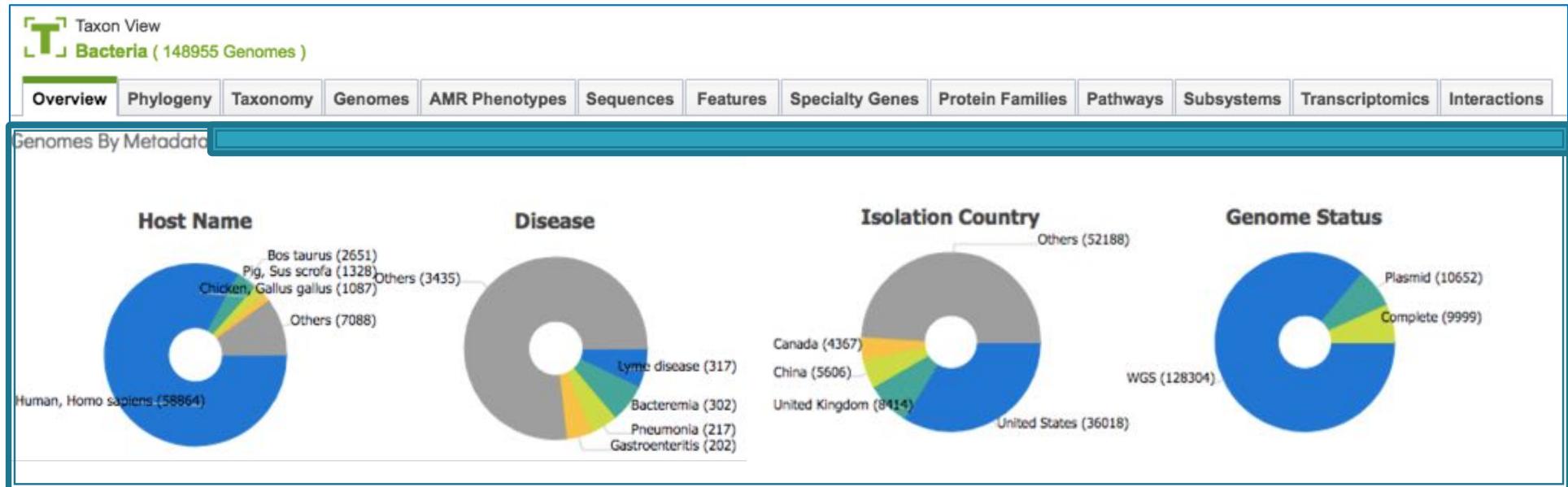
# Metadata filtering

	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	2996	United States	Human, Homo sapiens	2010		Blood
	Staphylococcus aureus P330170-177	1280.4993	WGS	58	2899	United States	Human, Homo sapiens	2011		Blood
	Staphylococcus aureus P330177-181	1280.4994	WGS	40	2804	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	1280.4955	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	2678	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	25	2683	United States	Human, Homo sapiens	2011		Blood
	Staphylococcus aureus P310806-176	1280.4982	WGS	29	2768	United States	Human, Homo sapiens	2011		Blood

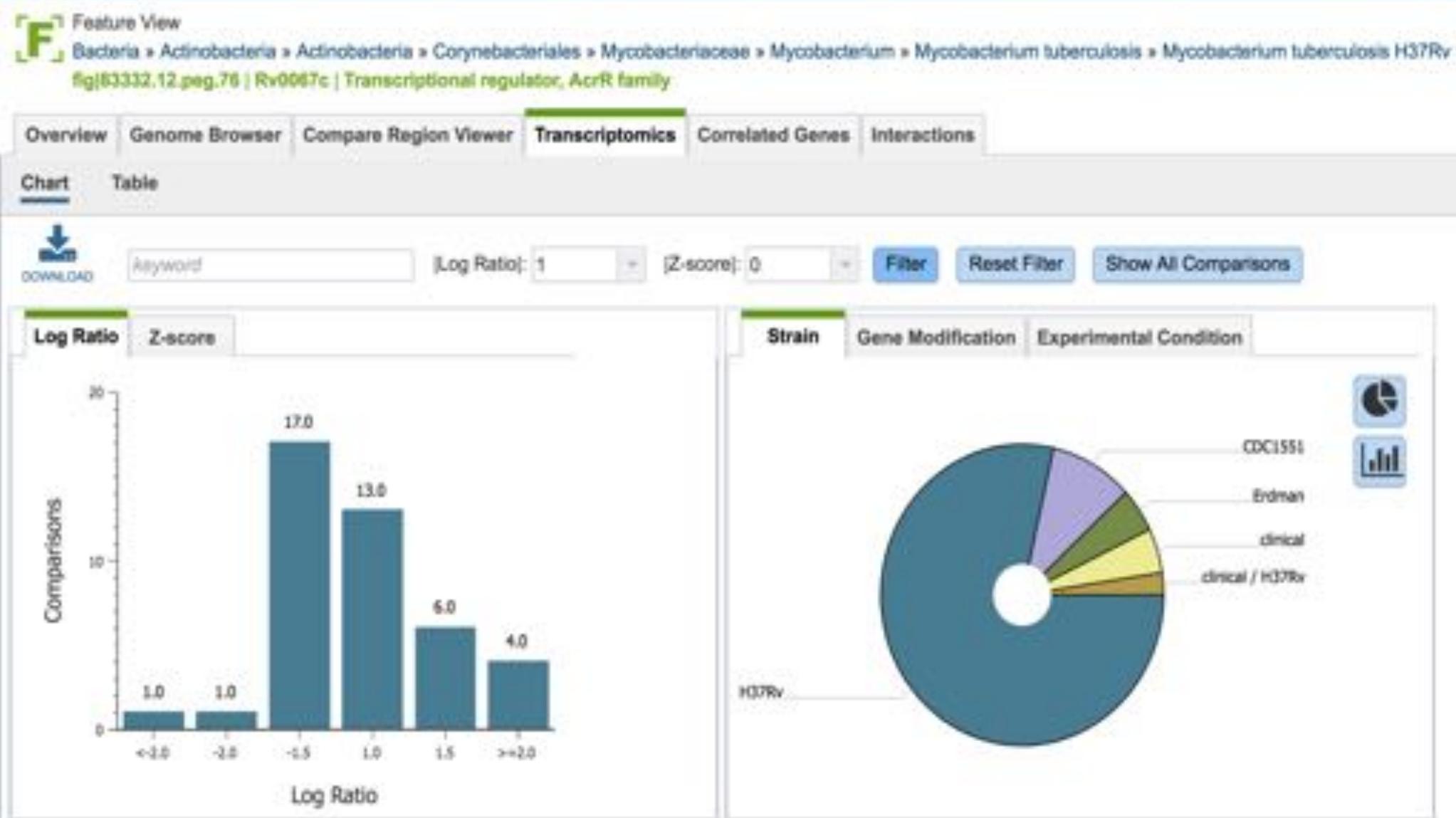
# Large scale summaries based on metadata – AMR



# Large scale summaries based on metadata



# How data is summarized at PATRIC: Consistencies across levels



# 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 Genes:

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

#### 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 select genera:

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

[View all AMR phenotype data](#)

#### 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.



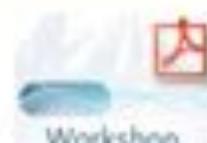
#### Workshop Guide: Genome Annotation

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.



Find additional PATRIC resources

Find additional PATRIC resources

Find additional PATRIC resources



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 (RBSS)

### 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 displaying the PATRIC website. The URL in the address bar is <https://www.patricdb.org>. The page title is "PATRIC WORKSHOP @ ARGONNE NATIONAL LABORATORY". Below the title, there is a brief description of the workshop, mentioning it will be offered on 2017 November 2-3, at Argonne National Laboratory in the suburbs of Chicago, IL. The workshop will run for three days, with the third day optional and dedicated solely to participants working on their own projects with help from the PATRIC team members. Included will be genome assembly, annotation, comparative analysis, and variation, as well as metabolic model construction, RNAseq analysis, T-RFLP analysis, and phylogenetic tree construction. Registration information is available [here](#). The workshop will be limited to 25 people on a first-come, first-served basis.



## Provide Feedback

X

Assembly failed

Job number

Select file to attach (optional):  No file chosen

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 Parnello, 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 PMID: 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].