

JBrowse as a Tool

Eric Rasche

What is it?

Screenshots

JBrowse in Galaxy

Features

GFF3/BED

BAM

Blast XML

BigWig

VCF/SNPs

Nice Features

Roadmap

Caveats

Q&A

# JBrowse as a Tool

Eric Rasche

2015-07-07

# JBrowse is a Genome Browser

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- Fast
- Features!
- Extensible

## Available Tracks

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

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



Reference sequence Zoom in to see sequence Zoom in to see sequence

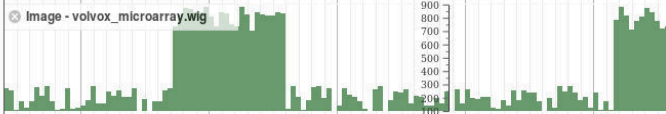
CanvasFeatures - transcripts  
Apple3 mRNA with both CDSs and UTRs

VCF - volvox-sorted variants

HTMLFeatures - Example Features  
f10 f11 f13 f14 f15

HTMLFeatures - mRNAs  
Apple2 mRNA with CDSs but no UTRs

Apple3 mRNA with both CDSs and UTRs



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Volvox Example

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

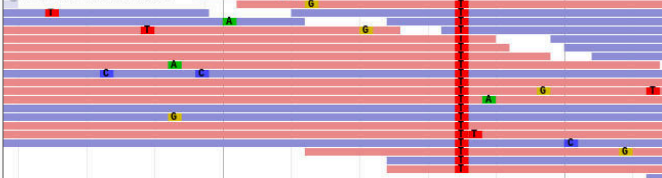
VCF - volvox-sorted variants

SNV C->T

BAM - volvox-sorted SNPs/Coverage



BAM - volvox-sorted.bam



# Why JBrowse as a Tool? Workflows!

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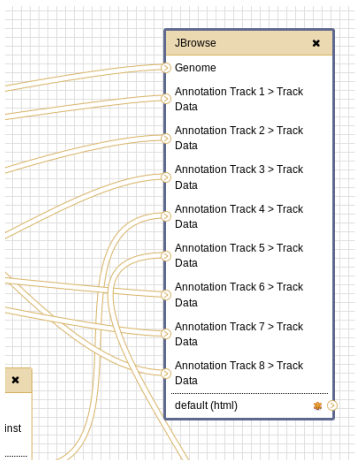
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# GFF3/BED

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The screenshot displays the Galaxy CPT interface for the JBrowse genome browser. The top navigation bar includes 'Galaxy / CPT' and various menu items like 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'Admin', 'Help', and 'User'. The main tool panel is titled 'JBrowse genome browser (Galaxy Tool Version 0.2)'. It features a 'Genome' dropdown set to '2: Miro.fa'. Below this are two 'Annotation Track' sections. The first track, '1: Annotation Track', is configured with 'Track Label' as 'Glimmer', 'Track Category' as 'Default', and 'Track Type' as 'GFF/GFF3/BED Features'. Its 'Track Data' is set to '58: Glimmer3 to GFF3 on data 2 and data 54 in GFF, GFF3, BED', with a note 'This is match/match\_part data' and 'Yes' selected. The second track, '2: Annotation Track', has 'Track Label' as 'MGA' and 'Track Category' as 'Default'. A right-hand sidebar shows a 'Hist' panel with a list of tracks including '58: G on d', '58: P on d', '51: J allgr (Bac)', '50: J allgr (Gaid)', '48: J leng', '42: J form', '453 form', 'HTML', '41: J Graj', '36: J allgr', '35: G data data', and '33: J Data'. At the bottom right, there are navigation icons for back, forward, and search.

# 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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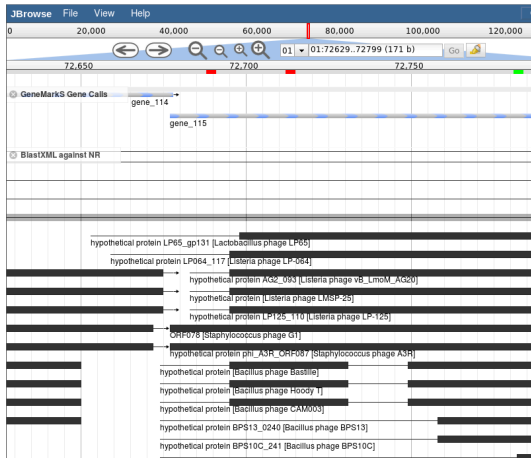
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# BigWig

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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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**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

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