In our beta app, JBrowse2 has been used to visualize 128 isolates from various species of *Phytophthora* .

The core visual elements of JBrowse2 include:

- Sequence tracks or assembly tracks
- Alignment tracks (BAM files need to be provided)
- Variant tracks (VCF) which are sorted, compressed and indexed gff files (.sorted.gff.tabix)
- Feature tracks : They are provided in the form of Bigwig files; binary files which are continuous signals across the entire genome.

Though JBrowse2 can have multiple views like Circos-style circular plots, dotplots, comparative views ; in Eumicrobedb Single Page Application (SPA), the linear genome view is used to visualize the data; where only one assembly ; which is essentially the sequence file of a reference genome along with its associated files or tracks; can be visualized at one time.

In the current beta version of the Eumicrobedb SPA, the user provides the basename of the files with different extensions of each isolate. The basename is a unique organism id which serves as an identifier for a particular isolate. The react framework stores this basename in a variable. The variable value is used to fetch three kinds of files:

- assembly or reference sequence track files : genomic fasta format file (fna) and indexed fna file(fna.fai)
- feature track files: A compressed general feature format file (gff.gz) and a tabix format of this file (gff.gz.tbi) of the particular organism
- variable tracks which include the bigwig files of the genomic locations of Simple Sequence Repeat (SSR) regions and of RXLR motifs present in that organism

These files are then provided to the JBrowse2 Linear Genome View function and can then be visualized as tracks in our SPA.

In the gff3 tabix track which is our feature track; core details and attributes of genomic features as well as subfeatures (mRNA) are present. This is displayed just on clicking a particular gene. The user also has the option of viewing and copying sequences of CDS, protein, cDNA, the selected gene with introns and the gene with bases added both upstream and downstream to its CDS.