## How to use JBrowse2

## Introduction

We are working on transitioning all our databases to JBrowse2. JBrowse2 has the same features as JBrowse1 but allows for multiple genomes to be viewed in the same session versus one genome per session. This does allow for syntemy to be viewed within JBrowse2.

Instead of putting every genome into JB2 like we did with JB1, we are currently only putting the key reference genomes for each crop into JB2 along with other good quality genomes (chromosome scale assemblies that are not highly fragmented) within each crop. We also did synteny analyses between genomes within the same crop type and between the 1-2 highly used (reference) genomes of each crop. We can add other genomes and comparisons as requested as well as update what the reference genomes are as the needs of the community change.

There are results from two different pairwise synteny analyses. The 'Synteny – Genome Sequence Based' category are results from minimap2 which compares the genome sequences on the nucleotide level. The 'Synteny – Ortholog Based' category are results from MCScan which is based on gene positions and mRNA sequences.

Please provide feedback on feature you would like us to add (provided we have data) and other training resources you feel are needed via the database contact form. You can also look at the <u>JBrowse2 documentation</u>.

## Starting a session

- 1.) Go to Tools  $\rightarrow$  JBrowse. From that page, there will be a link at the top of the page for a blank JBrowse session
- 2.) Click "Linear genome view"



3.) Select a genome and chromosome/scaffold to open (also have option to open all chromosome/scaffolds) and click "open".

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				Assembly V. caesariense W85-20 P0 v2 Select assembly to view	Vcev1_p0.Chr01 Enter sequence name, featu	Q 👔	OPEN	SHOW ALL REGIONS IN ASSEMBLY	

4.) From here, you will need to open the track selector (right-hand menu). Initially there is a large button in the center of the track to do so. After you open tracks, that disappears, and you will need to click on the tiny hamburger icon in the upper left of the track to open it again.

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			Marker and QTL Alignments •••
			Synteny - Genome Sequence Based ····
			Synteny - Ortholog Based •••

5.) The track selector is very similar to JB1 and you have to select the box in front of the track name to make it visible. The Reference sequence track is the genome sequence and can be zoomed to base level. The Genes track is the annotated genes and mRNA from the genome assembly. When enabling most of the tracks, you will get an error saying you need to zoom in to see them or you can click the "Force load" text.

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- 6.) Navigation is like JB1. Arrow keys to move left or right, but you can also click and drag left/right. To change chromosomes, either click the box and select another or start typing the name (can also add coordinates with following structure: chrName:start..stop). Also, you can type gene/mRNA/marker/SNP/trait names into box and search for those.
- 7.) Additional tracks We have a variety of tracks available for each genome.

Available tracks 👻	Ø	: _ ×			
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▼ Tracks •••					
<ul><li>✓ Reference sequence (</li><li>✓ Genes-Vcae_W85-20_</li></ul>	V. caesariense P0 •••	W85-20 P0 v2) •••			
Marker and QTL Alig	nments …				
Synteny - Genome Sequence Based •••					
Synteny - Ortholog Based •••					

8.) You can expand each section by clicking on the section title. Under the 'Marker and QTL Alignments' section, you will find mapped features that are also stored in the GDV database. Some of these positions are from the literature, some of the positions are from analyses that GDV performed. Click the box next to the name to make the track visible. Click on the three dots after the track name to see more information. We also have these tracks in JB1.



9.) In JB2 you can have multiple genomes open in the same session. To do this, go to the JB2 menu under 'Add' → 'Linear genome view'. You will get the option to select another genome or even the same genome but a different chromosome/scaffold.



## Viewing Synteny Data

 You can view the synteny data in 2 ways. First, just like any other track by clicking the check boxes under the Synteny sections. The 'Synteny – Genome Sequence Based' category are results from minimap2 which compares the genome sequences on the nucleotide level. The 'Synteny – Ortholog Based' category are results from MCScan which is based on gene positions and mRNA sequences.



2.) Or you can take advantage of the new 'Linear synteny view' by adding it from the 'Add' menu.



3.) The configuration window for the Linear synteny view allow you to select two or more genomes (click 'Add row' to add more genomes) and display syntenic relationships via connecting lines between the genomes. For each pairwise comparison, you also need to select a synteny analysis dataset from the pull-down menu. GDV provides the pairwise comparisons with minimap2 and MCscan. You can also upload your own files to temporarily display in JB2 (use 'New track' radio button).

Untitled view					
Select assemblies for linear synteny view Row 1: × Assembly V. caesariense W85-20 P0 v2	Synteny dataset to display between row 1 and 2 <ul> <li>None</li></ul>				
Row 2: × Assembly V. caesariense W85-20 P0 v2 × ADD ROW LAUNCH	Select a track from the select box below, the track will be shown when you hit "Launch". Vmac Ben Lear-Vcae W85-20 P0 (Minimap2) 👻				
≻ Untitled view					
Select assemblies for linear synteny view	Synteny dataset to display between row 2 and 3				
Row 1: X Assembly V. caesariense W85-20 P0 v2 -	○ None				
Row 2: X Assembly V. macrocarpon Stevens v1	Select a track from the select box below, the track will be shown when you hit "Launch".				
Row 3: X Assembly V. myrtillus NK2018 v1 V	Vmac Stevens-Vmyr NK2018 Simple Anchors (MCScan) 👻				
ADD ROW LAUNCH					

In the above example, we are doing a comparison between a blueberry, cranberry and bilberry genome. Click the arrow to the right of the genome pairs to select the synteny data for that pair. We have selected the simple anchors tracks for each pair. After clicking 'Launch' we see this, a genome wide view of the synteny. Check out <u>our video</u> for more info.

