BV-BRC Newsletter
February 22, 2024

BV-BRC
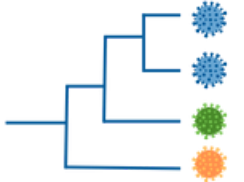Bacterial and Viral Bioinformatics Resource Center

BV-BRC Newsletter Plan

Happy New Year from the BV-BRC. We are excited to share our first newseletter of 2024 with you and to tell you what the team has been up to since the last one. We are always working on making the

Viral Sub-species Classification Workshop

Hear from subject matter experts in virology, computational tools and public health.

Get the chance to participate in the conversation and help facilitate the determination of a consistent objective use case-driven approach for the hierarchical grouping of virus strains below the species level.

REGISTER NOW ＞

Outreach Spotlight

The BV-BRC team spent the fall doing some outreach, which we wanted to highlight. The bacterial team went to the University of Florida and had a wonderful time. We held a joint workshop at Iowa State and were welcomed by a kind host, and an even more beautiful location. Simultaneously our bacterial team went to THISTI in India and hosted an AMR centered meeting.

Please follow along with all things BV-BRC on our LinkedIn page. This is also the new channel you will see on our homepage.

The back to the basics webinars are now complete and can be accessed on our youtube channel. Check them out here

Thank You to our 50,000 Registered Users

Website Updates

Taxonomic Classification Service Enhancements:
- Added support for 16S metagenomic analysis.

Comparative Systems Service Enhancements:
- Introducing a new filter by feature group function.
- Expanded genome metadata labels in the filter table and heat map view, including genome group, genome status, geographic group, isolation country, host, and collection year.
- Backend changes to support protein families heat map modifications.

Codon Tree Service Enhancements:
- Updated Bacterial Genome Tree to submit genome group lists.
- Revised the mechanism for submitting genome groups in codon tree jobs.
- Minor adjustments to codon tree metadata fields.
- Genome Group removed from metadata fields selection in Bacterial Genome Tree.

Sequence Submission Service Enhancement:
- Set address inputs under Submitter Information as required in Sequence Submission.

Other Minor Service Enhancements:
- Bug fixes for info/tooltip icons, ensuring correct help text display in Fastq Util and Viral Genome Tree pages.
- Bug fix for Primer Sequence tooltip button and updated icon.
- Bug fix for Input File info button to open the info dialog.

Website Bug Fixes and Enhancements:
- Updated taxon view phylogenetic trees to showcase new trees based on GTDB.
- Added/Fixed subsystems and pathways buttons in the action bar on the feature list page.

Scheduled Maintenance

Expect scheduled BV-BRC system maintenance on the second Thursday of each month going forward, which may result in limited or reduced access to the BV-BRC resources on that day.

BV-BRC VIRUS SPOTLIGHT
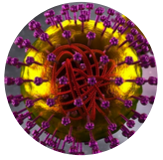
Measles morbillivirus

22653 Genomes*
Count as of 1/23/24

Measles is a highly contagious viral infection caused by the measles virus. It presents with symptoms like fever, cough, and a distinctive red rash. Measles can lead to serious complications, and vaccination with the MMR vaccine is crucial for prevention. Use the below BV-BRC tools to analyze Measles data:

Genome Annotation
BLAST
Primer Design
Similar Genome Finder
Viral Genome Tree
Gene/Protein Tree

MSA and SNP Analysis
Meta-CATS
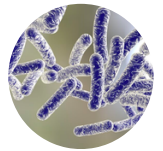Taxonomic Classification
Metagenomic Binning
Fastq Utilities

BV-BRC BACTERIA SPOTLIGHT

Legionella

Complete, WGS and Plasmid Genomes

Legionella is a Gram-negative bacteria causing respiratory infections like Legionnaires' disease. Found in water sources, it thrives in artificial systems. Transmission occurs through contaminated aerosols. Prevention involves water system hygiene and temperature control. Study it now with these BV-BRC tools:

Genome Assembly
Genome Annotation
Comprehensive Genome Analysis
BLAST
Primer Design
Similar Genome Finder
Genome Alignment
Variation Analysis
Tn-Seq Analysis
Bacterial Genome Tree
Gene/Protein Tree

Metagenomic Read Mapping
Fastq Utilities
Meta-CATS
Proteome Comparison
Comparative Systems
ID Mapping
Taxonomic Classification
Metagenomic Binning
Expression Import
RNA-Seq Analysis