

JBrowse as a Tool

Eric Rasche

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JBrowse is a Genome Browser

JBrowse as a Tool

Eric Rasche

- Fast
- Features!
- Extensible

Available Tracks

filter by text

Reference sequence

1

☒ Reference sequence

Miscellaneous

10

- ☒ HTMLFeatures - Example Features
- ☐ HTMLFeatures - Name test track has a really long track label
- ☐ HTMLFeatures - SNPs
- ☐ HTMLFeatures - Example motifs
- ☐ HTMLFeatures - Features with right-click menus
- ☐ HTMLFeatures - Fingerprinted BACs
- ☐ HTMLFeatures - ESTs
- ☐ FromConfig - Features in Configuration
- ☐ GFF3 - volvox.gff3 in-memory adaptor
- ☐ GTF - volvox.gtf in-memory adaptor

Transcripts

4

- ☐ CanvasFeatures - Protein-coding genes
- ☒ HTMLFeatures - mRNAs
- ☐ CanvasFeatures - mixed mRNAs and CDSs
- ☒ CanvasFeatures - transcripts

Pre-generated images

1

- ☒ Image - volvox_microarray.wig

BAM

4

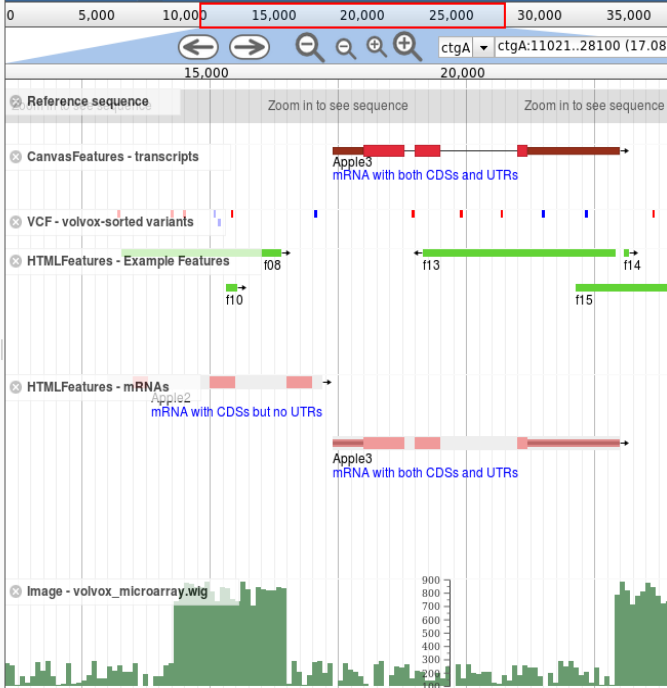
- ☐ Legacy BAM - volvox-sorted.bam
- ☐ BAM - volvox-sorted.bam
- ☐ BAM - volvox-sorted.SNPs/Coverage

Volvox Example

File

View

Help



Available Tracks

Reference sequence 1

☒ Reference sequence

Miscellaneous 10

- ☐ HTMLFeatures - Example Features
- ☐ HTMLFeatures - Name test track has a really long track label
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Transcripts 4

- ☐ CanvasFeatures - Protein-coding genes
- ☐ HTMLFeatures - mRNAs
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- ☐ CanvasFeatures - transcripts

Pre-generated images 1

☐ Image - volvox_microarray.wig

BAM 4

- ☐ Legacy BAM - volvox-sorted.bam
- ☒ BAM - volvox-sorted.bam
- ☒ BAM - volvox-sorted SNPs/Coverage

Volvox Example

File

View

Help

0 5,000 10,000 15,000 20,000 25,000 30,000 35,000



ctgA ctgA:17010..17074 (66 b)

17,025

17,050

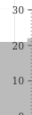
Reference sequence

G	S	V	K	S	R	T	P	L	S	K	R	E	R	R	Q	E	N	F	S	A	L	D	I	K	
g	t	t	c	a	g	t	c	a	a	a	t	c	g	a	a	a	g	a	g	a	g	c	g	c	a
c	a	a	g	t	c	a	c	t	t	t	a	g	c	t	t	t	t	c	t	c	c	g	c	g	t
T				H		F		R		G		L		S		A		C		F		E		I	L
N	E	T	F	D	V	E		F		L	P	A	S	N	A	S	Y	L							

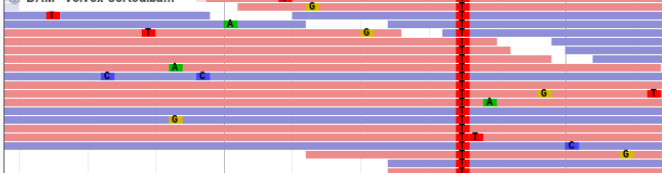
VCF - volvox-sorted variants

SNV C -> T

BAM - volvox-sorted SNPs/Coverage



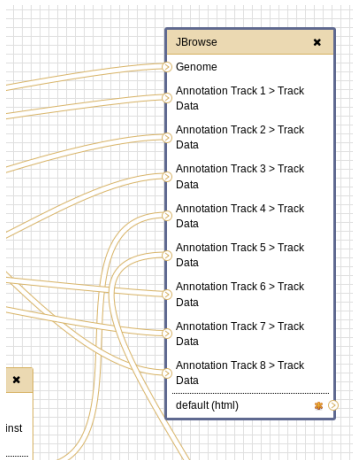
BAM - volvox-sorted.bam



Why JBrowse as a Tool? Workflows!

JBrowse as a Tool

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GFF3/BED

JBrowse as a Tool

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The screenshot displays the JBrowse genome browser interface within the Galaxy CPT environment. The top navigation bar includes links for 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'Admin', 'Help', and 'User'. The main tool title is 'JBrowse genome browser (Galaxy Tool Version 0.2)'. Below this, the 'Genome' section shows a dropdown menu set to '2: Miro.fa'. The 'Annotation Track' section contains two tracks:

- Track 1: Annotation Track**
 - Track Label:** Glimmer
 - Track Category:** Default (with a note: 'Organise your tracks into Categories for a nicer end-user experience')
 - Track Type:** GFF/GFF3/BED Features
 - Track Data:** 58: Glimmer3 to GFF3 on data 2 and data 54 (with a note: 'In GFF, GFF3, BED')
 - This is match/match_part data:** Yes (selected), No
- Track 2: Annotation Track**
 - Track Label:** MGA
 - Track Category:** Default (with a note: 'Organise your tracks into Categories for a nicer end-user experience')

On the right side, a vertical track list shows various tracks with green highlights, including '58: Glimmer3 to GFF3 on data 2 and data 54', '51: Jvarkit alignment', '50: Jvarkit alignment', '48: Jvarkit alignment', '42: Jvarkit alignment', '453: Jvarkit alignment', '41: Jvarkit alignment', '36: Jvarkit alignment', '35: Jvarkit alignment', '33: Jvarkit alignment', and '32: Jvarkit alignment'. The bottom of the interface features a series of navigation icons for zooming and panning.

BAM

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Track Type

BAM Pileups

Track Data



No bam dataset available.

in BAM

Autogenerate SNP Track

Yes

No

Not recommended for deep coverage BAM files

Blast XML

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Track Type

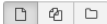
Blast XML

BlastXML Track Data



No blastxml dataset available.

Features used in Blast Search



73: Intein Detection on data 28 and data 15

in GFF3. This is required so we know where to map features. E.g. where results of which CDS Protein32 match up to. The c should MATCH some feature IDs in your GFF3 file.

Minimum Gap Size

10

before a new match_part feature is created

Is this a protein blast search?

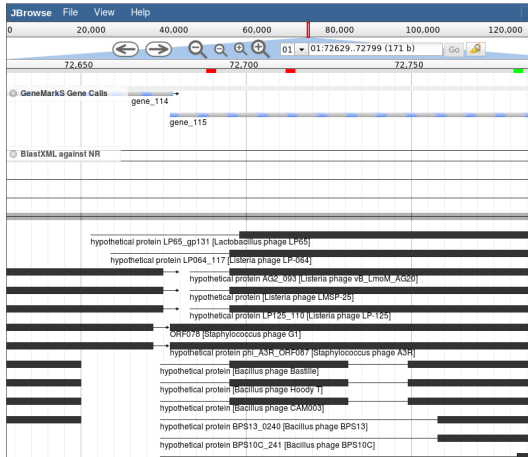
Yes

No

Gapped Blast XML

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BigWig

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Track Type

BigWig XY

Track Data



73: Intein Detection on data 28 and data 15

in BigWig

Use XYPlot

☒ Yes ☐ No

instead of continuous coloured band

Show variance band

☒ Yes ☐ No

Only for XYPlots

Track Scaling

Autoscale (local)

VCF/SNPs

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Track Type

VCF SNPs

SNPs



No vcf dataset available.

in VCF

Nice Features

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- Lots of formats
- “Sugar” to support non-standard data for JBrowse like BlastXML
- Just an HTML dataset, download, view, deploy to production servers

Planned Features

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- Soon more raw JBrowse configuration
- Color/track styling implemented
- Will be easier to configure “production” JBrowse instances

Caveats/TODOs

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- This is still a **work-in-progress** (but it's close!)
- Still some bugs in dependencies & their installation process
- Broken upstream perl modules, yay!
- JBrowse-in-Galaxy will not display BAM/BigWig files if you aren't using X_SENDFILE (but I think we can fix this)

Q&A

JBrowse as a Tool

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- Development:
<https://github.com/galaxyproject/tools-iuc>
- Twitter: @Eric_Rasche
- Bugs/feature requests welcome!