

PATRIC Bioinformatics Resource Center

Argonne National Lab

Lemont, Illinois

August 14–16, 2017



www.patricbrc.org



Search



PATRIC User Registration

USERNAME

FIRST NAME

LAST NAME

EMAIL ADDRESS

ORGANIZATION

ORGANISMS

INTERESTS

Register New User

Today's instructors

- ▶ Robert Olson
- ▶ Andrew Warren
- ▶ Rebecca Wattam
- ▶ Fangfang Xia

NIH/NIAID BRC Program

Provide publicly accessible database to:

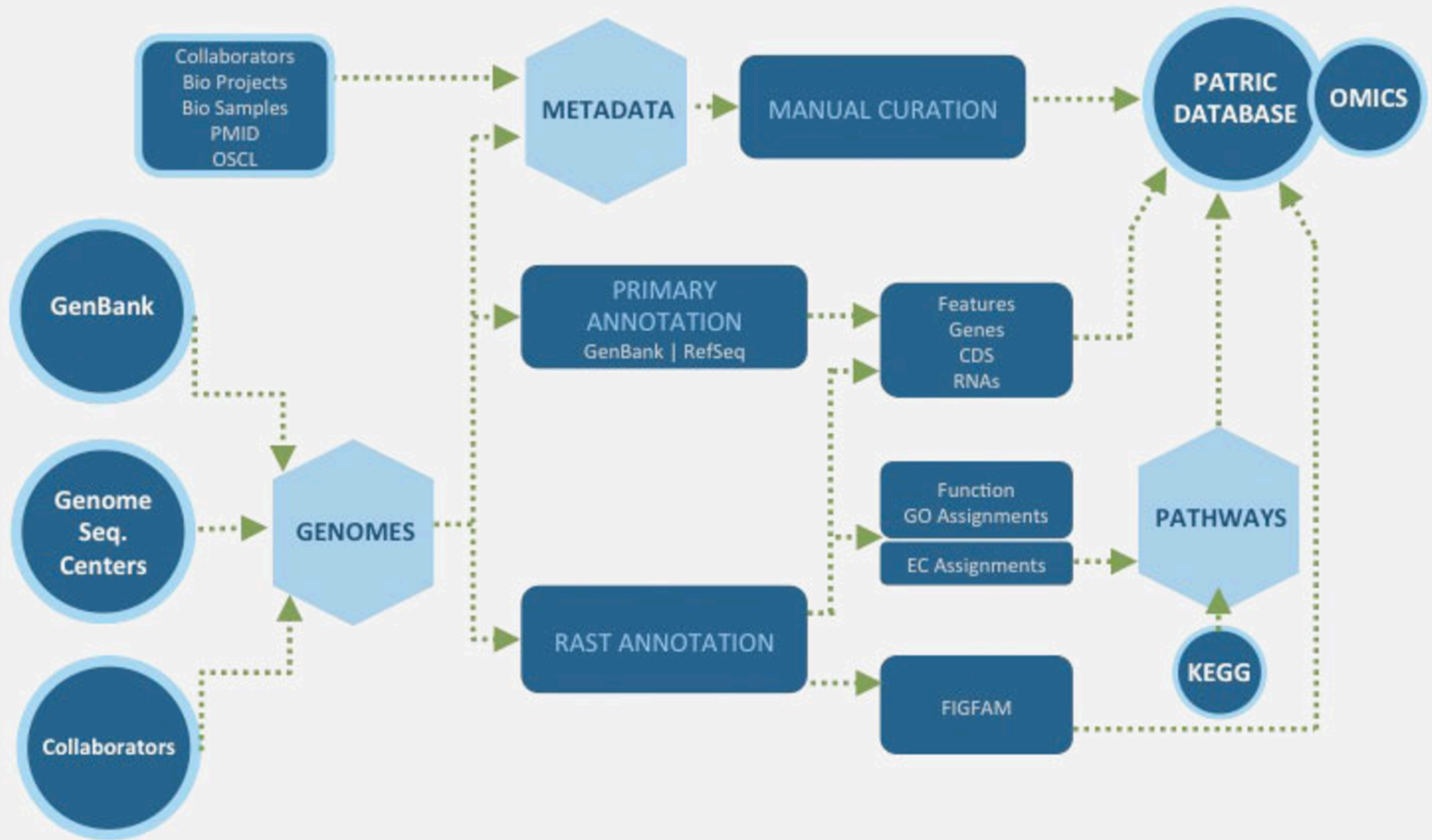
- Store, update, integrate and display genome sequence data, annotation and associated data for human pathogens.
- Provide query, analysis and visualization of information with user friendly interfaces.
- Serve as public repository for NIAID-supported genome-scale programs.
- Collaborate on experimental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

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**

PATRIC data processing



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

Computational Services in PATRIC

- ▶ **Genome Assembly**—Many Assemblers, Compare Assembly Output
- ▶ **Genome Annotation**—High-Speed Annotation using RAST Algorithms
- ▶ **Differential Expression Analysis**—Upload your microarray/RNA-seq data

BYOD: Bring Your Own Data and analyze it in PATRIC

- ▶ **BLAST Service**—BLAST against all or user-created groups
- ▶ **TN-Seq**—Align reads, measure essentiality
- ▶ **Flux Balance Analysis Modeling**—Predict essential genes, compare models
- ▶ **“Virtual Integration”**—Access comparative genomics features with your data

Most recent addition!

- ▶ Build your own phylogenetic tree

Comparative Analysis, Visualization and Search

▶ Comparative Analysis and Visualizations

- metabolic pathways, disease, metadata, PPI
- protein family (isofunctional homologs) sorter
- gene list, gene set, projections, heatmaps
- transcriptome analysis, up/down fold changes

▶ Comprehensive Searching

- AMR genes (ARDB, CARD), genome features, external ID mapping, similarity, gene pages, gene collections, correlated genes, genome finder, transcriptome, EC, GO, etc.

How data is summarized at PATRIC: Consistencies across levels



Feature View

Bacteria » Actinobacteria » Actinobacteria » Corynebacteriales » 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



DOWNLOAD

keyword

|Log Ratio|: 1

|Z-score|: 0

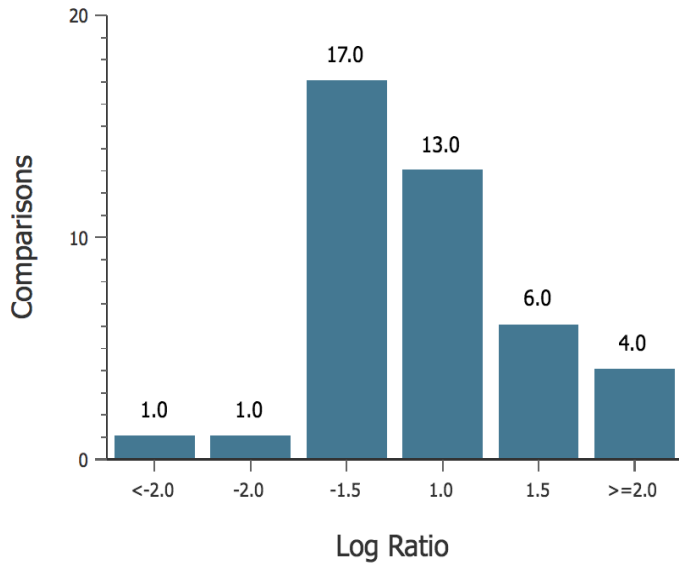
Filter

Reset Filter

Show All Comparisons

Log Ratio

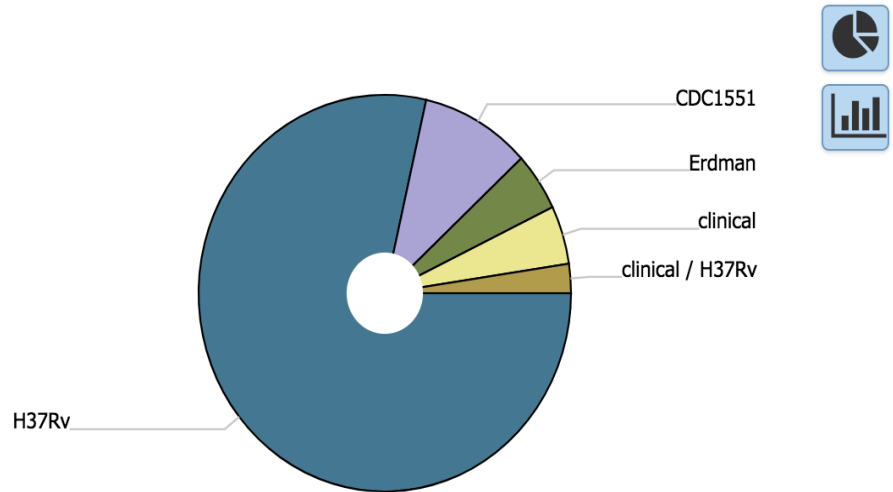
Z-score



Strain

Gene Modification

Experimental Condition



New Antimicrobial Data

Data Types

Antibiotic Resistance

Genomes

Genomic Features

Pathways

Protein Families

Specialty Genes

Transcriptomics

Specialty Data Collections

PATRIC Collaborations

PATRIC DBPs

NIAID Clinical Proteomics

NIAID Genome Sequencing

NIAID Structural Genomics

NIAID Systems Biology

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 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 workshop

- ▶ The recent discovery of a plasmid-borne colistin resistance gene, *mcr-1*, heralds the emergence of truly pan-drug resistant bacteria.
- ▶ We'll explore this genome, and show how a researcher might bring their new reads on such a genome and analyze them in PATRIC

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].

mcr-1 comes to the United States

May 2016

Accepted Manuscript Posted Online

AAC Accepted Manuscript Posted Online 26 May 2016
Antimicrob. Agents Chemother. doi:10.1128/AAC.01103-16
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1 *Escherichia coli* Harboring *mcr-1* and *bla*_{CTX-M} on a Novel IncF Plasmid: First report of
2 *mcr-1* in the USA

3 Patrick McGann^{1#*}, Erik Snestrud^{1*}, Rosslyn Maybank¹, Brendan Corey¹, Ana C. Ong¹, Robert
4 Clifford¹, Mary Hinkle¹, Timothy Whitman², Emil Lesho¹, and Kurt E. Schaecher^{3#}

5 ¹Multidrug-resistant Organism Repository and Surveillance Network, Walter Reed Army
6 Institute of Research, Silver Spring, Maryland, USA.

7 ² Department of Infectious Diseases, Walter Reed National Military Medical Center, MD, USA .

8 ³ Department of Pathology, Walter Reed National Military Medical Center, MD, USA.

Facts of the case

- ▶ *Escherichia coli* MRSN 388634 was cultured from the urine of a 49 year-old female with a urinary track infection in Pennsylvania.
 - The patient reported no travel history within the prior 5 months.
- ▶ Colistin MIC was confirmed by microbroth dilution and *mcr-1* detected by real-time PCR.

Today's schedule (August 14)

- ▶ 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 Proteomic Comparison
- ▶ 2:00 pm Break
- ▶ 2:15 pm Comparative Genomics
- ▶ 3:45 pm Running PATRIC's Tree Building Service
- ▶ 4:30 pm Question and Answer Session
- ▶ 5:00 pm Adjourn

Schedule (August 15)

- ▶ 9:00 am BLAST at PATRIC
- ▶ 9:45 am Similar Genome Finder Service
- ▶ 10:00 am Break
- ▶ 10:15 am RNA-Seq Pipeline
- ▶ 11:15 am Expression Import Service
- ▶ 12:00 pm Lunch
- ▶ 1:00 pm Comparative Transcriptomics
- ▶ 2:00 pm SNP and MNP Variation Service
- ▶ 3:00 pm Tn-Seq Service
- ▶ 3:30 pm Building a Metabolic Model
- ▶ 4:30 pm Question and Answer Session
- ▶ 5:00 pm Adjourn

Schedule (August 16)

- ▶ 9:00 am Introduction to PATRIC Command Line Interface
- ▶ 11:00 am Break
- ▶ 11:15 am Work with Your Private Data
- ▶ 12:00 pm Lunch
- ▶ 1:00 pm Work with Your 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: Comparison

Workshop Guide: BLAST

Workshop Guide: Variation

Provide Feedback



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

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How to Cite PATRIC

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How to cite PATRIC

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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!

Argonne National Lab



On to assembly....