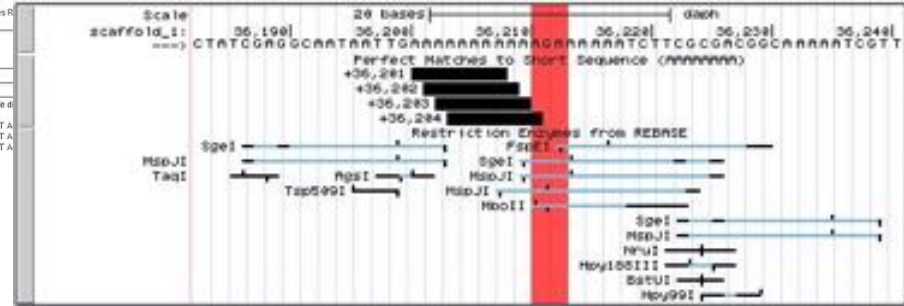
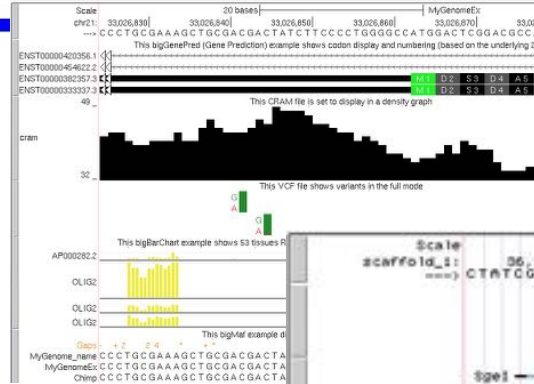


Custom Annotations in the Browser

Custom Tracks (Text/Binary)

Track Hubs

Assembly Hubs



Custom Annotations in the Browser

Custom Tracks (Text/Binary)

Track Hubs

Assembly Hubs

The screenshot shows the 'Add Custom Tracks' interface in the UCSC Genome Browser. At the top, there is a navigation bar with links for Genomes, Genome Browser, Tools, Mirrors, Downloads, My Data, and Help. Below this, the 'Add Custom Tracks' section is highlighted. It features a form with three dropdown menus: 'clade' set to 'Mammal', 'genome' set to 'Human', and 'assembly' set to 'Feb. 2009 (GRCh37)'. Below the form, there is a paragraph of text explaining that users can display their own data as custom annotation tracks. The text lists supported data formats: bigBed, bigChain, bigGenePred, bigMaf, bigPsl, bigWig, BAM, VCF, BED, BED detail, BEDGraph, broadPeak, CRAM, GFF, GTF, MAE, narrowPeak, Personal Genome SNP, PSL, or WIG. It also mentions that data can be provided via a URL or embedded in a track line. Below the text, there are two input options: 'Paste URLs or data:' followed by a large empty text box, and 'Or upload:' followed by a 'Choose File' button and 'no file selected' text. To the right of the text box is a 'Submit' button, and below it is a 'Clear' button. On the right side of the interface, there is a vertical menu with links for 'My Sessions', 'Public Sessions', 'Track Hubs', and 'Custom Tracks'.

Custom Annotations in the Browser

Custom Tracks (Text/Binary)

Track Hubs

Assembly Hubs



track name=ex1 description="Blue example BED3 track" color=0,0,255,

chr21 33030000 33040000

chr21 33050000 33060000

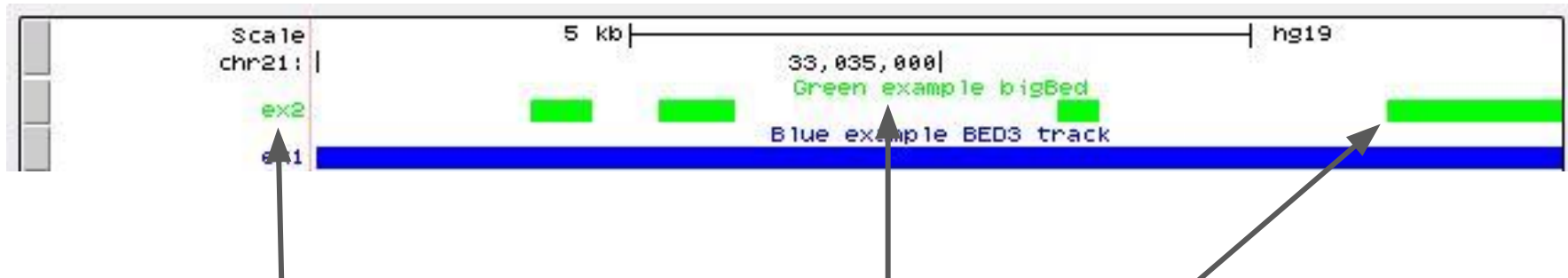
...

Custom Annotations in the Browser

Custom Tracks (Text/Binary)

Track Hubs

Assembly Hubs



track name=ex2 description="Green example bigBed" color=0,255,0, **type=bigBed**
bigDataUrl=http://genome.ucsc.edu/goldenPath/help/examples/bigBedExample.bb

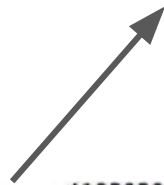
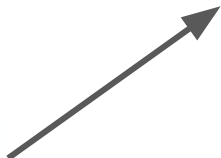
Custom Annotations in the Browser

Custom Tracks (Text/Binary)

Track Hubs

Assembly Hubs

bedToBigBed in.bed chrom.sizes out.bb



```
scaffold_1 3890 3896
scaffold_1 4063 4069
scaffold_1 4236 4242
scaffold_1 4755 4761
scaffold_1 5976 5982
scaffold_1 6022 6028
scaffold_1 6023 6029
scaffold_1 6398 6404
scaffold_1 6399 6405
scaffold_1 26373 26379
scaffold_1 26374 26380
scaffold_1 29767 29773
scaffold_1 29790 29796
scaffold_1 29917 29923
scaffold_1 29918 29924
scaffold_1 30872 30878
scaffold_1 32125 32131
scaffold_1 32218 32224
scaffold_1 32219 32225
scaffold_1 32220 32226
```

```
scaffold_1 4193030
scaffold_3 3777634
scaffold_2 3740169
scaffold_4 3075709
scaffold_5 2511979
scaffold_6 2406117
scaffold_8 2335496
scaffold_7 2324446
scaffold_9 2251199
scaffold_12 2218424
```

The resulting binary file **out.bb** can be hosted at your institution:

bigDataUrl=<http://path.lab.edu/to/out.bb>

Serving files requires byte-range requests, which allows only portions of file to transfer. Some locations, like Dropbox, prevent such requests as people can then watch videos from their servers.

Custom Annotations in the Browser

Custom Tracks (Text/Binary)

Track Hubs

Assembly Hubs

bedToBigBed and other standalone command-line utilities are downloadable tools available on Linux and UNIX platforms.

Genomes Genome Browser Tools Mirrors Downloads My Data

Add Custom Tracks

clade Mammal genome Human assembly

Display your own data as custom annotation tracks in the browser. [bigBed](#), [bigChain](#), [bigGenePred](#), [bigMaf](#), [bigPsl](#), [bigWig](#), [BAM](#), [VCF](#), [bedGraph](#), [broadPeak](#), [CRAM](#), [GFF](#), [GTF](#), [MAF](#), [narrowPeak](#), [Per Wig](#) formats. To configure the display, set [track](#) and [browser](#) line a [User's Guide](#). Data in the bigBed, bigWig, bigGenePred, BAM and VCF formats can be provided via only a URL or embedded in a track line in the box below. Examples are [here](#).

Paste URLs or data: Or upload: No file chosen

- Genome Data
- Source Code
- Genome Browser Store
- Utilities
- FTP
- MySQL Access

Custom Annotations in the Browser

Custom Tracks (Text/Binary)

Track Hubs

Assembly Hubs

Track hubs are web-accessible directories of genomic data.

<http://path.lab.edu/to/>

hubDirectory

|

|_hub.txt

|_genomes.txt

|_hg19

|_trackDb.txt

hub.txt can be as short as four lines, it points to genomes.txt

genomes.txt can be as short as two lines and points to trackDb.txt

The trackDb.txt file is typically much larger and shares how to display tracks and where to find data files.

bigDataUrl=<http://path.lab.edu/to/file1.bb>

bigDataUrl=<http://path.lab.edu/to/file2.bb>

bigDataUrl=<http://path.lab.edu/to/file3.bb>

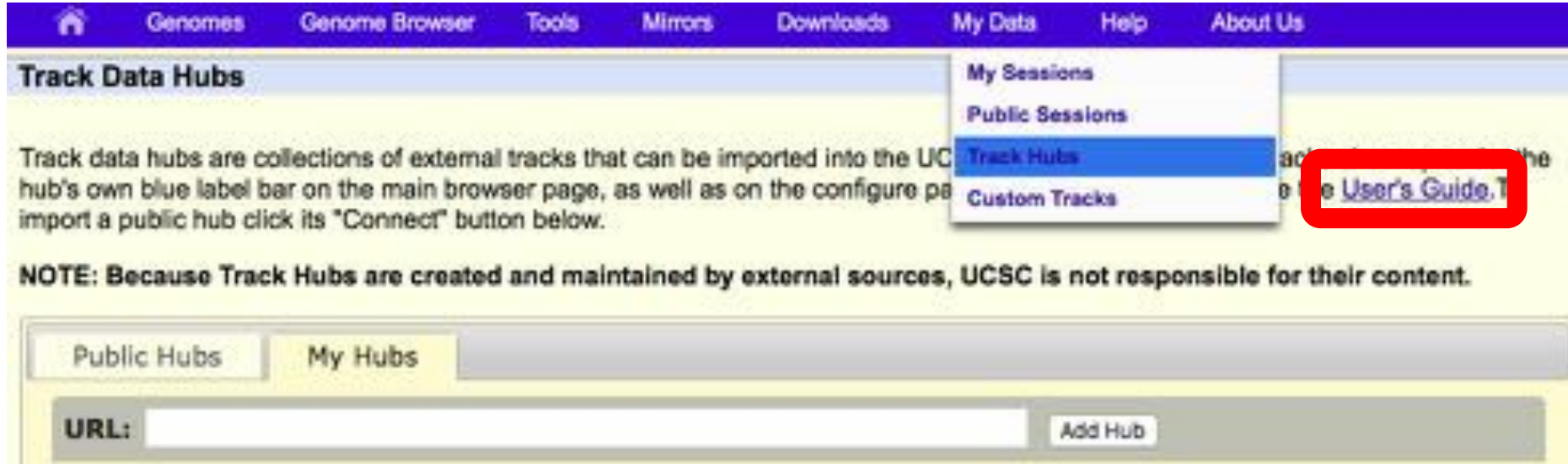
...

Custom Annotations in the Browser

Custom Tracks (Text/Binary)

Track Hubs

Assembly Hubs



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, showing options: My Sessions, Public Sessions, Track Hubs (highlighted in blue), and Custom Tracks. To the right of the dropdown, a link labeled 'User's Guide.1' is circled in red. Below the dropdown, there is a text block explaining that track data hubs are collections of external tracks that can be imported into the UCSC Genome Browser. A note states: 'NOTE: Because Track Hubs are created and maintained by external sources, UCSC is not responsible for their content.' At the bottom, there are two tabs: 'Public Hubs' and 'My Hubs'. Below the tabs is a form with a 'URL:' label, an input field, and an 'Add Hub' button.

`http://your/path/to/remote/files/hub.txt`

Custom Annotations in the Browser

Custom Tracks (Text/Binary)

Track Hubs

Assembly Hubs

`faToTwoBit` and other standalone command-line utilities are available under the Downloads → Utilities menu




A BAM file (.bam) is the binary version of a SAM file.

```
samtools view -S -b sample.sam > sample.bam
```



```
PRESLEY_0030:6:5:16900:1343200/2 65 chr1 10047 254 67995 + 0 CCTAACCCCTAACCCCTAACCC
faJhfafeJa_cfaddfcaffw_efabfcefcf*cace^cvo/aakajYZZZ\K^VZTa00000000
PRESLEY_0030:6:26:17171949000/2 65 chr1 10053 254 61ML55 + 0 CCTAACCCCTAACCCCTAACCC
f_tceeffhhfaecffoffffcfctffccff|cb^bbf0|ob^w^*_*_*_Y^0000000000000000
PRESLEY_0030:5:69:17883:1556700/2 65 chr1 10060 255 2573ML5 + 0 AACTAACCCCTAACCCCTAA
hgfgghhhhHhhhhhhhhhgghhhhhhhghhhhhhhHfhghdHhchghfchfhadhhhea|_cfc|
PRESLEY_0030:5:75:7248:1501400/2 65 chr1 10060 255 2573ML5 + 0 AACTAACCCCTAACCCCTAA
hfhfgghhgthhhffhghhgghcgthhhfhchfhcgcedfaff_hdfeehaacc[RcMhh]egbd|bb
PRESLEY_0030:5:10:18596:330500/2 65 chr1 10060 255 2573ML5 + 0 AACTAACCCCTAACCCCTAA
hhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhgghhhhhhhahhghd_dhgcgded^a^
PRESLEY_0030:7:79:7804:1526200/2 65 chr1 10060 255 2573ML5 + 0 AACTAACCCCTAACCCCTAA
hhhhhhghfghghghghthhhhhhhhhhhh_dhhffcchhdadhfhf[hhhhghhhc]cRffcccheglgR
PRESLEY_0030:7:91:10770:1928100/2 65 chr1 10060 255 2572ML5 + 0 AACTAACCCCTAACCCCTAA
NghhhhhhhhhhhHhhhhfghhhhhhhhhchhhghdhhhhghhhghcghhhhehfhad|cff_fbe^'BB
PRESLEY_0030:7:10:18643:2126700/2 65 chr1 10060 255 2573ML5 + 0 AACTAACCCCTAACCCCTAA
Hhfhhhhhghghhhghfghhhfgghhhffaghhhhchcdcafaffffaffiff|cccf_deegepacacaR
|br|on|ec|g|w|d|e| -15 head -n 40 tempdelete
PRESLEY_0030:7:82:16832:942100/2 73 chr1 10042 255 68985 + 0 CTAACCCCTAACCCCTAACCC
hhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhghhhhhghhgfhghhchghfghhgcc0LCPHWjYa
PRESLEY_0030:6:7:18371:1669000/2 65 chr1 10043 254 71ML55 + 0 TAACCCCTAACCCCTAACCC
Yffhghghghghghghhghhg_fffchfhghffffhhfhchfffff|accocff|fb|e|eb|Tj|_ "y0eY"
PRESLEY_0030:6:5:16900:1343200/2 65 chr1 10047 254 67995 + 0 CCTAACCCCTAACCCCTAACCC
```

Sequence Alignment Map (SAM) text file



The resulting binary file **sample.bam** (with an additional accompanied index file *sample.bam.bai*) can have data more easily extracted and can also be viewed in Genome Browsers.

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

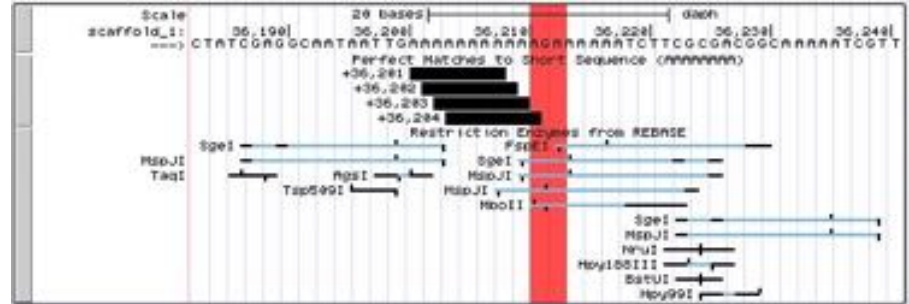


```
>scaffold_1
GTTGTAAATACTCTATTCTACAATAAAACCAAAGATAACTCTTTATCAG
TCATAGGTTGAATTGGCGTTGAAGTAAACAAAAATACTGCTCAAAAGG
...
>scaffold_2
AGTTATGACAAACTATAAAAAAGTCGGTAGAGACAAAAGCGAAAAGGATCT
TCGTTTCGTGGACGAAGCGACCAAACTGAGCACAAGATAAATCCCGAATA
...
>scaffold_3
CATAAATTCATAAATCAATTCATGAAGAATAATTTTAGAAAAATGGTTCA
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.

Viewing Your Genome at UCSC

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



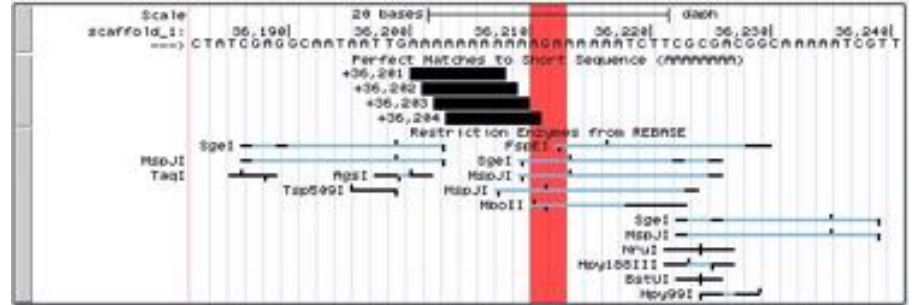
bigDataUrl *http://location_of/file.bam*



Viewing Your Genome at UCSC

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

Browser accesses the 2bit genome to
create window of ATCGs



bigDataUrl http://location_of/file.bam

Browser displays a window of bam
alignments upon the 2bit genome pulled
from the bigDataUrl location.

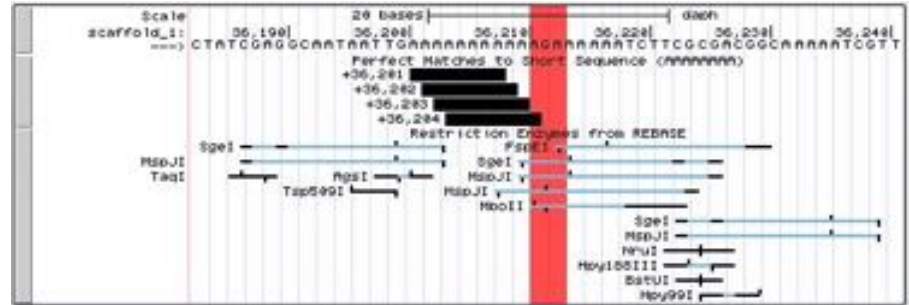
Viewing Your Genome at UCSC

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 Your Genome 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

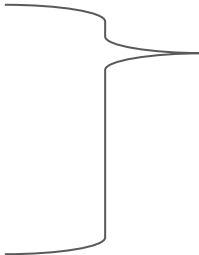


hub.txt

The **hub.txt** file defines how to show and label data (**shortLabel**, **longLabel**). The file has a 2nd stanza to specify the **genome** to display data upon and then multiple **track** stanzas (3rd, 4th, 5th, ect..) for annotations.

Viewing Your Genome 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
(hub no longer requires many
directories)

```
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 Your Genome 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 genome stanza shares where to find the 2bit (and information about the your genome)

The **twoBitPath** must point to an online location of the binary-indexed data that can accept byte-range requests.

Viewing Your Genome 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

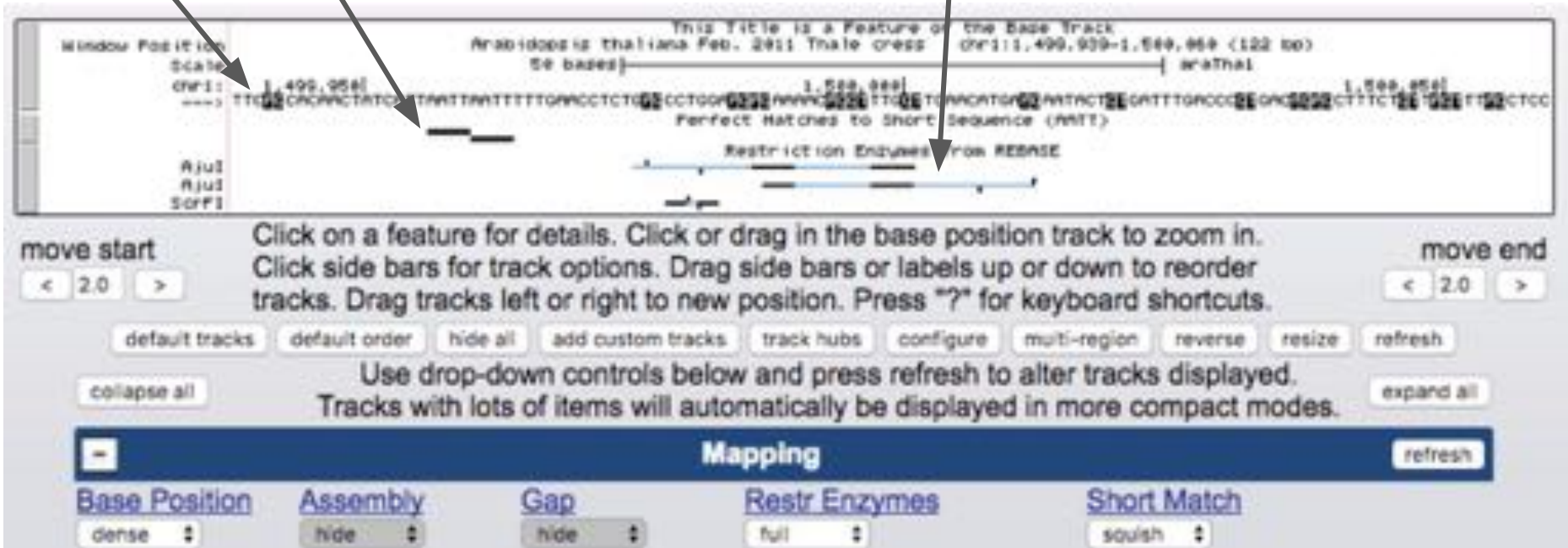
track cytoBandIdeo
longLabel Chromosome ideogram with cytogenetic bands
shortLabel cytoBandIdeo
[bigDataUrl cytoBandIdeo.bigBed](#)
type bigBed

The multiple track stanzas share where to find the annotation tracks and their data type (bam, bigBed...)

The **bigDataUrl** must point to an online location of the binary-indexed data that can accept byte-range requests.

Viewing Your Genome at UCSC

A Base track, Short DNA Match track and Restriction Enzyme track come with the 2bit



Additional Track Types

multiple types

others types:

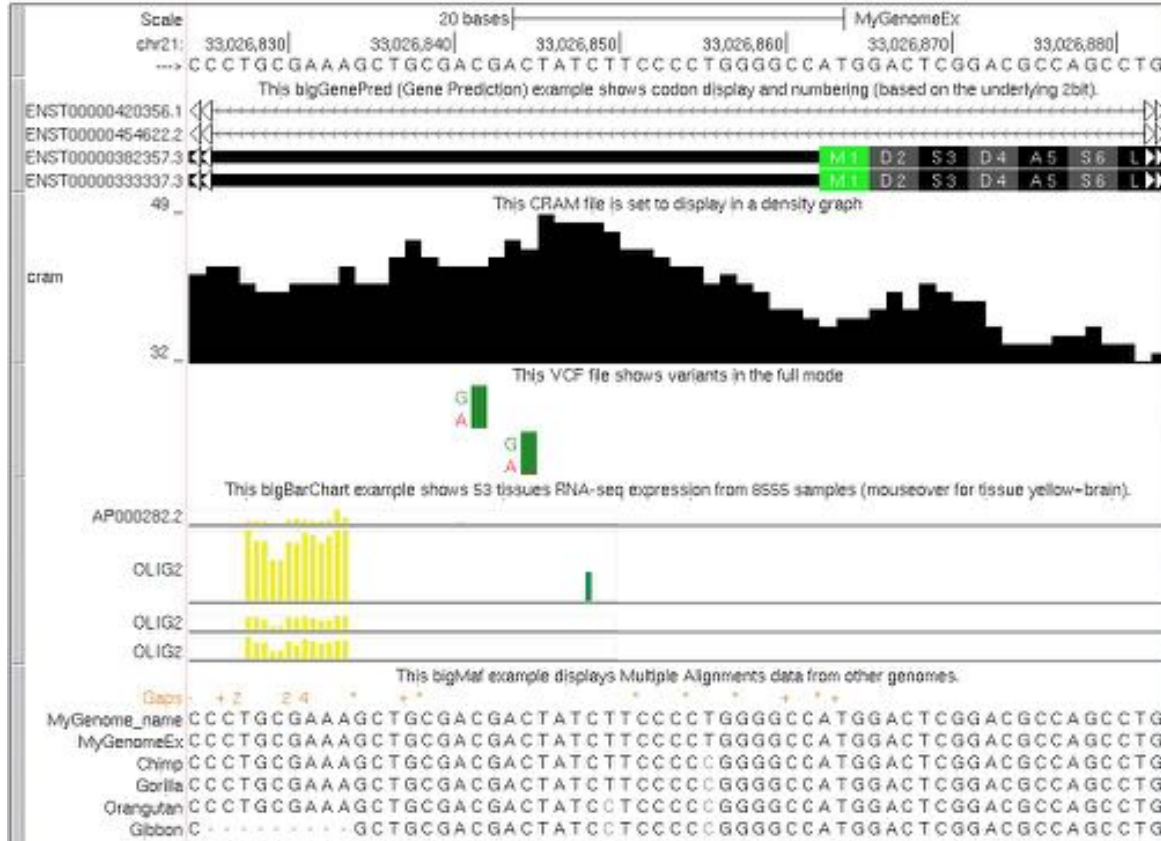
bigGenePred:

CRAM:

VCF:

bigBarChart:

bigMaf:



BAM,

bigPsl,

bigChain,

bigMaf,

bigNarrowPeak,

bigWig,

bigBed...

An example hub hosted at CyVerse



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[Products](#) ▾

[Learning](#)

[Events](#)

[News](#)

[Launch](#) ▾

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

Sign-up for a
CyVerse
Account

A screenshot of the CyVerse "Sign Up" form. The form is titled "Sign Up" and features the CyVerse logo at the top. Below the title, there are three steps: "1 Account", "2 Institution", and "3 Demographics". The "Account" step is active. The form contains several input fields: "First Name" with the value "Brian", "Last Name" with the value "Lee", "Username" with the value "brianleesoe" (underlined and followed by a green checkmark), and "Email" with the value "brianlee@soe.ucsc.edu" (followed by a green checkmark). A blue "NEXT" button is located at the bottom right of the form.

Hosting your data at CyVerse

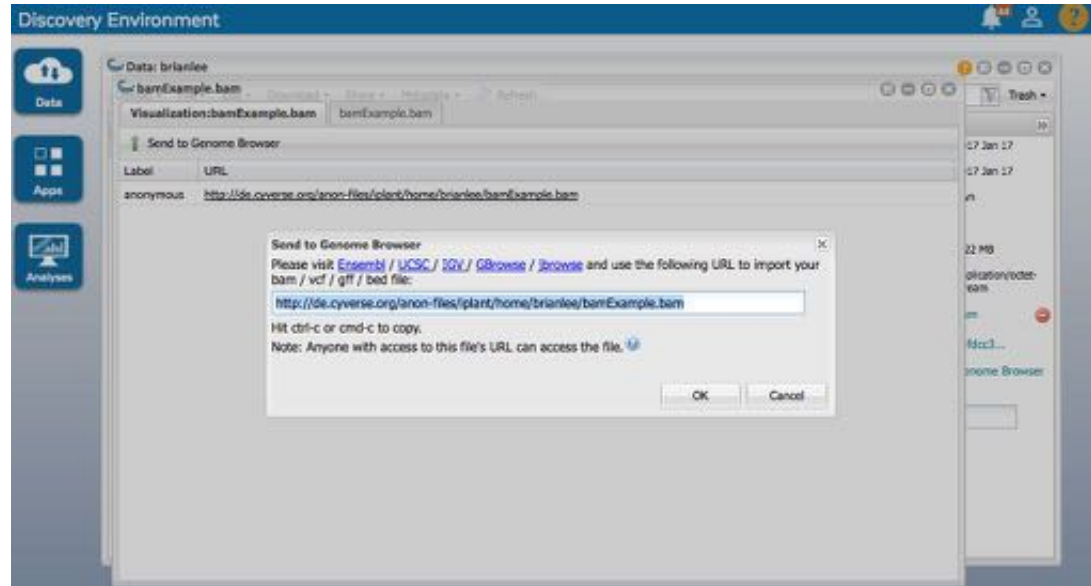


Discovery Environment

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: 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>

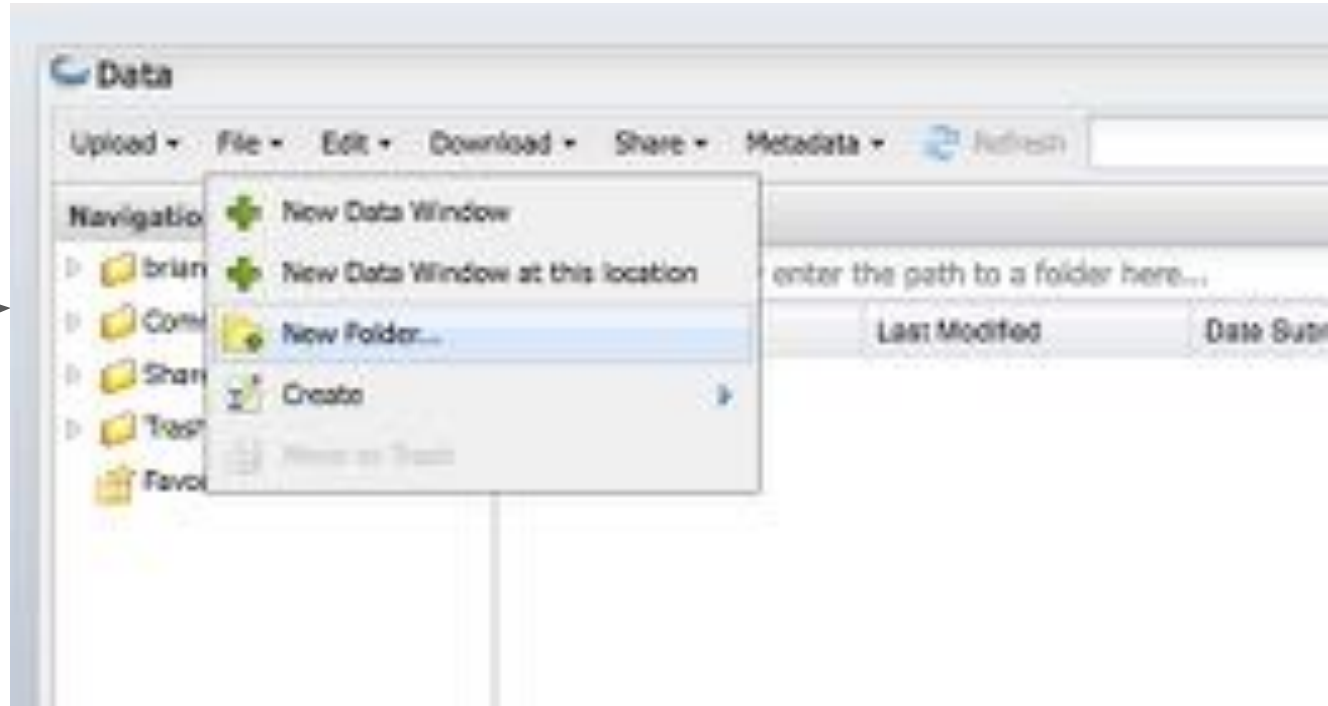
Hit ctrl-c or cmd-c to copy.

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

OK Cancel

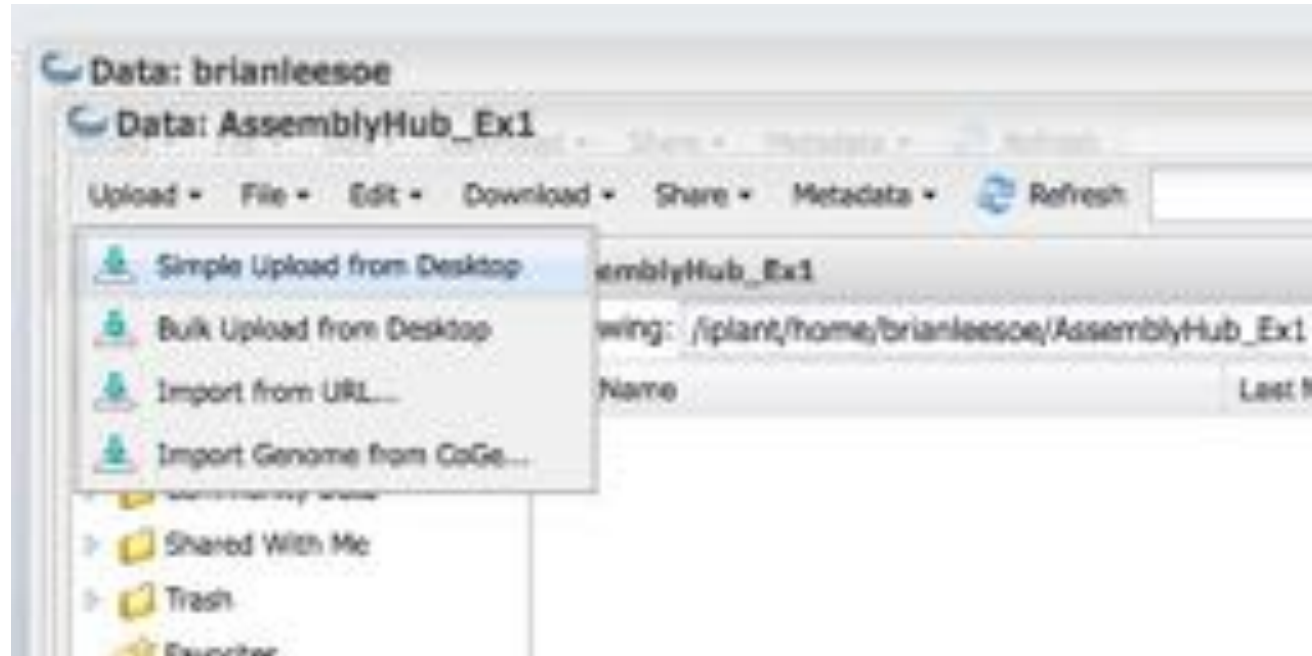
Hosting your data at CyVerse

Make a New Folder for Your Genome Data



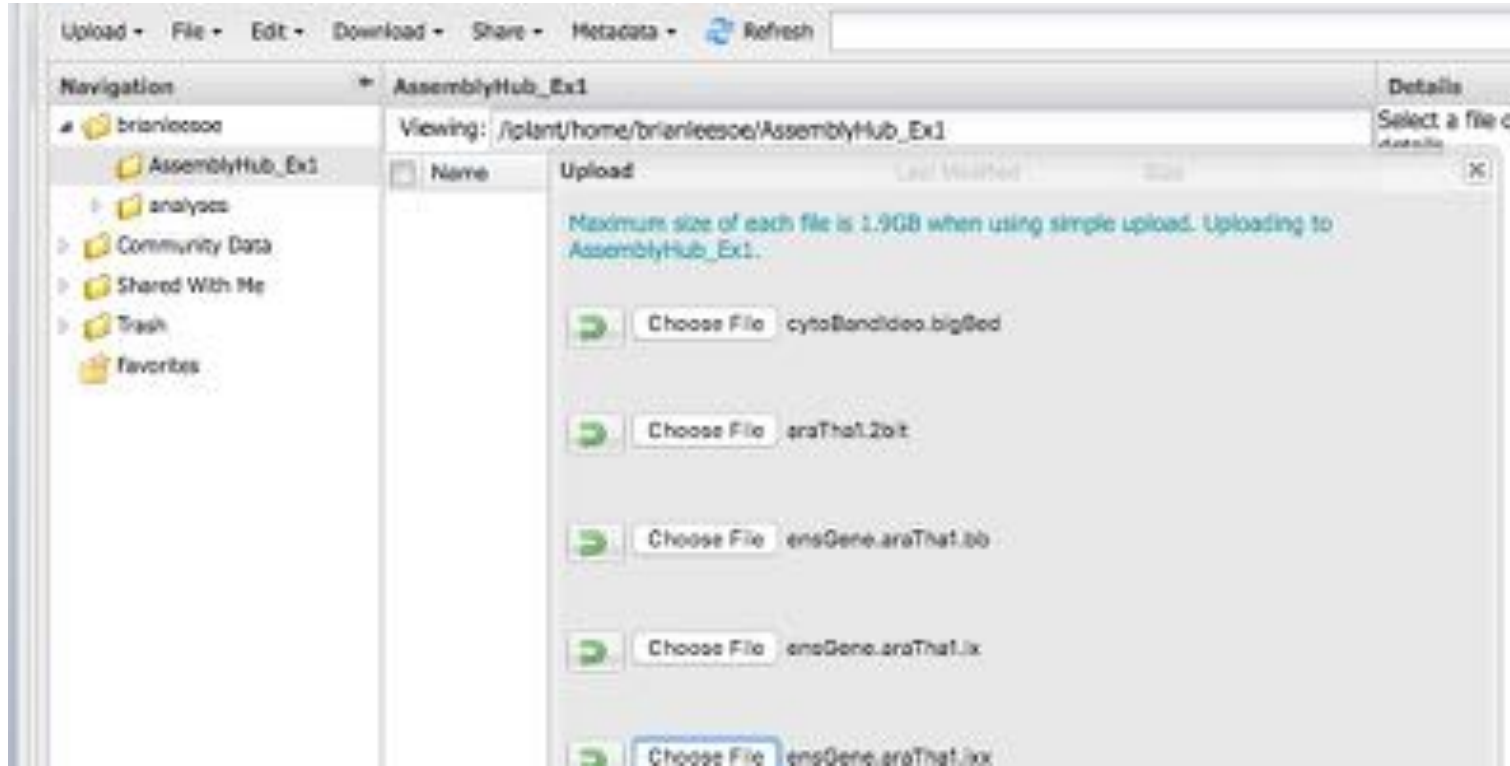
Hosting your data at CyVerse

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)

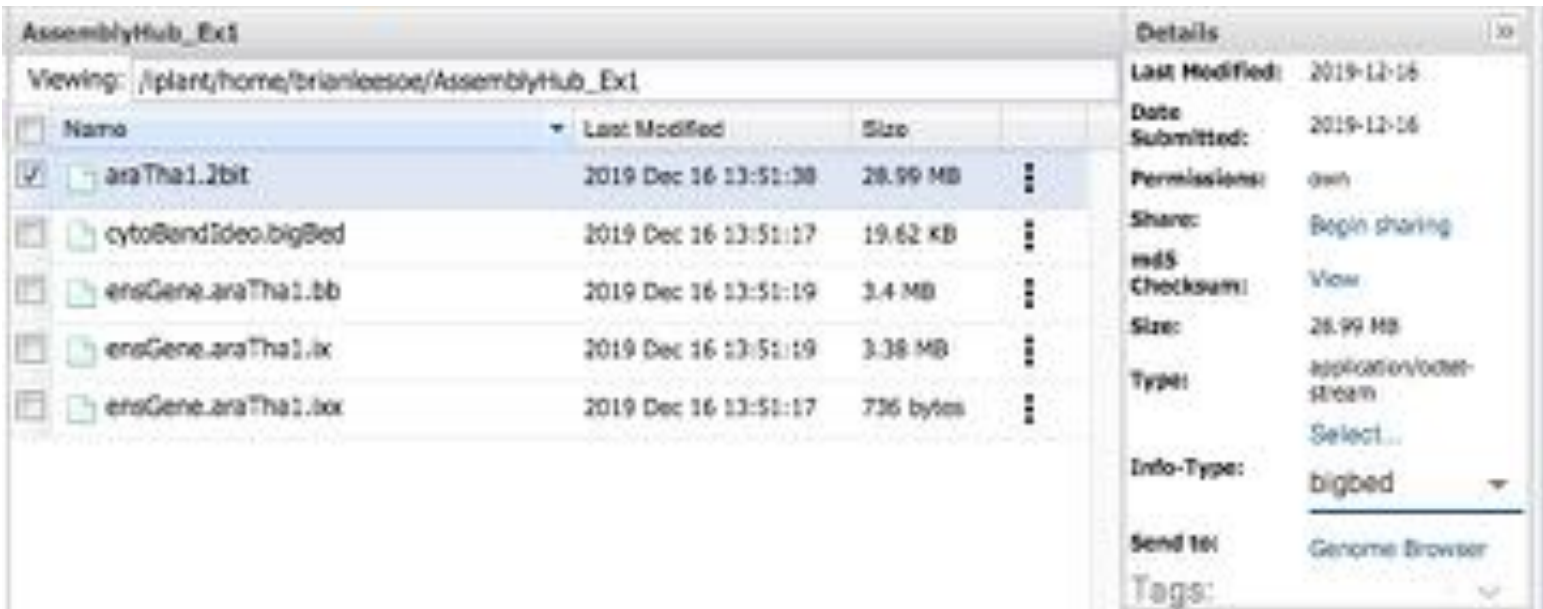


The screenshot displays the CyVerse web interface for a user named 'brianleesoe'. The main area shows a file upload interface for the 'AssemblyHub_Ex1' hub. The interface includes a navigation pane on the left with folders like 'analyses', 'Community Data', 'Shared With Me', 'Trash', and 'favorites'. The main content area shows a table with columns for 'Name' and 'Upload'. Below the table, there is a message: 'Maximum size of each file is 1.9GB when using simple upload. Uploading to AssemblyHub_Ex1.' and several 'Choose File' buttons for files named 'cyto@brianleesoe.bigBed', 'araThat1.2bit', 'ensGene.araThat.bb', 'ensGene.araThat.ix', and 'ensGene.araThat.jx'. The 'Choose File' button for 'ensGene.araThat.jx' is highlighted with a blue border.

Name	Upload
	Maximum size of each file is 1.9GB when using simple upload. Uploading to AssemblyHub_Ex1.
	<input type="button" value="Choose File"/> cyto@brianleesoe.bigBed
	<input type="button" value="Choose File"/> araThat1.2bit
	<input type="button" value="Choose File"/> ensGene.araThat.bb
	<input type="button" value="Choose File"/> ensGene.araThat.ix
	<input type="button" value="Choose File"/> ensGene.araThat.jx

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 and sharing options.

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 for 'araTha1.2bit':

- Last Modified: 2019-12-16
- Date Submitted: 2019-12-16
- Permissions: own
- Share: Begin sharing
- mDS
- 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

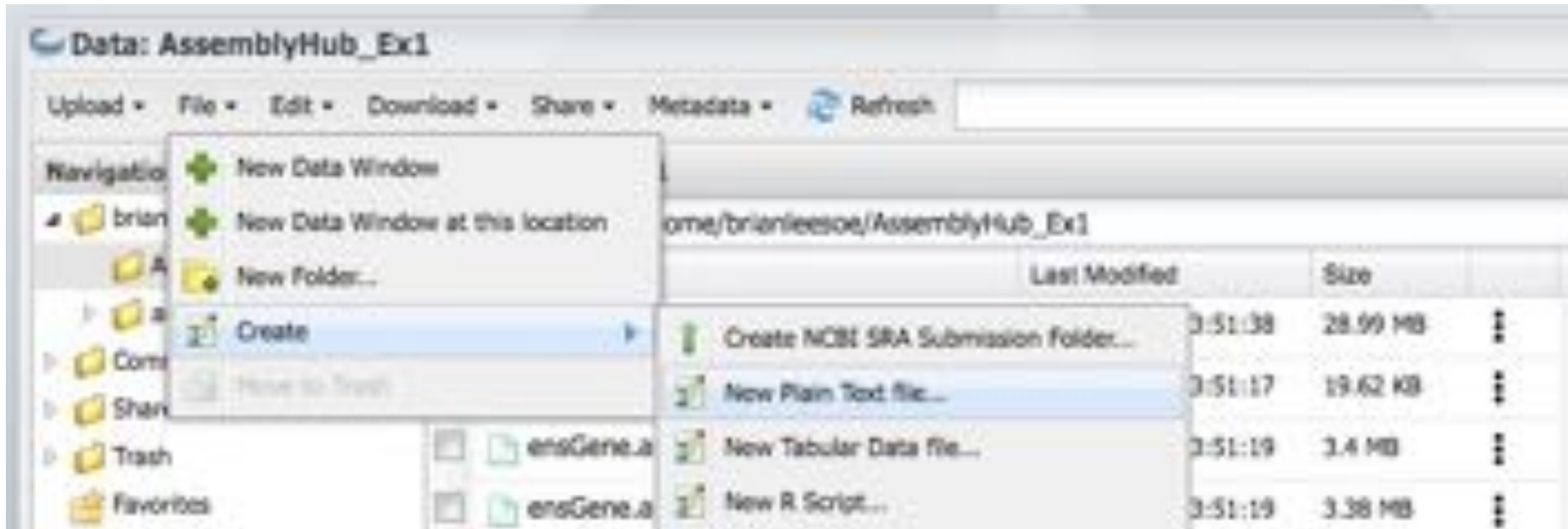
Creating a Link that Accepts Byte-Ranges: “Send to Genome Browser”



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

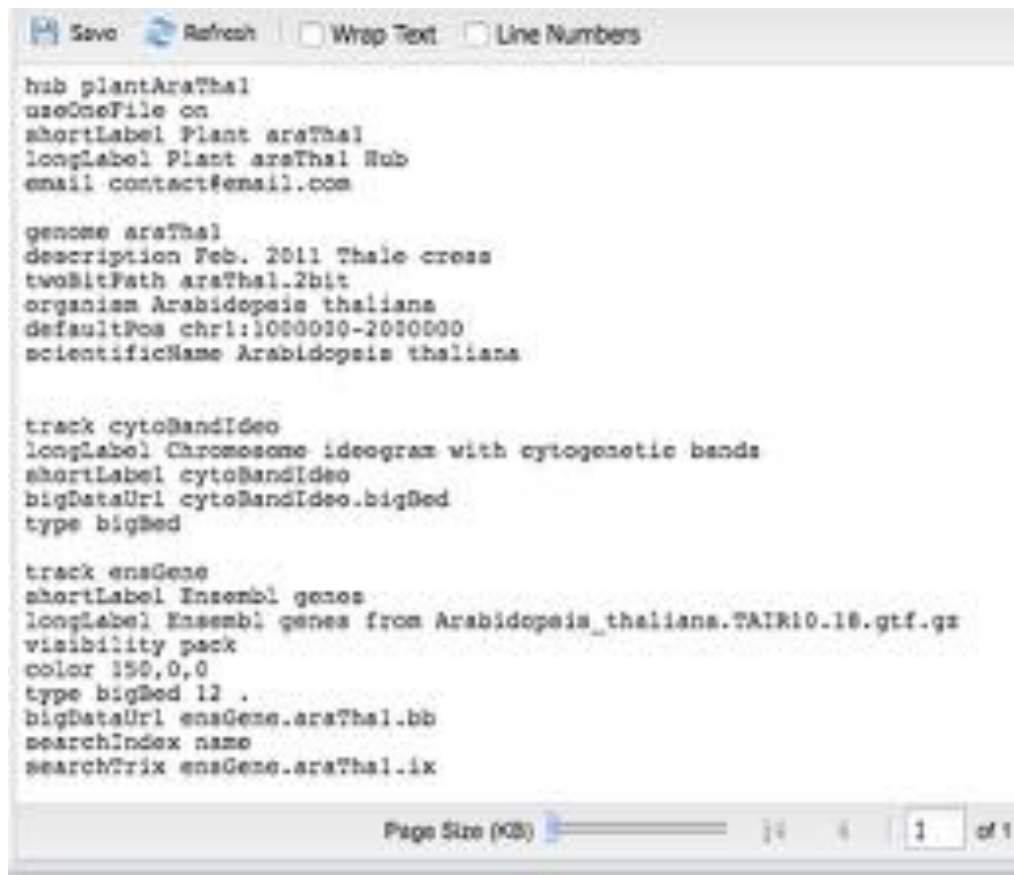
Hosting your data at CyVerse

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

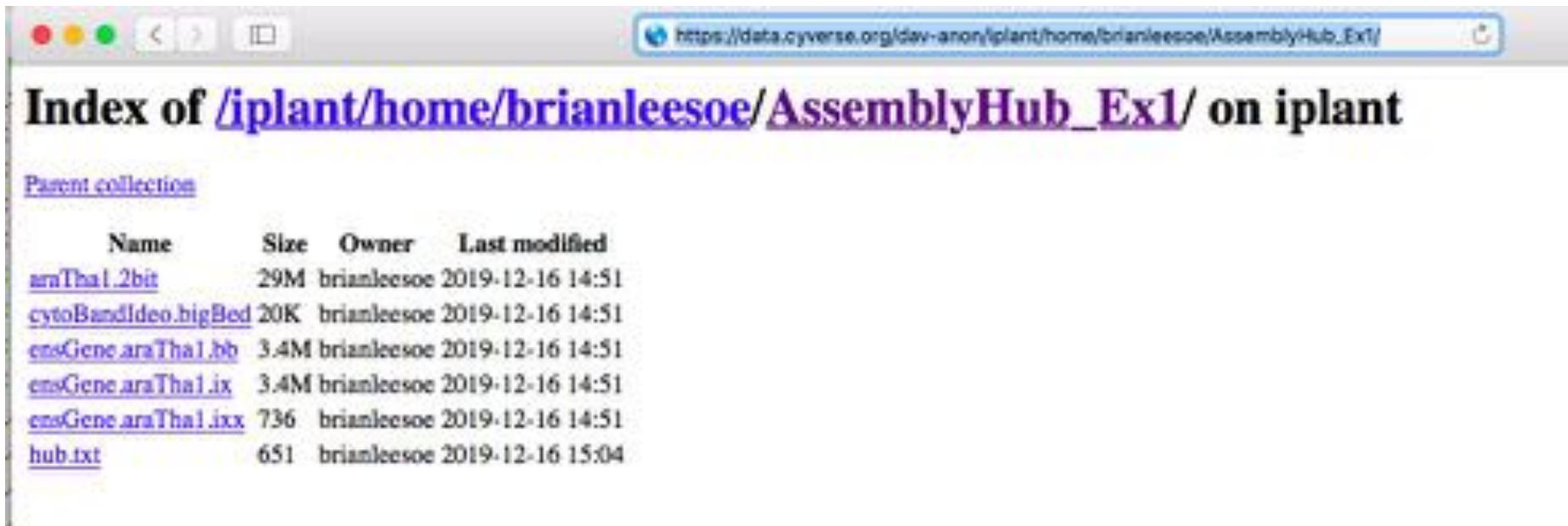
genome araThal
description Feb. 2011 Thale cross
twoBitPath araThal.2bit
organism Arabidopsis thaliana
defaultPos chr1:1000000-2000000
scientificName Arabidopsis thaliana

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 peak
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



The screenshot shows a web browser window with the address bar containing the URL https://data.cyverse.org/dav-anon/iplant/home/brianleesoe/AssemblyHub_Ex1/. The main content of the page is the title "Index of [/iplant/home/brianleesoe/AssemblyHub_Ex1/](#) on iplant" and a link to the "Parent collection". Below this is a table listing files with columns for Name, Size, Owner, and Last modified.

Name	Size	Owner	Last modified
araThal.2bit	29M	brianleesoe	2019-12-16 14:51
cytoBandIdeo.bigBed	20K	brianleesoe	2019-12-16 14:51
ensGene.araThal.bb	3.4M	brianleesoe	2019-12-16 14:51
ensGene.araThal.ix	3.4M	brianleesoe	2019-12-16 14:51
ensGene.araThal.ixx	736	brianleesoe	2019-12-16 14:51
hub.txt	651	brianleesoe	2019-12-16 15:04

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 hub'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.

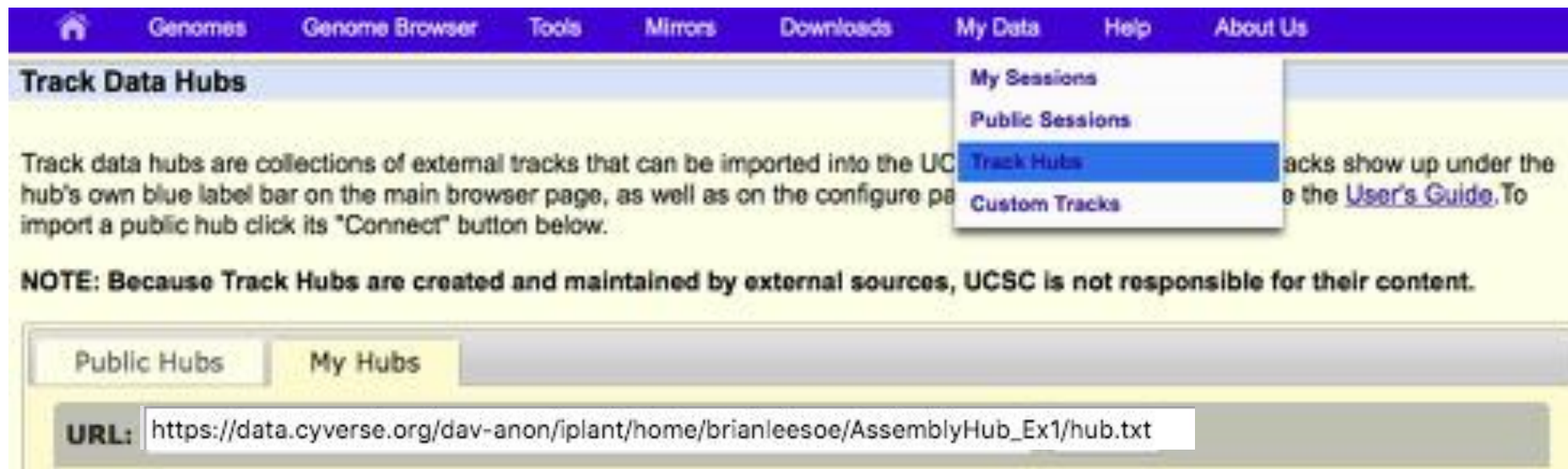
NOTE: Because Track Hubs are created and maintained by external sources, UCSC is not responsible for their content.

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 hubs show up under the user's own blue label bar on the main browser page and on the configuration page. It also provides a link to the 'User's Guide To' (partially visible). A note states: 'NOTE: Because Track Hubs are created and maintained by external sources, UCSC is not responsible for their content.' At the bottom, there are two tabs: 'Public Hubs' and 'My Hubs'. Below the tabs is a text input field with the URL: `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. 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.

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Public Hubs My Hubs

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

Hosting your data at CyVerse

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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

Ensembl genes from Arabidopsis thaliana Feb. 2011 Thale cress Assembly (araTha1)

move start < 2.0 > move end < 2.0 >

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

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.

collapse all expand all

Mapping and Sequencing

refresh

Base Position Restr. Enzymes Short Match

derose ↓ hide ↓ hide ↓

other

refresh

Ensembl genes

pack ↓

Viewing Your Genome at UCSC

Host all data at Remotely

Binary indexed files:

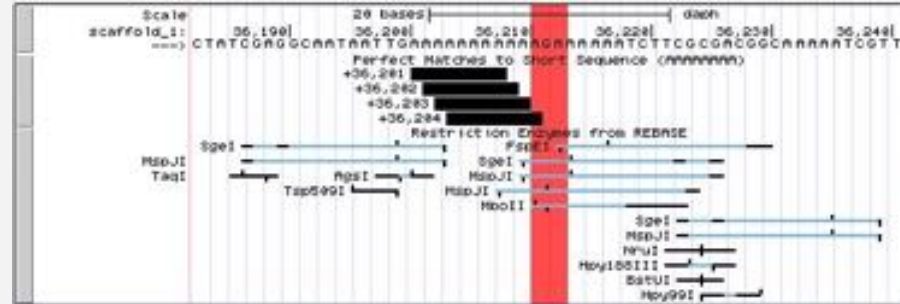
twoBitPath,
bigDataUrl

Text files: hub.txt

```
>scaffold_1
GTTGTAATACTCTATTCTACAATAAAACCAA
TCATAGGTTGAATTGGCGTTGAAGTAAAAACAAA
...
>scaffold_2
AGTTATGACAAACTATAAAAAAGTCGGTAGAGACAAAAG
TCGTTTCGTGGACGAAGCGACCAAACTGAGCACAAAGAT
...
>scaffold_3
CATAAATTCATAAATCAATTCATGAAGAATAATT
TAGAAAATTTCCAGGAAGTTTGAAGTTGCTAT
...
```

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

Visualize at UCSC



API extraction of UCSC Data

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

The image shows a screenshot of the UCSC REST API data interface website. At the top, there is a dark blue navigation bar with the UCSC logo on the left and several menu items: Genomes, Genome Browser, Tools, Mirrors, Downloads, My Data, Projects, Help, and About Us. Below the navigation bar is a light orange header section with the text "REST API data interface". A dropdown menu is open, showing a list of links: Genome Data, Source Code, Genome Browser Store, Utilities, FTP, MySQL Access, and REST API (which is highlighted in blue). To the left of the dropdown menu is a dark blue section titled "Contents" with 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 of the page, there is a dark blue footer section with the text "What is REST?".

API extraction of UCSC Data

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



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REST API data interface

<https://api.genome.ucsc.edu/getData/sequence?genome=hg38;chrom=chr1;start=470000;end=470111>

downloadTime: "2020:01:13T21:55:42Z"

downloadTimeStamp: 1578952542

genome: "hg38"

chrom: "chr1"

start: 470000

end: 470111

▼ dna: "tgaagaactgaggctcctcagtcctacaaatggagagaaactgaatctagctaagaacctgtgagtgagctgggaagaagatccaccctcagttgaaatttaagatgacAT"

API extraction of UCSC Data

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



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<https://api.genome.ucsc.edu/getData/track?genome=hg38;track=geneHancerInteractionsDoubleElite;chrom=chr1;start=470000;end=5000000>

```
genome: "hg38"
trackType: "bigInteract"
track: "geneHancerInteractionsDoubleElite"
chrom: "chr1"
chromSize: 248956422
bigDataUrl: "/gdb/hg38/geneHancer/geneHancerInteractionsDoubleElite.v2.hg38.tb"
start: 470000
end: 5000000
geneHancerInteractionsDoubleElite:
  0:
    chrom: "chr1"
    chromStart: 522927
    chromEnd: 828801
    name: "ENSG00000237894/GH1.300026"
    score: 16
    value: "35.59"
    geneAssociationMethods: "eQTLs,TF_co-expression"
    color: "77,198,238"
    geneHancerChrom: "chr1"
    geneHancerStart: 826199
    geneHancerEnd: 828801
    geneHancerIdentifier: "GH1.300026"
    geneHancerStrand: "-"
    geneChrom: "chr1"
    geneStart: 522927
    geneEnd: 522928
    geneName: "ENSG00000237894"
    geneStrand: "-"
```


API extraction of UCSC Data

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



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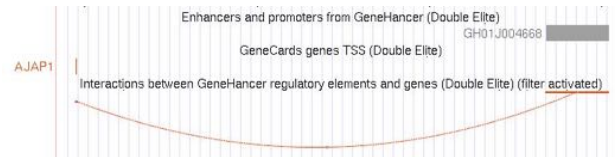
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REST API data interface

<https://api.genome.ucsc.edu/getData/track?genome=hg38;track=geneHancerInteractionsDoubleElite;chrom=chr1;start=470000;end=500000>

```
name: "AJAP1/GH01J004668"
score: 2
value: "0.87"
geneAssociationMethods: "eRNA_co-expression,Distance"
color: "217,83,25"
geneHancerChrom: "chr1"
geneHancerStart: 4668332
geneHancerEnd: 4678223
geneHancerIdentifier: "GH01J004668"
geneHancerStrand: "-"
geneChrom: "chr1"
geneStart: 4654731
geneEnd: 4654732
geneName: "AJAP1"
geneStrand: "+"
itemsReturned: 205
```



API extraction of UCSC Data

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



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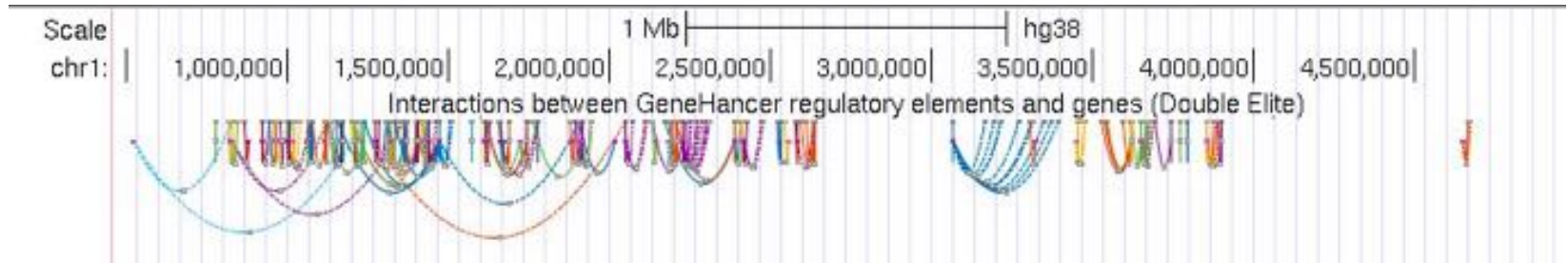
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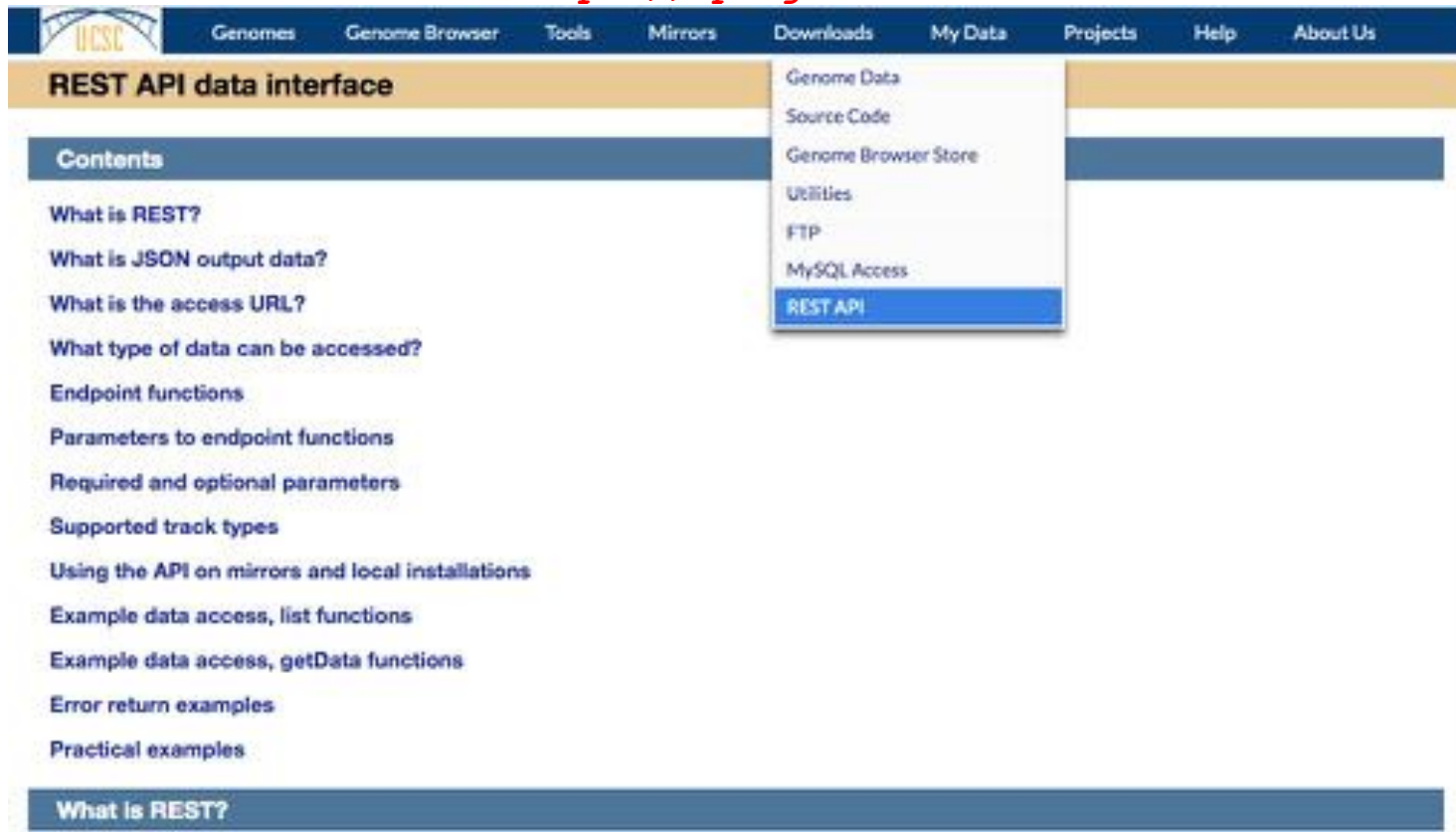
REST API data interface

[https://genome.ucsc.edu/cgi-bin/hgTracks?db=hg38&position=chr1:470000-500000
&geneHancer=full](https://genome.ucsc.edu/cgi-bin/hgTracks?db=hg38&position=chr1:470000-500000&geneHancer=full)



API extraction of Hub Data

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



The screenshot shows the UCSC Genome Browser website with a navigation menu at the top. The 'REST API data interface' section is highlighted in orange. A dropdown menu is open, showing options: Genome Data, Source Code, Genome Browser Store, Utilities, FTP, MySQL Access, and REST API (which is highlighted in blue). The main content area lists various topics under 'Contents', including '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'. A blue bar at the bottom contains the text 'What is REST?'.

UCSC
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REST API data interface

- Genome Data
- Source Code
- Genome Browser Store
- Utilities
- FTP
- MySQL Access
- REST API**

Contents

- 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
- Practical examples

What is REST?

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

API extraction of Hub Data

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



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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"
```

API extraction of Hub Data

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



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[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)

chrom:	"chr3"
start:	4321
end:	4333
dna:	"TATATATGTT"

API extraction of Hub Data

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



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http://api.genome.ucsc.edu/getData/track?genome=araTha1&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: "araTha1"
chromSize: 38427671
start: 4321
end: 4333
bigDataUrl: "https://data.cyverse.org/dav-anon/iplant/home/brianleesoe/AssemblyHub_Ex1/ensGene.araTha1.db"
trackType: "bigBed 12 ."
```

```
ensGene:
  0:
    chrom: "chr1"
    chromStart: 3638
    chromEnd: 5899
    name: "AT1G01950.1"
    score: 0
    strand: "+"
    thickStart: 3759
    thickEnd: 5638
    reserved: ""
    blockCount: 6
    blockSizes: "283,281,128,398,153,461,"
    chromStarts: "8,365,855,1075,1543,1888,"
ItemsReturned: 1
```

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

API extraction of Hub Data

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



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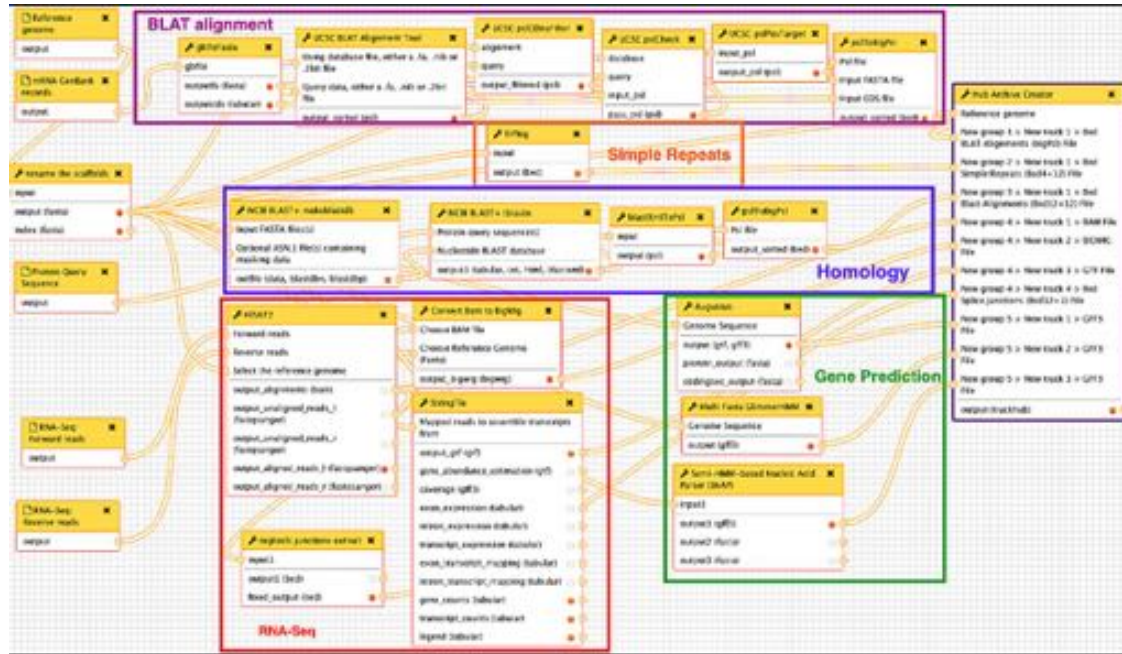
http://api.genome.ucsc.edu/getData/track?genome=araThal&chrom=chr1&start=4321&end=4333&track=ensGene&hubUrl=https://data.cyverse.org/dav-anon/iplant/home/brianleesoe/AssemblyHub_Ex1/hub.txt

```
chrom: "chr1"
chromStart: 3634
chromEnd: 5899
name: "AT1G01010.1"
score: 0
strand: "+"
thickStart: 3759
thickEnd: 5634
reserved: ""
blockCount: 6
blockSizes: "263,203,120,390,153,461,"
chromStarts: "0,365,855,1075,1543,1000,"
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 automatically generating assembly hubs

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

