

## BV-BRC Newsletter Plan

We took a break from newsletters, and now we are back and ready to share all the amazing work happening within the BV-BRC. Going forward, look out for a regular BV-BRC Newsletter with information about the latest bacterial and viral data, analysis services, website updates, workshops, and more from the BV-BRC team.

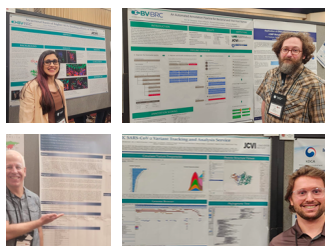
## Outreach Spotlight

The BV-BRC team attended three conferences this summer: ASV, ISMB and NIAMRE. We hosted a joint BV-BRC workshop for bacterial and viral researchers and three bacterial workshops. Our viral team attended the Virus Evolution and Molecular Epidemiology workshop and gave multiple talks.

We launched BV-BRC [LinkedIn](#) page this summer. Please follow us to stay connected!



We loved the chance to meet users at ASV. We had a great time hearing how everyone uses the services and the opportunity to share our work and make the BV-BRC more useful for users like you!



## Bacterial Bioinformatics Coursera

Are you interested in learning more about bacterial bioinformatics? Do you want to get a free certificate to show your knowledge and expertise? [Check out our Coursera here now!](#)

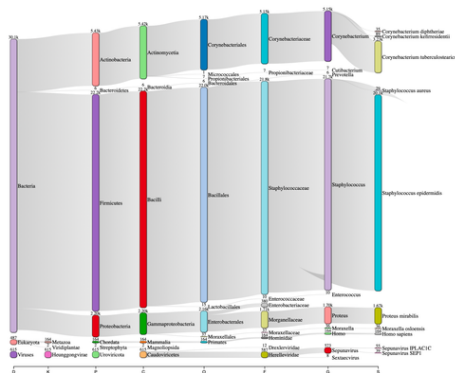


## Website Updates

We have revamped the sequence submission platform to increase access and support for sequence submission. We have unified the subspecies classification service using tree based approach. If you do microbiome analysis, check out our taxonomic classification service.

### Enhanced Taxonomic Classification Service

- We now support whole genome sequencing (WGS) and 16S metagenomic analysis.
- Two WGS pipelines:
  - Microbiome analysis
  - Species Identification
- Host removal for 10 species
- Multisample comparisons
- Interactive charts and graphs for individual and multiple samples
- Outputs include Alpha and Beta statics, Krona plots, Snakey diagrams, MultiQC reports and more!



### Updates to Comparative Services

- Ability to identify groups from the table and heatmap

### Updates to Bacterial Genome Tree

- Ability to visualize metadata like county of isolation, host, and genome group by coloring the tree

### Updates to Sequence Submission

If you are a user who utilizes the sequence submission tool, we are excited to announce that you can now add your corresponding university to the submission. This is just one of many improvements to the sequence submission tool in the coming months, we look forward to making this service even more useful to our users.

## Migration to BV-BRC

At the beginning of this year, our team completed the [merger of PATRIC, IRD, and ViPR into BV-BRC](#). If you were a user of any of these resources, we are excited to have you on our new platform, BV-BRC. Things may look a bit different, but it has the tools you love and use ready for you. One major difference is that IRD and ViPR had separate portal for each of the families, whereas BV-BRC has unified data sets and analysis tools across families to provide better access.

## Scheduled Maintenance



Expect monthly scheduled maintenance on the second Thursday going forward. 11/9, 12/14, 1/11 and so on. There will be limited or reduced access to the BV-BRC on this day. Please be advised to keep this in mind.

## Upcoming Workshops

### OCTOBER 26-27, 2023

The Bacterial team will be at the University of Florida hosting a workshop.

### NOVEMBER 13-17, 2023

We are excited to work with our friends over at Iowa State to give a workshop on antimicrobial resistance and our virology tools.

### NOVEMBER 18-20, 2023

We will be traveling to India at THSTI to deliver a workshop on antimicrobial resistance and bacterial metagenomics.

## ONLINE BACK TO SCHOOL SERIES

Check out the information below for the back to school series on how to use the BV-BRC. Click the weeks for registration on the next page.

[REGISTER NOW](#)



## Command Line Interface

Recently, we have been receiving requests from users about bulk data analysis. Our Command Line Interface (CLI) is a ideal for that. Check out CLI tutorial here: [www.bv-brc.org/docs/cli\\_tutorial/cli\\_installation.html](http://www.bv-brc.org/docs/cli_tutorial/cli_installation.html)



## BACK TO THE BASICS: VIRAL ANALYSIS

WEDNESDAYS 11:00-12:00 PDT



### Week 2: October 25th

Week 2 will allow you to begin to do some analysis within the BV-BRC. Check out this presentation if you're interested in our Annotation tools within the BV-BRC.

[REGISTER NOW](#) >

### Week 3: November 8th

Week 3 will allow you to get comfortable putting together phylogenetic trees in the BV-BRC and aligning sequences using our multi-sequence alignment tool.

[REGISTER NOW](#) >

### Week 4: November 29th

Check out our sequence submission tool in week 4, along with other influenza specific tools!

[REGISTER NOW](#) >

### Week 5: December 5th

All things Protein! Join this session to learn all about analyzing protein data in the BV-BRC

[REGISTER NOW](#) >

## COMMAND LINE ESSENTIALS

How-to get started with the CLI to run large analysis jobs

### Using macOS

**Step 1:** Go to “<https://github.com/BV-BRC/BV-BRC-CLI/releases>”

**Step 2:** Scroll down to Assets and click “BV-BRC-1.040.dmg”

**Step 3:** Download the DMG for the BV-BRC app

**Step 4:** Open the BV-BRC App on your MAC, you may need to the first time “Control-click the app icon, then choose Open from the shortcut menu. Click Open.”

### Using Windows

**Step 1:** Go to “<https://github.com/BV-BRC/BV-BRC-CLI/releases>”

**Step 2:** Scroll down to Assets and click “BV-BRC-1.040.dmg”

**Step 3:** Download the BV-BRC Installer File and double click the file to start the installation

**Step 4:** Use the command line, go to “Start Menu” --> “All Programs” --> “BV-BRC”

### Using Linux

**Step 1:** Have either dpkg or gdebi installed

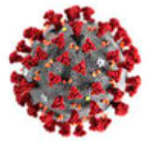
#### DPKG Commands

```
curl -O -L https://github.com/BV-BRC/BV-BRC-CLI/releases/download/1.040/bvbrcli-1.040.deb
sudo dpkg -i bvbrcli-1.040.deb
sudo apt-get -f install
```

#### GDEBI Commands

```
sudo apt-get install gdebi-core
sudo gdebi bvbrcli-1.040.de
```

## BV-BRC VIRUS SPOTLIGHT



### SARS-COV-2

**8454850 Genomes\***

Count as of 10/16/23

Cases of SARS-CoV-2 are rising again this fall which makes this virus an important public health target. We even have generated phylogenetic trees of circulating lineages which is highlighted on our [SARS-CoV-2 variant tracker phylogenetic tree page](#). There are many tools for analysis within the BV-BRC for SARS-CoV-2, check them out below:

<a href="#">Genome Annotation</a>	<a href="#">Gene/Protein Tree</a>
<a href="#">SARS-CoV-2 Genome</a>	<a href="#">MSA and SNP</a>
<a href="#">Analysis</a>	<a href="#">Analysis</a>
<a href="#">BLAST</a>	<a href="#">Meta-CATS</a>
<a href="#">Primer Design</a>	<a href="#">Taxonomic</a>
<a href="#">Similar Genome Finder</a>	<a href="#">Classification</a>
<a href="#">Viral Genome Tree</a>	<a href="#">Metagenomic Binning</a>
	<a href="#">Fastq Utilities</a>

## BV-BRC BACTERIA SPOTLIGHT



### *Vibrio vulnificus*

**36 Complete, 413 WGS and 12 Plasmid Genomes**

This flesh-eating bacterium, one of the causes of necrotizing fasciitis, is on the rise. CDC has recently issued a health advisory to notify the medical community about its rise. BV-BRC tools that can be used to analyze this organism include:

<a href="#">Genome Assembly</a>	<a href="#">Metagenomic Read</a>
<a href="#">Genome Annotation</a>	<a href="#">Mapping</a>
<a href="#">Comprehensive Genome</a>	<a href="#">Fastq Utilities</a>
<a href="#">Analysis</a>	<a href="#">Meta-CATS</a>
<a href="#">BLAST</a>	<a href="#">Proteome Comparison</a>
<a href="#">Primer Design</a>	<a href="#">Comparative Systems</a>
<a href="#">Similar Genome Finder</a>	<a href="#">ID Mapping</a>
<a href="#">Genome Alignment</a>	<a href="#">Taxonomic</a>
<a href="#">Variation Analysis</a>	<a href="#">Classification</a>
<a href="#">Tn-Seq Analysis</a>	<a href="#">Metagenomic Binning</a>
<a href="#">Bacterial Genome Tree</a>	<a href="#">Expression Import</a>
<a href="#">Gene/Protein Tree</a>	<a href="#">RNA-Seq Analysis</a>

