



UCSC Genome Browser



UNIVERSITY OF CALIFORNIA
SANTA CRUZ | Genomics
Institute

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CyVerse's “*Send to Genome Browser*” option creates links accepting byte-range requests for binary index data.

Examples of Visualizing binary indexed data in the UCSC Genome Browser

A 2bit file is a binary indexed version of a FASTA file
(stores sequence ACGT as 00 01 11 10)

faToTwoBit input.fasta output.2bit




```
>scaffold_1
GTTGTAAATACTCTATTCTACAATAAAACCAAAGATAACTCTTTATCAG
TCATAGGTTGAATTGGCGTTGAAGTAAACAAAAATACTGCTCAAAAGG
...
>scaffold_2
AGTTATGACAAACTATAAAAAAGTCGGTAGAGACAAAAGCGAAAAGGATCT
TCGTTTCGTGGACGAAGCGACCAAACTGAGCACAAGATAAATCCCGAATA
...
>scaffold_3
CATAAATTCATAAATCAATTCATGAAGAATAATTTTAGAAAAATGGTTCA
TAGAAAAATTTCCAGGAAGTTTGAAGTTGCTATAATGATTATTTCTCTTG
...
>scaffold_4
ATACTGCCCCATGCCTCATCTACTCCCTTCTTAACCTTTTCATCAACAACT
TGCTTAAGTTGGTCATCACTGACTGAGTGAGCCCAAACCTGGAATAGCTGT
...
```

The resulting indexed binary file
output.2bit can have data more easily
extracted and can also be viewed in the
UCSC Genome Browser.

Extracting a specific window location of data from a BAM and 2bit file


samtools view http://location_of/file.bam "chr1:1499900-1500055" > output.sam



```
PRESLEY_0030:6:5:16900:3432#0/2 65 chr1 10047 254 67M9S * 0 0 CCTAACCTAACCTAACCTAACCC
fa]hfafe]a_cfaddfcaffW_edfabfcdfcf*cace^c\d\aaWaJYZZ\K^VZTaBB00000000
PRESLEY_0030:6:26:1717:9490#0/2 65 chr1 10053 254 61M15S * 0 0 CCTAACCTAACCTAACCTAACCC
f_fcdefhfaecffdf]ffdcf]ffcff]cb`bb[d]db*W*^^^_Y^BB0000000000000000
PRESLEY_0030:5:69:17803:15567#0/2 65 chr1 10060 255 2573M1S * 0 0 AACTAACCTAACCTAA
hgfgghhhhhhhhhhhhhghghhhhhhhhhhhhhhhghghhhchghfchfhhadbhhea_cfcfa[
PRESLEY_0030:5:75:7248:15014#0/2 65 chr1 10060 255 2573M1S * 0 0 AACTAACCTAACCTAA
hfhfgghhgfhhhffhghhdghcagfhhhhfchhhfcfhcgcedfaff_hdfeeehaacc[Rchhh]egbd[bb
PRESLEY_0030:5:101:10596:3305#0/2 65 chr1 10060 255 2573M1S * 0 0 AACTAACCTAACCTAA
hhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhghhhghhhhhhhhhghd_dnhgceded^a^
.....
```

twoBitToFa -seq=chr1 -start=1499900 -end=1500055

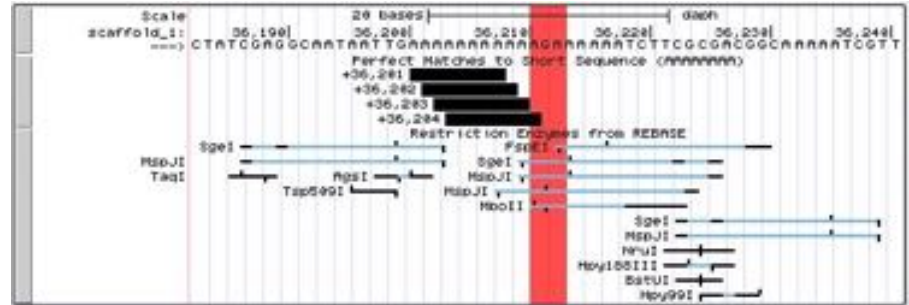
<http://yourGenome/your.2bit> output.fa



```
>chr1:1499900-1500055
GCTACCATCACCCAAAAAGCTGAGGAGTTTGAATTCCTTCAGCACAACT
ATCATTAAATTAATTTTTGAACCTCTGAGCCTGGAAGAGAAAAACAGGTTTG
GTTCAACATGAAGAATACTGTGATTTGACCCGTGACAGAGCTTTTCTGTTA
```

Viewing Data at UCSC

bigDataUrl http://location_of/file.bam



twoBitPath <http://yourGenome/your.2bit>



Hosting your data at CyVerse

CyVerse Storage Solution

<https://de.cyverse.org/> Discovery Environment



The image is a screenshot of the CyVerse Discovery Environment landing page. At the top left is the CyVerse logo, which consists of three curved lines forming a stylized 'C' followed by the word 'CYVERSE™'. To the right of the logo is the tagline 'Transforming SCIENCE through DATA-DRIVEN DISCOVERY'. Below the logo and tagline is the heading 'Discovery Environment' in a bold, blue font. Underneath the heading is a paragraph: 'The Discovery Environment integrates powerful, community-recommended software tools into a system that:'. This is followed by a bulleted list of three features: 'Makes big data management easy. Upload, organize, edit, view and search with ease!', 'Has 500+ scientific apps that utilize compute clusters and HPC resources as needed.', and 'Hides the complexity needed to do these tasks.'. On the right side of the page, there is a white box with a thin blue border. Inside this box, at the top, is an orange button with the text 'Log in with your CyVerse ID'. Below the button are two links: 'Forgot Password?' and 'Register Now'. At the bottom of the box, in a smaller font, is the text 'Minimum screen resolution supported: 1024 x 768'.

CYVERSE™ Transforming SCIENCE through
DATA-DRIVEN DISCOVERY

Discovery Environment

The Discovery Environment integrates powerful, community-recommended software tools into a system that:

- Makes big data management easy. Upload, organize, edit, view and search with ease!
- Has 500+ scientific apps that utilize compute clusters and HPC resources as needed.
- Hides the complexity needed to do these tasks.

Log in with your CyVerse ID

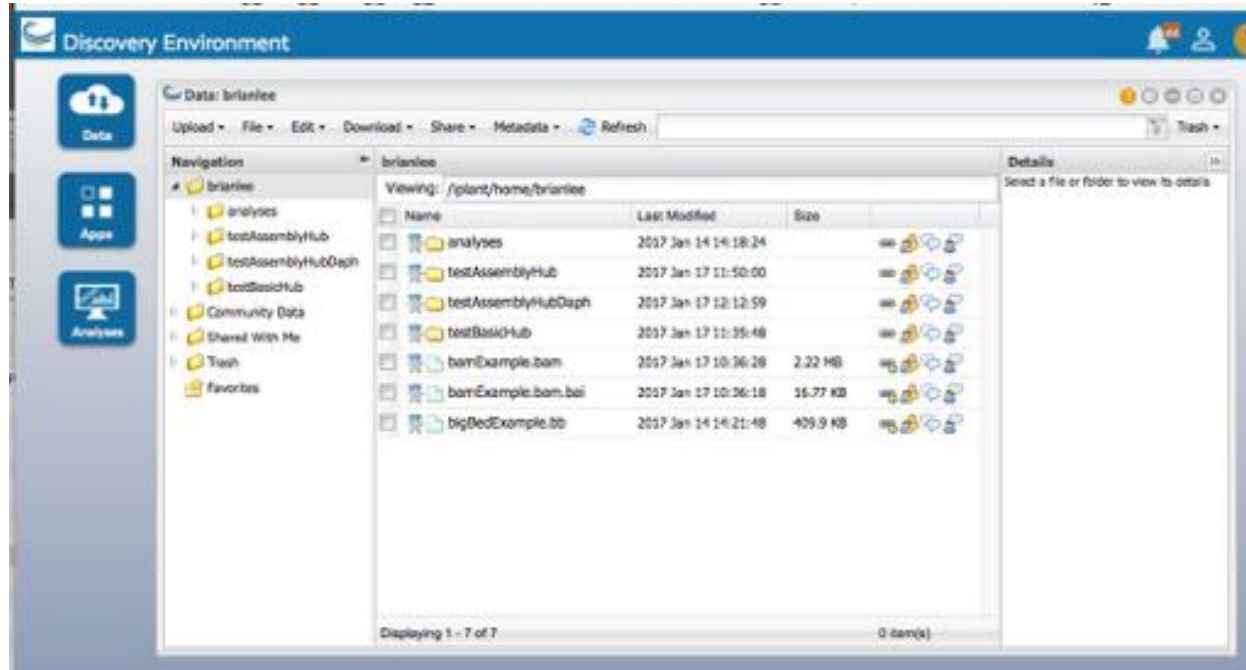
[Forgot Password?](#) [Register Now](#)

Minimum screen resolution supported: 1024 x 768

Hosting your data at CyVerse

CyVerse Storage Solution

<https://de.cyverse.org/> Discovery Environment



Hosting your data at CyVerse

CyVerse Storage Solution

Creating a Link that Accepts Byte-Ranges: “Send to Genome Browser”

**Share
Menu:**

**Send to
Genome
Browser**

The screenshot shows the CyVerse Data browser interface. The 'Share' menu is open, and the 'Send to Genome Browser' option is highlighted. The file 'bamExample.bam' is selected in the file list. The file details on the right show the 'Info-Type' as 'bam'.

Name	Last Modified	Size
bamExample.bam	2017 Jan 17 10:36:28	2.22 MB
bamExample.bam.bai	2017 Jan 17 10:36:18	16.77 KB
bigBedExample.bb	2017 Jan 14 14:21:48	409.9 KB

Details for 'bamExample.bam':

- Last Modified: 2017 Jan 17
- Date Submitted: 2017 Jan 17
- Permissions: own
- Share: 1
- Size: 2.22 MB
- Type: application/octet-stream
- Info-Type: bam
- md5 Checksum: 0f1d0c3...
- Send to: Genome Browser

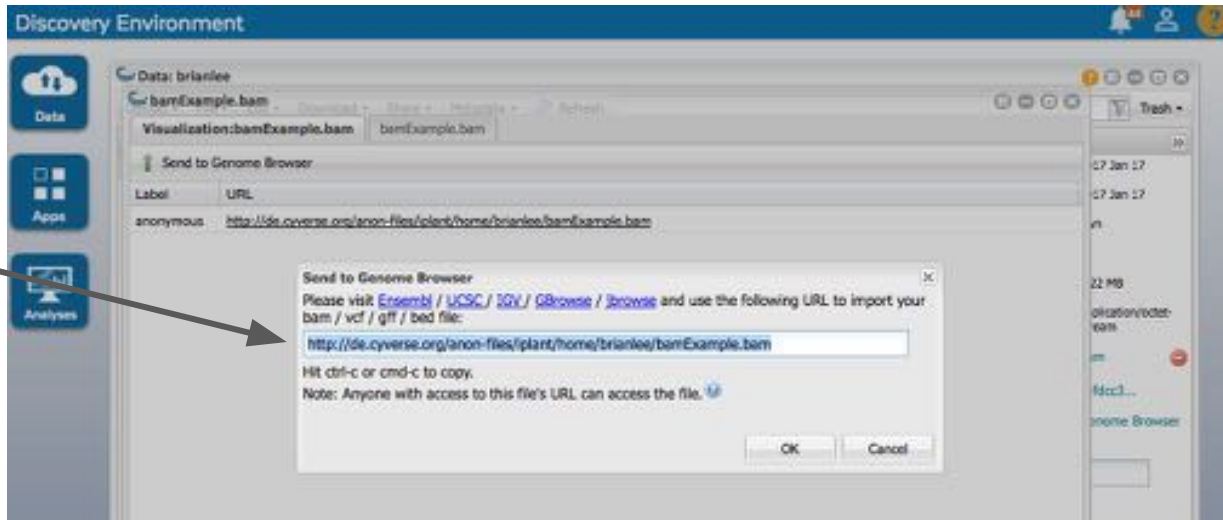
**Info-Type:
bam**

Hosting your data at CyVerse

CyVerse Storage Solution

Creating a Link that Accepts Byte-Ranges: “Send to Genome Browser”

Results in a link you can use in later visualization: ***bigDataUrl***



https://data.cyverse.org/dav-anon/iplant/home/brianleesoe/Bam_Ex1/DNase_example.bam

Hosting your data at CyVerse

CyVerse Storage Solution

Creating a Link that Accepts Byte-Ranges: “Send to Genome Browser”

Paste the link into
the BAM as
Custom Track on
any Assembly or
Assembly Hub

The screenshot shows the 'Add Custom Tracks' interface in the CyVerse Genome Browser. The top navigation bar includes 'Genomes', 'Genome Browser', 'Tools', 'Mirrors', 'Downloads', 'My Data', 'Projects', 'Help', and 'About Us'. The 'Add Custom Tracks' section is active, displaying a dropdown menu with options: 'My Sessions', 'Public Sessions', 'Track Hubs', 'Custom Tracks' (highlighted), and 'Track Collection Builder'. Below the menu, there is a text area for pasting URLs or data, with a 'Submit' button and a 'Clear' button. An arrow points from the text on the left to the text input area.

https://data.cyverse.org/dav-anon/iplant/home/brianleesoe/Bam_Ex1/DNase_example.bam

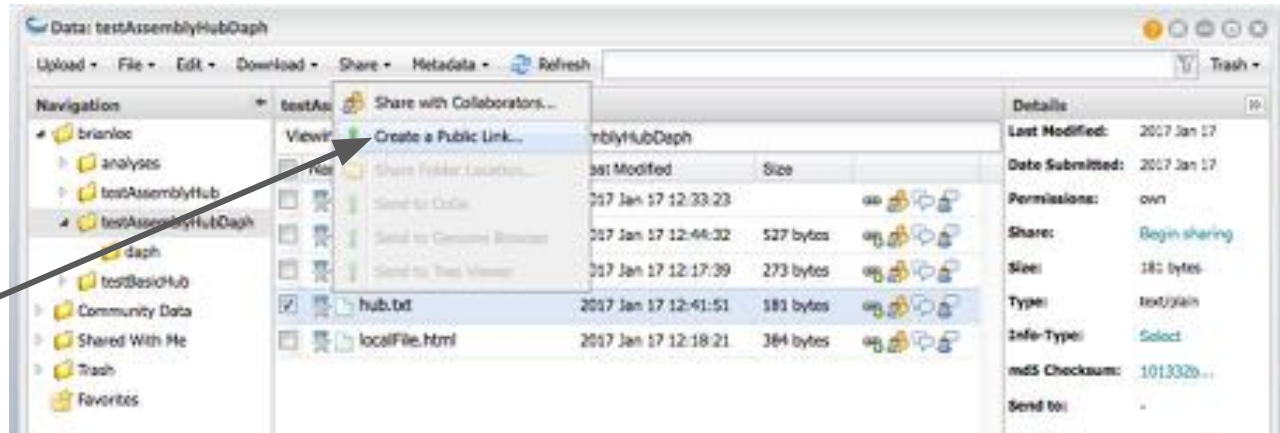
Hosting your data at CyVerse

CyVerse Storage Solution

NOTE: The “Create a Public Link” is not the same as “Send to Genome Browser”

The “**Create a Public Link**” option will work for static interactions, like downloading text/data files.

It will not work for data byte-range requests needed for visualization.



<https://de.cyverse.org/dl/d/ABC-123-ECT-B3D95682-4E68A6/fileName>
Will not work to visualize data in the Browser

Viewing the CyVerse hosted 2bit at UCSC

```
twoBitToFa -seq=chr1 -start=1499900 -end=1500055
```

<https://data.cyverse.org/dav-anon/iplant/home/your.2bit> output.fa



```
>chr1:1499900-1500055  
GCTACCATCACCCAAAAAGCTGAGGAGTTTGAATTCACCTTCAGCACAACT  
ATCATTAAATTAATTTTTGAACCTCTGAGCCTGGAAGAGAAAACAGGTTTG  
GTTCAACATGAAGAATACTGTGATTTGACCCGTGACAGAGCTTTCTGTTA
```


Viewing the CyVerse hosted 2bit at UCSC

hub plantAraTha1
useOneFile on
shortLabel Plant araTha1
longLabel Plant araTha1 Hub
email contact@email.com

genome araTha1
description Feb. 2011 Thale cress
twoBitPath araTha1.2bit
organism Arabidopsis thaliana
defaultPos chr1:1000000-2000000
scientificName Arabidopsis thaliana

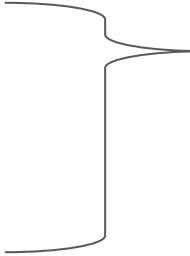
track cytoBandIdeo
longLabel Chromosome ideogram
shortLabel cytoBandIdeo
bigDataUrl cytoBandIdeo.bigBed
type bigBed

hub.txt



Viewing the CyVerse hosted 2bit at UCSC

hub plantAraTha1
useOneFile on
shortLabel Plant araTha1
longLabel Plant araTha1 Hub
email contact@email.com



The hub stanza sets **useOneFile on**, limiting hub to only one genome

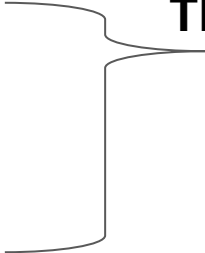
genome araTha1
description Feb. 2011 Thale cress
twoBitPath araTha1.2bit
organism Arabidopsis thaliana
defaultPos chr1:1000000-2000000
scientificName Arabidopsis thaliana

track cytoBandIdeo
longLabel Chromosome ideogram with cytogenetic bands
shortLabel cytoBandIdeo
bigDataUrl cytoBandIdeo.bigBed
type bigBed

Viewing the CyVerse hosted 2bit at UCSC

hub plantAraTha1
useOneFile on
shortLabel Plant araTha1
longLabel Plant araTha1 Hub
email contact@email.com

genome araTha1
description Feb. 2011 Thale cress
twoBitPath araTha1.2bit
organism Arabidopsis thaliana
defaultPos chr1:1000000-2000000
scientificName Arabidopsis thaliana



The genome stanza shares where to find the 2bit (and what to call the new genome)

track cytoBandIdeo
longLabel Chromosome ideogram with cytogenetic bands
shortLabel cytoBandIdeo
bigDataUrl cytoBandIdeo.bigBed
type bigBed

Viewing the CyVerse hosted 2bit at UCSC

```
hub plantAraTha1
useOneFile on
shortLabel Plant araTha1
longLabel Plant araTha1 Hub
email contact@email.com

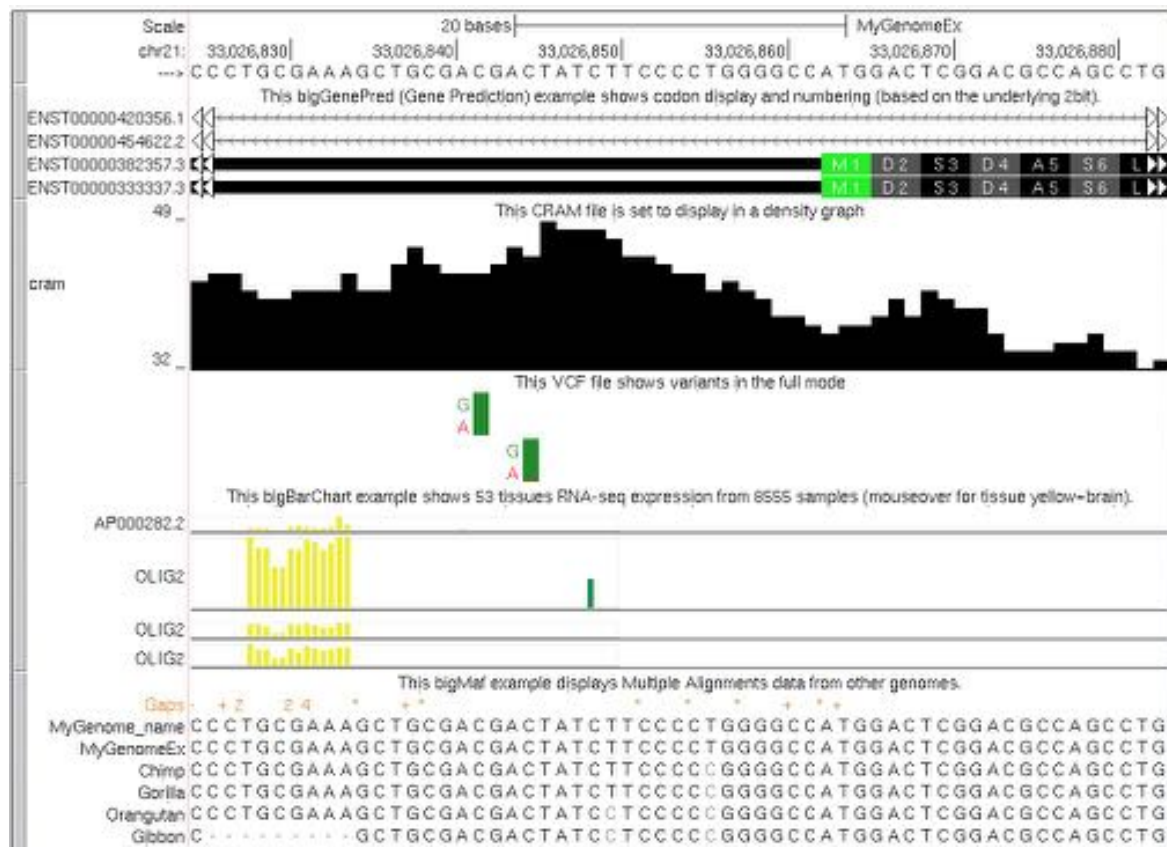
genome araTha1
description Feb. 2011 Thale cress
twoBitPath araTha1.2bit
organism Arabidopsis thaliana
defaultPos chr1:1000000-2000000
scientificName Arabidopsis thaliana
```

```
track cytoBandIdeo
longLabel Chromosome ideogram with cytogenetic bands
shortLabel cytoBandIdeo
bigDataUrl cytoBandIdeo.bigBed
type bigBed
```

The multiple track stanzas share where to find the annotation tracks and what to name them and the data type (BAM, CRAM, VCF, bigGenePred, bigBarChart, bigPsl, bigChain, bigMaf, bigNarrowPeak, bigWig, bigBed, others).

The [bigDataUrl](#) must point to an online location of the binary-indexed data that can accept byte-range requests.

Additional Track Types



Viewing the CyVerse hosted 2bit at UCSC

Host all data at CyVerse

Binary indexed files:

twoBitPath,

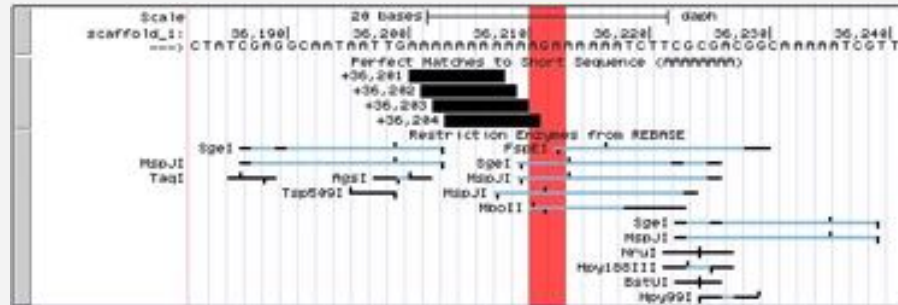
bigDataUrl

Text files: hub.txt

```
>scaffold_1
GTTGTAATACTCTATTCTACAATAAAACCAA
TCATAGGTTGAATTGGCGTTGAAGTAAAAACAAA
...
>scaffold_2
AGTTATGACAAACTATAAAAAAGTCGGTAGAGACAAAAG
TCGTTTCGTGGACGAAGCGACCAAAACTGAGCACAAGAT
...
>scaffold_3
CATAAATTCATAAATCAATTCATGAAGAATAATT
TAGAAAATTTCCAGGAAGTTTGAAGTTGCTA
...
```

```
hubDirectory
|__hub.txt
|__genomes.txt
|__hg19
|__trackDb.txt
```

Visualize at UCSC



Viewing the CyVerse hosted 2bit at UCSC

Easily move all data with CyVerse `iCommands` (`rsync` becomes `irsync`) that allows transfer of 2-100GB files and any recursive directory structures:

```
$ irsync -r local_directory_name i:data_store_directory_name
```

hubDirectory

```
|  
|_hub.txt  
|_genomeFile.2bit  
|_trackAnnotation.bigBed
```

Move all your local BAMS, VCFs, and related Assembly Hub files with the single `irsync` command.

Then make the files publicly accessible with the `ichmod` command.

<https://data.cyverse.org/dav-anon/>

```
$ ichmod read anonymous data_store_directory_name
```

Hosting your data at CyVerse



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[Launch](#) ▾

[Log In](#) | [Register](#)

Sign-up for a
CyVerse
Account

A screenshot of the CyVerse "Sign Up" form. The form is titled "CYVERSE Sign Up" and has three steps: "1 Account", "2 Institution", and "3 Demographics". The "Account" step is active. The form contains the following fields:

- First Name *: Brian
- Last Name *: Lee
- Username *: brianleesoe ✓
- Email *: brianlee@soe.ucsc.edu ✓

A blue "NEXT" button is located at the bottom right of the form.

Hosting your data at CyVerse

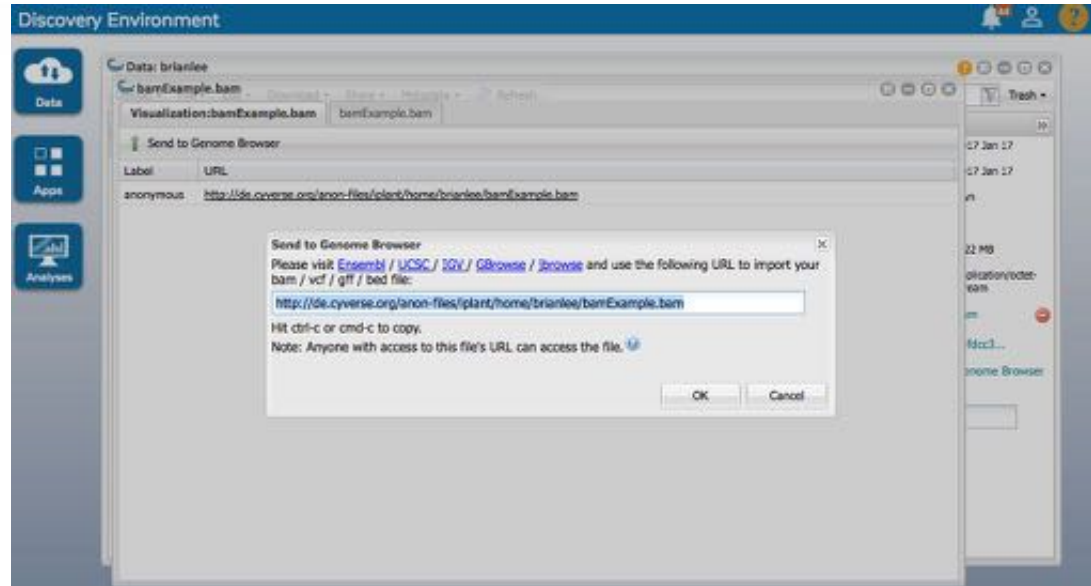


Discovery Environment

LAUNCH

Use hundreds of bioinformatics apps and manage data in the CyVerse Data Store from a simple web interface

Launch the Discovery Environment and click Data



Discovery Environment

Data

Apps

Analysis

Data: brianlee

bamExample.bam

Visualization: bamExample.bam

Send to Genome Browser

Label	URL
anonymous	http://de.cyverse.org/anon-files/plant/home/brianlee/bamExample.bam

Send to Genome Browser

Please visit [Ensembl](#) / [UCSC](#) / [IGV](#) / [GBrowse](#) / [JBrowse](#) and use the following URL to import your bam / vcf / gff / bed file:

<http://de.cyverse.org/anon-files/plant/home/brianlee/bamExample.bam>

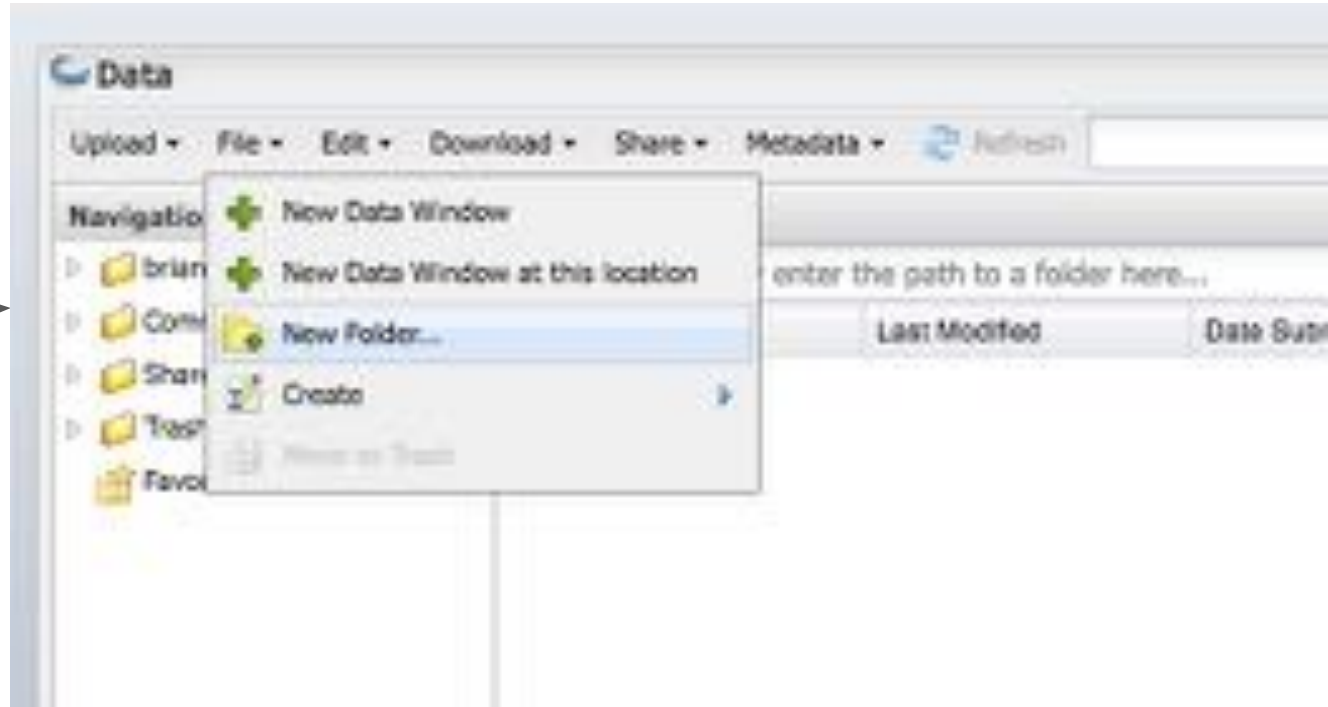
Hit ctrl-c or cmd-c to copy.

Note: Anyone with access to this file's URL can access the file.

OK Cancel

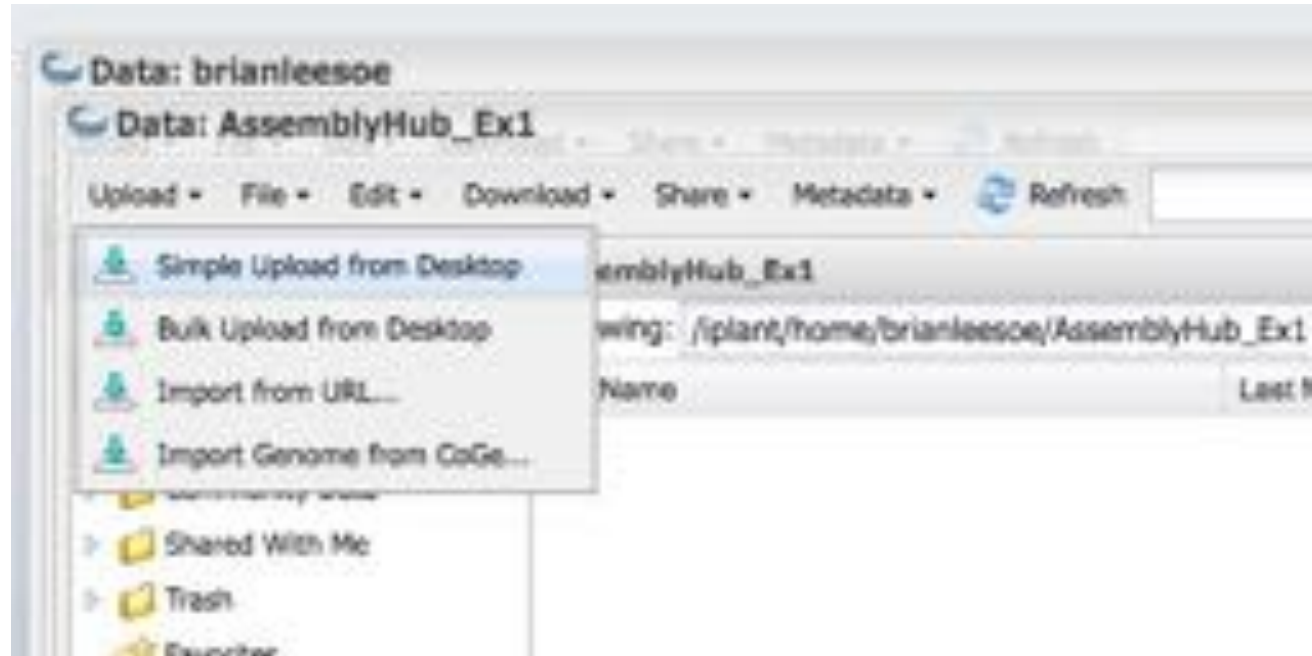
Hosting your data at CyVerse

Make a New Folder for Your Genome Data



Hosting your data at CyVerse

Upload your files from your created 2bit files from your Desktop to CyVerse



Hosting your data at CyVerse

Choose the
Files to
Upload
(supporting
hub files here)



Upload • File • Edit • Download • Share • Metadata • Refresh

Navigation AssemblyHub_Ex1 Details

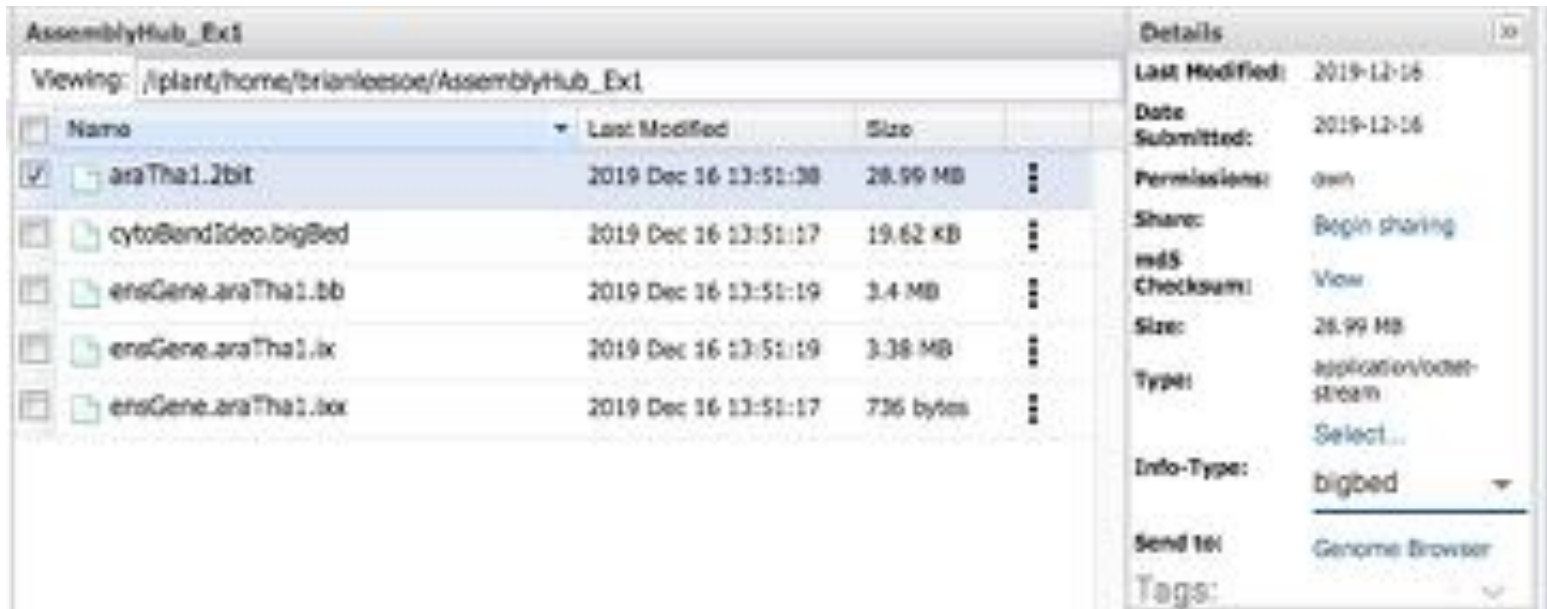
Viewing: /iplant/home/brianleesoe/AssemblyHub_Ex1

Select a file to upload

Name	Upload	Last Modified	Size
	Maximum size of each file is 1.9GB when using simple upload. Uploading to AssemblyHub_Ex1.		
	<input type="button" value="Choose File"/>	cyto@lanlideo.big@ed	
	<input type="button" value="Choose File"/>	araThat1.2@it	
	<input type="button" value="Choose File"/>	ensGene.araThat1.bb	
	<input type="button" value="Choose File"/>	ensGene.araThat1.ix	
	<input type="button" value="Choose File"/>	ensGene.araThat1.ix	

Hosting your data at CyVerse

Creating a Link that Accepts Byte-Ranges: “Send to Genome Browser”



The screenshot shows the CyVerse file manager interface. The main window displays a file list with columns for Name, Last Modified, and Size. The file 'araTha1.2bit' is selected. The details panel on the right shows the file's metadata, including its type and the 'Send to' option set to 'Genome Browser'.

Name	Last Modified	Size
araTha1.2bit	2019 Dec 16 13:51:38	28.99 MB
cytoBand2dec.bigBed	2019 Dec 16 13:51:17	19.62 KB
ensGene.araTha1.bb	2019 Dec 16 13:51:19	3.4 MB
ensGene.araTha1.ix	2019 Dec 16 13:51:19	3.38 MB
ensGene.araTha1.ix	2019 Dec 16 13:51:17	736 bytes

Details	
Last Modified:	2019-12-16
Date Submitted:	2019-12-16
Permissions:	own
Share:	Begin sharing
m&S	
Checksum:	View
Size:	28.99 MB
Type:	application/octet-stream
Info-Type:	bigbed
Send to:	Genome Browser
Tags:	

Select each file and set the **Type** to **bigBed** and then click the **Send to: Genome Browser**



Hosting your data at CyVerse

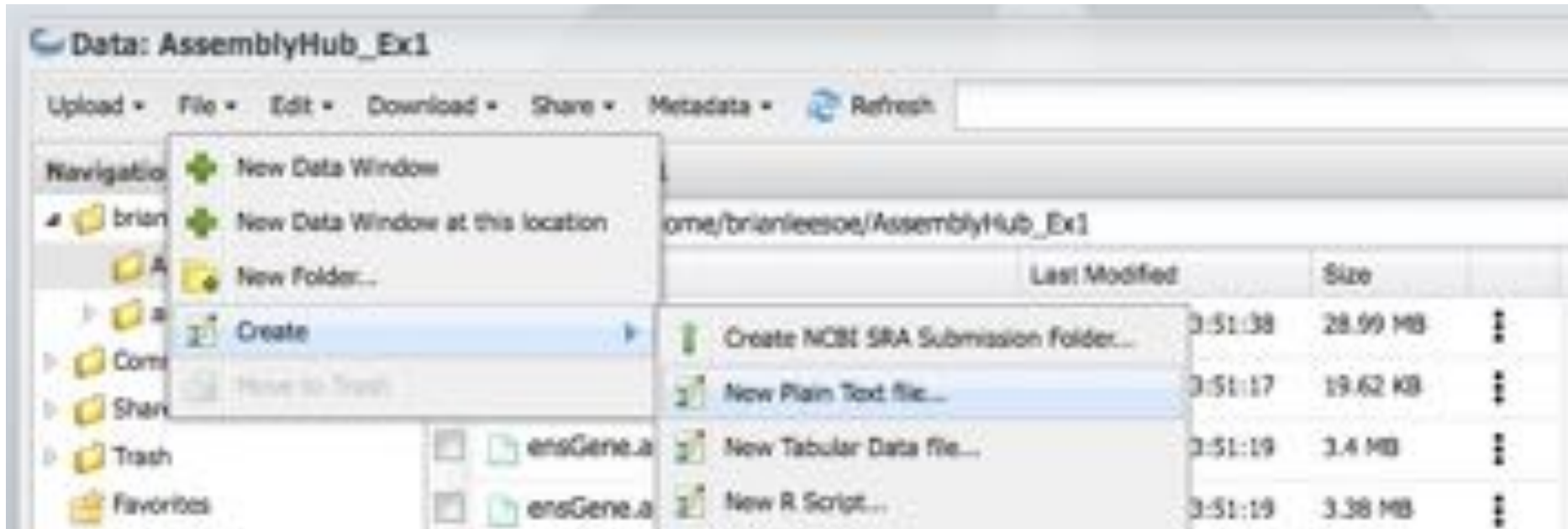
Creating a Link that Accepts Byte-Ranges: “Send to Genome Browser”

These generated **View in Genome Browser** links, which allow byte-range access to the data.



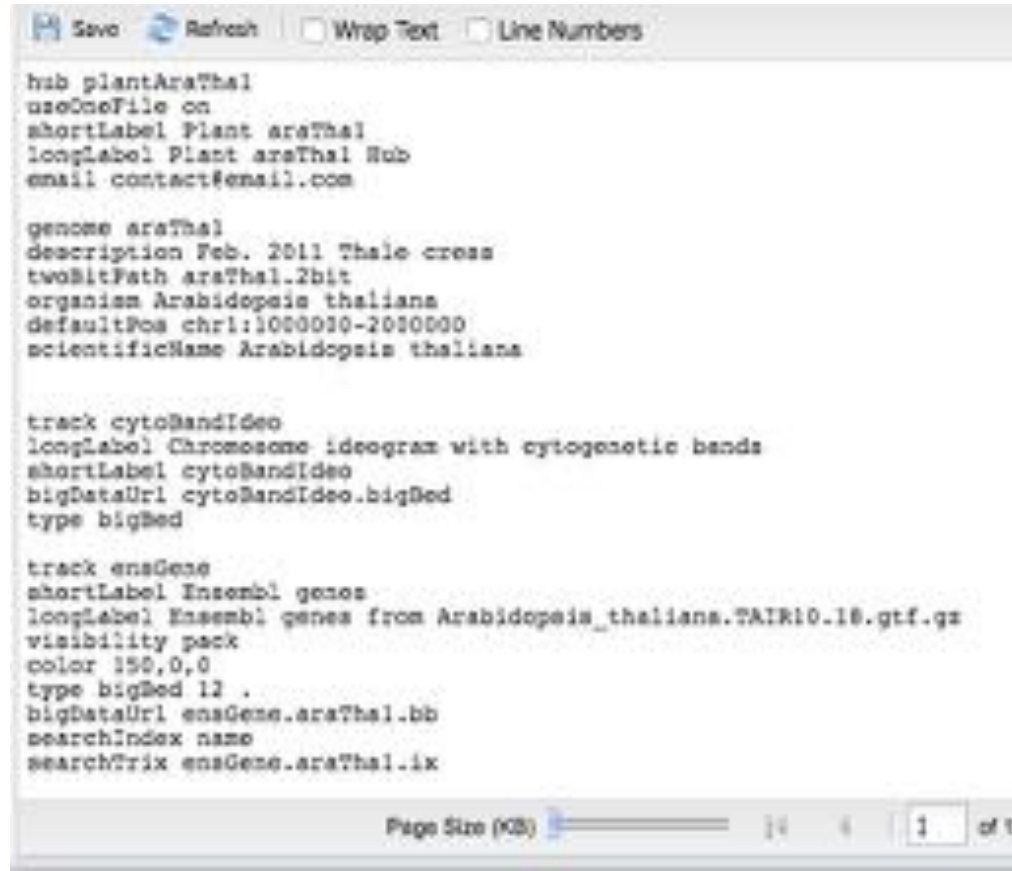
Hosting your data at CyVerse

Create a new Text File (or just upload one) for the **hub.txt**



Selected folder: /iplant/home/brianleeso/AssemblyHub_Ex1
File Name: hub.txt

Hosting your data at CyVerse



```
hub plantAraThal
useOneFile on
shortLabel Plant araThal
longLabel Plant araThal Hub
email contact@email.com

genome araThal
description Feb. 2011 Thale cross
twoBitPath araThal.2bit
organism Arabidopsis thaliana
defaultPos chr1:1000000-2000000
scientificName Arabidopsis thaliana

track cytoBandIdeo
longLabel Chromosome ideogram with cytogenetic bands
shortLabel cytoBandIdeo
bigDataUrl cytoBandIdeo.bigBed
type bigBed

track ensGene
shortLabel Ensembl genes
longLabel Ensembl genes from Arabidopsis_thaliana.TAIR10.10.gtf.gz
visibility pack
color 150,0,0
type bigBed 12 .
bigDataUrl ensGene.araThal.bb
searchIndex name
searchTrix ensGene.araThal.ix
```

Page Size (KB) | 1 of 1

Hosting your data at CyVerse

View in Genome Browser

Please visit [Ensembl](#) / [UCSC](#) / [IGB](#) / [IGV](#) / [GBrowse](#) / [jbrowse](#) / [WashU EPIGenome Browser](#) and use one of the following URLs to import your bam / vcf / gff / bed / bigBed / bigWig file:

`https://data.cyverse.org/dav-anon/iplant/home/brianleesoe/AssemblyHub_Ex1/hub.txt`

Copy to clipboard

Genomes Genome Browser Tools Mirrors Downloads My Data Help About Us

Track Data Hubs

Track data hubs are collections of external tracks that can be imported into the UCSC Genome Browser. Hubs show up under the user's own blue label bar on the main browser page, as well as on the configure page. To import a public hub click its "Connect" button below.

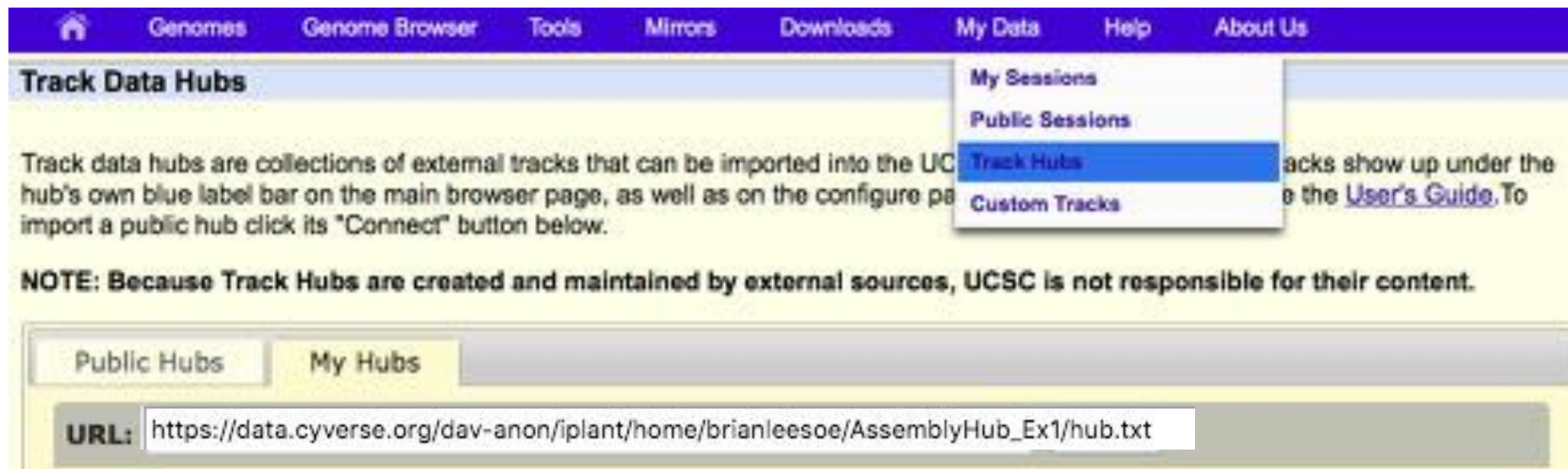
NOTE: Because Track Hubs are created and maintained by external sources, UCSC is not responsible for their content.

Public Hubs My Hubs

URL: Add Hub

- My Sessions
- Public Sessions
- Track Hubs
- Custom Tracks

Hosting your data at CyVerse



The screenshot shows the UCSC Genome Browser interface. At the top is a navigation bar with links: Home, Genomes, Genome Browser, Tools, Mirrors, Downloads, My Data, Help, and About Us. Below this is the 'Track Data Hubs' section. A dropdown menu is open from the 'Track Data Hubs' header, showing options: My Sessions, Public Sessions, Track Hubs (highlighted), and Custom Tracks. The main content area contains text explaining that Track Data Hubs are collections of external tracks that can be imported into the UCSC Genome Browser. It mentions that these hubs show up under the user's own blue label bar on the main browser page and on the configuration page. A note states that because Track Hubs are created and maintained by external sources, UCSC is not responsible for their content. At the bottom, there are tabs for 'Public Hubs' and 'My Hubs', and a URL input field containing the address: `https://data.cyverse.org/dav-anon/iplant/home/brianleesoe/AssemblyHub_Ex1/hub.txt`.

Track Data Hubs

Track data hubs are collections of external tracks that can be imported into the UCSC Genome Browser. These hubs show up under the user's own blue label bar on the main browser page, as well as on the configuration page. To import a public hub click its "Connect" button below.

NOTE: Because Track Hubs are created and maintained by external sources, UCSC is not responsible for their content.

Public Hubs My Hubs

URL: `https://data.cyverse.org/dav-anon/iplant/home/brianleesoe/AssemblyHub_Ex1/hub.txt`

Hosting your data at CyVerse

Genomes Genome Browser Tools Mirrors Downloads My Data View Help About Us

UCSC Genome Browser on Arabidopsis thaliana Feb. 2011 Thale cress Assembly (araTha1)

move <<< << < > >> >>> zoom in 1.5x 3x 10x base zoom out 1.5x 3x 10x 100x

chr1:1,475,000-1,524,999 50,000 bp. go

Scale chr1: 1,400,000 1,405,000 1,410,000 1,415,000 1,420,000 1,425,000 1,430,000 1,435,000 1,440,000 1,445,000 1,450,000 1,455,000 1,460,000 1,465,000 1,470,000 1,475,000 1,480,000 1,485,000 1,490,000 1,495,000 1,500,000 1,505,000 1,510,000 1,515,000 1,520,000

move start < 20 > move end < 20 >

Click on a feature for details. Click or drag in the base position track to zoom in. Click side bars for track options. Drag side bars or labels up or down to reorder tracks. Drag tracks left or right to new position. Press "?" for keyboard shortcuts.

default tracks default order hide all add custom tracks track hubs configure multi-region reverse resize refresh

collapse all Use drop-down controls below and press refresh to alter tracks displayed. Tracks with lots of items will automatically be displayed in more compact modes. expand all

Mapping and Sequencing refresh

Base Position Restr. Enzymes Short Match

hide hide hide

other refresh

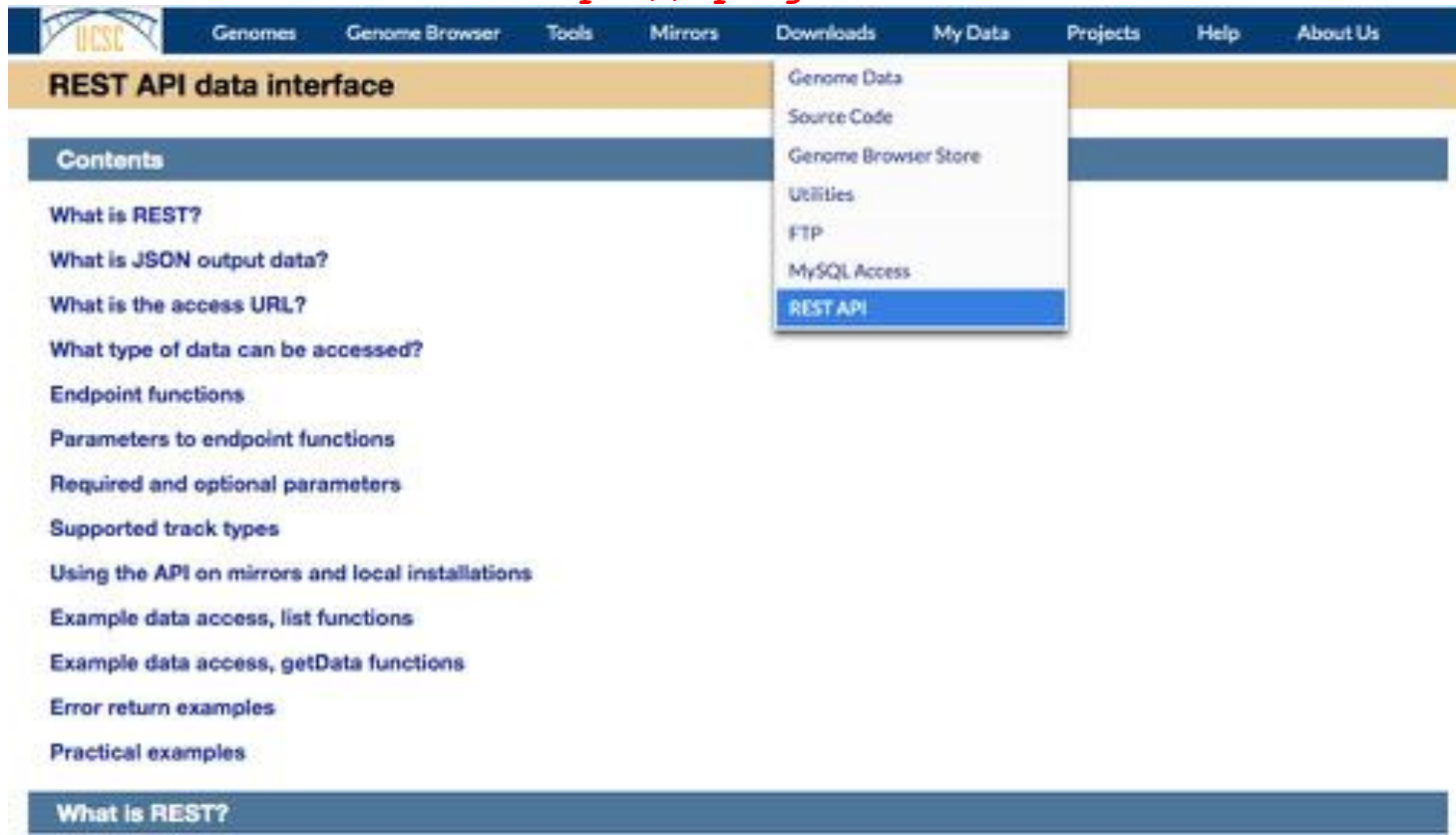
Ensembl genes

hide

https://data.cyverse.org/dav-anon/iplant/home/brianleesoe/AssemblyHub_Ex1/hub.txt

Hosting your data at CyVerse

<https://api.genome.ucsc.edu>



The screenshot shows the UCSC Genome Browser REST API data interface. At the top is a dark blue navigation bar with the UCSC logo and links for Genomes, Genome Browser, Tools, Mirrors, Downloads, My Data, Projects, Help, and About Us. Below this is a light orange header for the REST API data interface. A dropdown menu is open, listing options: Genome Data, Source Code, Genome Browser Store, Utilities, FTP, MySQL Access, and REST API (which is highlighted in blue). The main content area has a dark blue 'Contents' header followed by a list of links: What is REST?, What is JSON output data?, What is the access URL?, What type of data can be accessed?, Endpoint functions, Parameters to endpoint functions, Required and optional parameters, Supported track types, Using the API on mirrors and local installations, Example data access, list functions, Example data access, getData functions, Error return examples, and Practical examples. At the bottom, a dark blue footer contains the text 'What is REST?'.

https://data.cyverse.org/dav-anon/iplant/home/brianleesoe/AssemblyHub_Ex1/hub.txt

Hosting your data at CyVerse

<https://api.genome.ucsc.edu>



Genomes

Genome Browser

Tools

Mirrors

Downloads

My Data

Projects

Help

About Us

REST API data interface

[http://api.genome.ucsc.edu/getData/sequence?genome=araTha1&chrom=chr1
&start=4321&end=4333&hubUrl=https://data.cyverse.org/dav-anon/iplant/
home/brianleesoe/AssemblyHub_Ex1/hub.txt](http://api.genome.ucsc.edu/getData/sequence?genome=araTha1&chrom=chr1&start=4321&end=4333&hubUrl=https://data.cyverse.org/dav-anon/iplant/home/brianleesoe/AssemblyHub_Ex1/hub.txt)

```
downloadTime: "2019-12-18T20:12:18Z"  
downloadTimeStep: 1576599938  
+ hubUrl: "https://data.cyverse.org/dav-anon/iplant/home/brianleesoe/AssemblyHub_Ex1/hub.txt"  
genome: "araTha1"  
chrom: "chr1"  
start: 4321  
end: 4333  
dna: "tatatatGTGGT"
```


Hosting your data at CyVerse

<https://api.genome.ucsc.edu>



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REST API data interface

http://api.genome.ucsc.edu/getData/track?genome=araThal&chrom=chr1&start=4321&end=4333&track=ensGene&hubUrl=https://data.cyverse.org/dav-anon/iplant/home/brianleesoe/AssemblyHub_Ex1/hub.txt

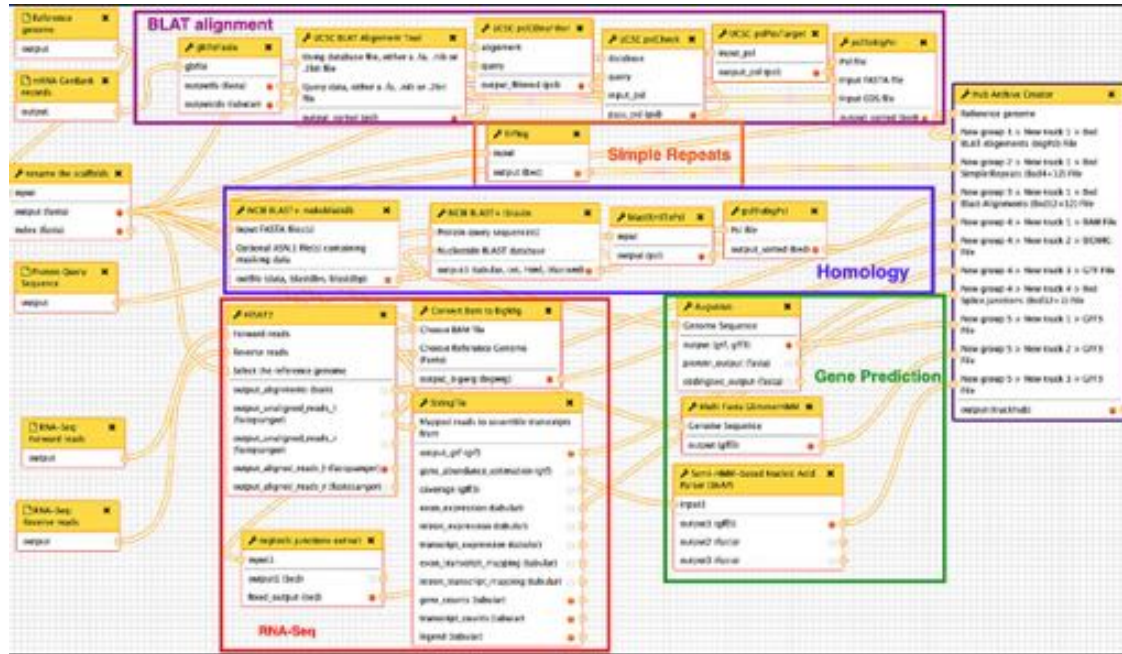
```
hubUrl: "https://data.cyverse.org/dav-anon/iplant/home/brianleesoe/AssemblyHub_Ex1/hub.txt"
genome: "araThal"
chromSize: 30427671
start: 4321
end: 4333
bigDataUrl: "https://data.cyverse.org/dav-anon/iplant/home/brianleesoe/AssemblyHub_Ex1/ensGene.araThal.bed"
trackType: "bigBed 12 ."
```

```
ensGene:
  0:
    chrom: "chr1"
    chromStart: 3630
    chromEnd: 5899
    name: "AT1G01010.1"
    score: 0
    strand: "+"
    thickStart: 3759
    thickEnd: 5630
    reserved: "0"
    blockCount: 6
    blockSizes: "283,281,120,390,153,461,"
    chromStarts: "0,365,655,1075,1543,1800,"
ItemsReturned: 1
```

Assembly Track Hub Creation Resources

G-OnRamp Galaxy workflow turning data like RNA-Seq into Assembly Hubs

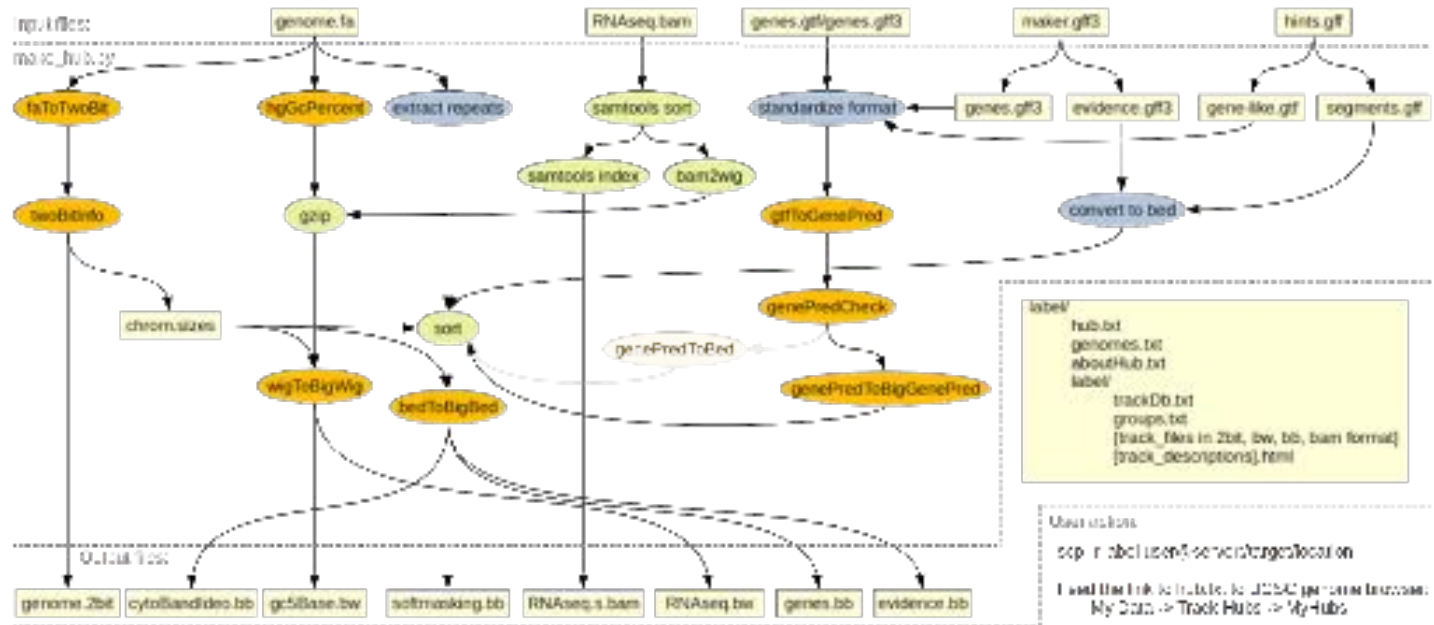
<http://gonramp.wustl.edu/>



Assembly Track Hub Creation Resources

MakeHub Command line tool for the fully automatic generation of assembly hubs

<https://github.com/Gaius-Augustus/MakeHub>





Thank You!



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