JBrowse Supports Diverse Data

Configure Multiple Tracks

Dynamically Open

Append via URL

Statically Configure

Customizable Views

- BAM
- BigWig
- GFF
- GTF
- GBK
- VCF
- FASTA
- FASTAi
- SPARQL
- **custom types (e.g., REST end-point like mygene.info)**

```
addStores={"url":{"type":"JBrowse/Store/SeqFeature/
GFF3","urlTemplate":"http://host/genes.gff"}}
&addTracks=[{"label":"genes","type":"JBrowse/View/Track/
CanvasFeatures","store":"url"}]
```

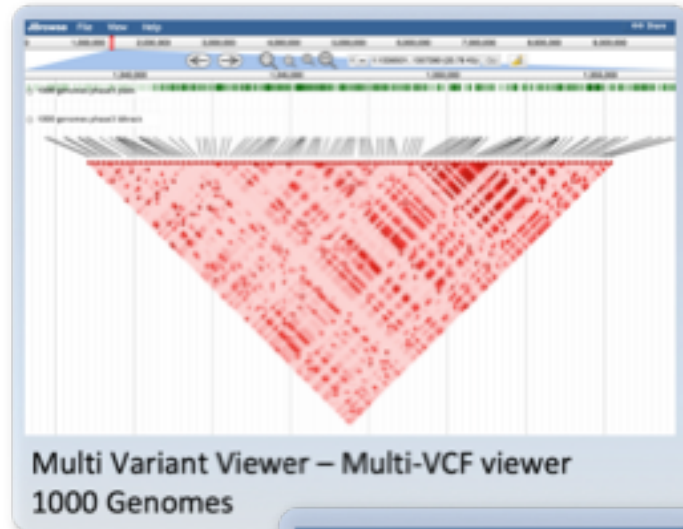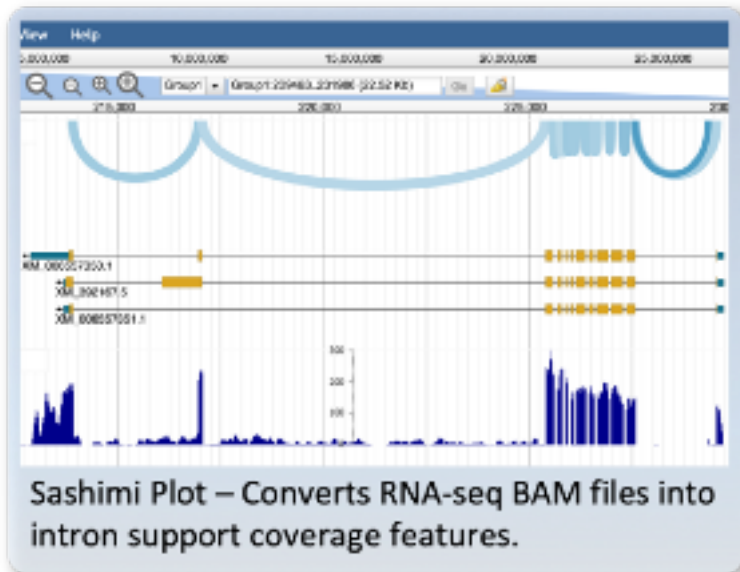The GMOD Plugin Directory

https://gmod.github.io/jbrowse-registry/

Expansive JBrowse Plugin Registry

https://gmod.github.io/jbrowse-registry/

44 registered plugins

Multi Variant Viewer – Multi-VCF viewer
1000 Genomes

@cmdcolin

Sashimi Plot – Converts RNA-seq BAM files into
intron support coverage features.

Lollipop, SVG Tracks with
MyVariants.info plugin