

Comparative Genomics Analyses

- *Brucella*
- *Mycobacterium*
- *Helicobacter*
- *Corynebacterium*
- *Staphylococcus*

Bioinformatic Pipelines and Tools

- Protein Family Sorter
- Comparative Pathway Viewer
 - RASTtk
 - Protein families
- Antimicrobial resistance identification

Pathosystems Resource Integration Center

PATRIC

Supported by the National Institute of Allergy and Infectious Diseases
since 2004

NIAID Priority Pathogens



Category A

- *Bacillus anthracis* (anthrax)
- *Clostridium botulinum* toxin (botulism)
- *Yersinia pestis* (plague)
- Variola major (smallpox) and other related pox viruses
- *Francisella tularensis* (tularemia)
- Viral hemorrhagic fevers
- Arenaviruses
 - LCM, Junin virus, Machupo virus, Guanarito virus
 - Lassa Fever
- Bunyaviruses
 - Hantaviruses
 - Rift Valley Fever
- Flaviruses
 - Dengue
- Filoviruses
 - Ebola
 - Marburg

Category B

- *Burkholderia pseudomallei*
- *Coxiella burnetii* (Q fever)
- *Brucella* species (brucellosis)
- *Burkholderia mallei* (glanders)
- *Chlamydia psittaci* (Psittacosis)
- Ricin toxin (from *Ricinus communis*)
- Epsilon toxin of *Clostridium perfringens*
- *Staphylococcus enterotoxin B*
- Typhus fever (*Rickettsia prowazekii*)
- Food- and Waterborne Pathogens
 - Bacteria
 - Diarrheagenic *E. coli*
 - Pathogenic Vibrios
 - *Shigella* species
 - *Salmonella*
 - *Listeria monocytogenes*
 - *Campylobacter jejuni*
 - *Yersinia enterocolitica*

Category C

Emerging infectious disease threats such as Nipah virus and additional hantaviruses.

NIAID priority areas:

- Tickborne hemorrhagic fever viruses
 - Crimean-Congo Hemorrhagic fever virus
- Tickborne encephalitis viruses
- Yellow fever
- Multi-drug resistant TB
- Influenza
- Other Rickettsias
- Rabies
- Prions
- Chikungunya virus
- Severe acute respiratory syndrome associated coronavirus (SARS-CoV)
- Antimicrobial resistance, excluding research on sexually transmitted organisms*

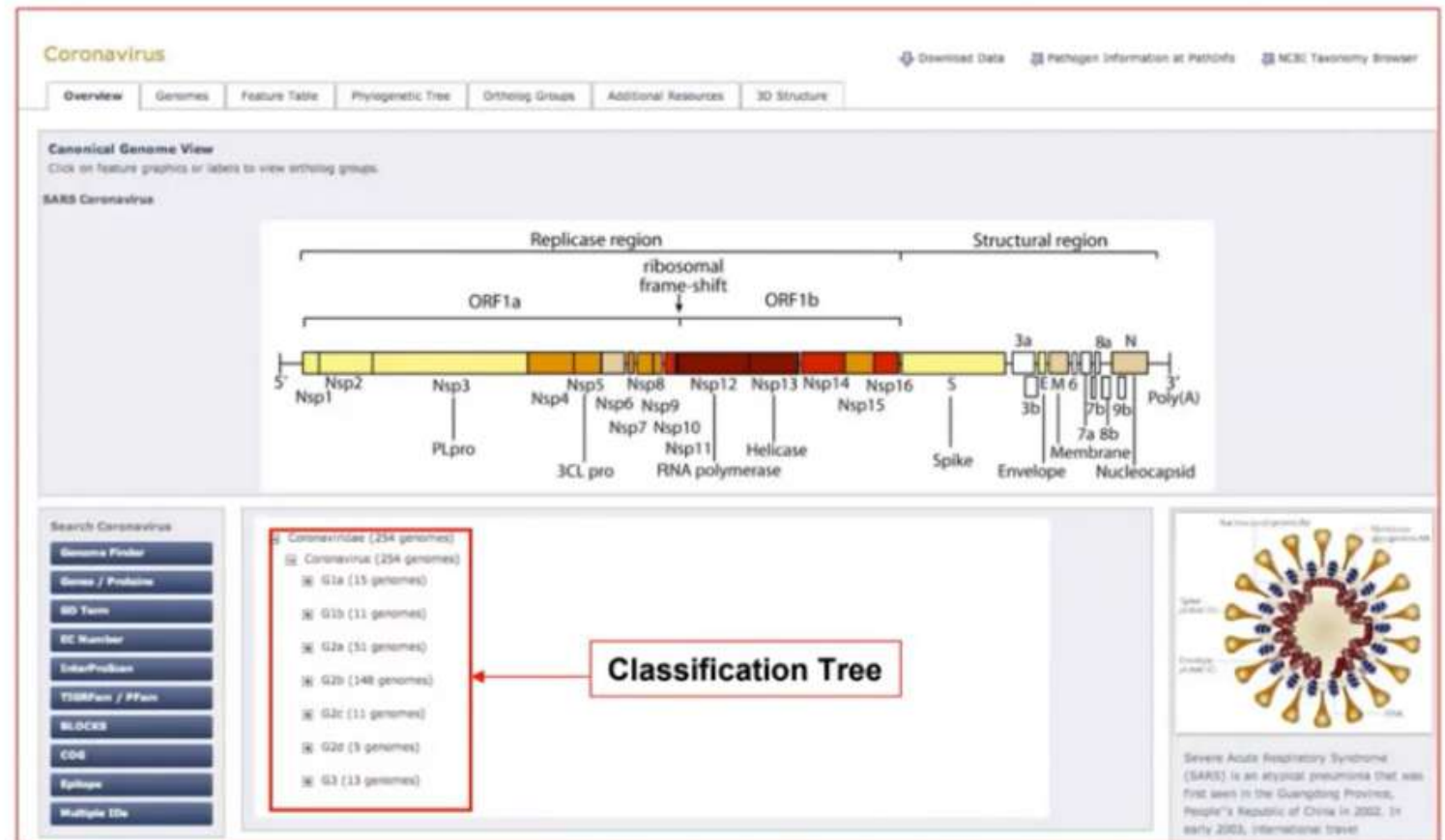
PATRIC 1 (2004-2009)

- Bacteria

- *Brucella*
- *Coxiella*
- *Rickettsia*

- Viruses

- Caliciviridae
- **Coronavirus**
- Hepatitis A Virus
- Hepatitis E Virus
- Lyssavirus



Organism Overview Page

PATRIC 2 Data Merge



PATRIC 2-3 (2009 – 2019)



Viruses:
IRD/ViPR
UTSW, Northrop



Viruses:
IRD/ViPR
Northrop, JCVI



Bacteria:
PATRIC
VT, UChicago



Bacteria:
PATRIC
UChicago, VT



Eukaryotes:
EuPathDB
UPenn, UGA



Eukaryotes:
EuPathDB
UPenn, UGA



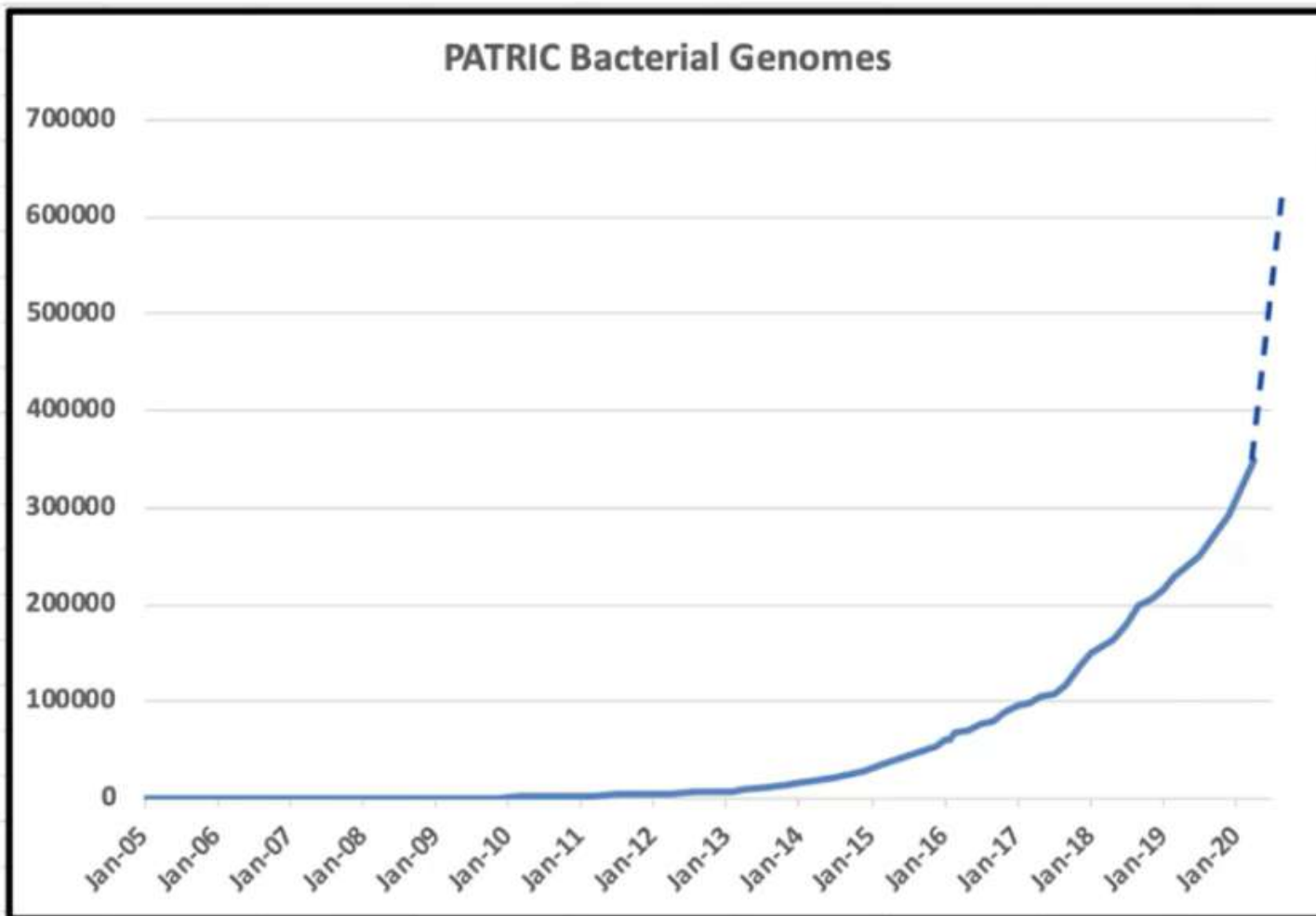
Vectors:
Notre Dame
EBI/EMBL



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Notre Dame
EBI/EMBL



PATRIC: Data Growth



- Started with ~15 bacterial genomes in 2004
- Doubling every 2 years
- Will add about 250K viral genomes soon

Number of Jobs Submitted

Year

Legend:

- Fastq Utils
- Taxonomic Classification
- Metagenomic Read Mapping
- Genome Alignment
- Comprehensive Genome Analysis
- Metagenome Binning
- Phylogenetic Tree
- Variation
- RNA-Seq
- Proteome Comparison
- Model Reconstruction
- Assembly
- Annotation

Bacterial and Viral BRC (2019-2024)



Viruses:
IRD/ViPR
Northrop, JCVI



Bacteria:
PATRIC
UChicago, VT



Eukaryotes:
EuPathDB
UPenn, UGA



Vectors:
Notre Dame
EBI/EMBL



Bacteria and Viruses:
BV-BRC
UChicago, JCVI, UVA



Eukaryotes and Vectors:
VEuPathDB
UPenn, UGA
Notre Dame, EBI/EMBL

patrickbrc.org

Genomics

Assembly **new**
Annotation
Comprehensive Genome
Analysis
BLAST
Similar Genome Finder
Variation Analysis
Tn-Seq Analysis
Phylogenetic Tree
Genome Alignment

Metagenomics

Metagenomic Read Mapping
Taxonomic Classification
Metagenomic Binning

Transcriptomics

Expression Import
RNA-Seq Analysis

Protein Tools

Protein Family Sorter
Proteome Comparison

Metabolomics

Comparative Pathway
Model Reconstruction

Data

ID Mapper
Fastq Utilities