Web Load Wireframes





Help



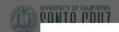
Host address: https://local.xena.ucsc.edu:7223

A Local Xena Hub is an application on your computer for loading and storing data.

We support most types of genomic and/or phenotypic/clinical/annotation data. This data can be your own or from another source, like GEO or a publication.

Data on a Local Xena Hub can only be viewed or accessed by the same computer on which it is running.

0 Cohorts, 0 Datasets



# Launching ...

If you see a browser dialog, click 'Open localxenahub.us'

If this is your first time, download and run a Local Xena Hub

A Local Xena Hub is an application on your computer for loading and storing data.



CLOSE



#### Local Xena Hub

Load Data

Help



Host address: https://local.xena.ucsc.edu:7223

A Local Xena Hub is an application on your computer for loading and storing data.

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### 7 Cohorts, 11 Datasets

new (2 datasets)

newnew (1 dataset)

newone (1 dataset)

Own (3 datasets)

second mine (1 dataset)

trial (2 datasets)

wholenew (1 dataset)



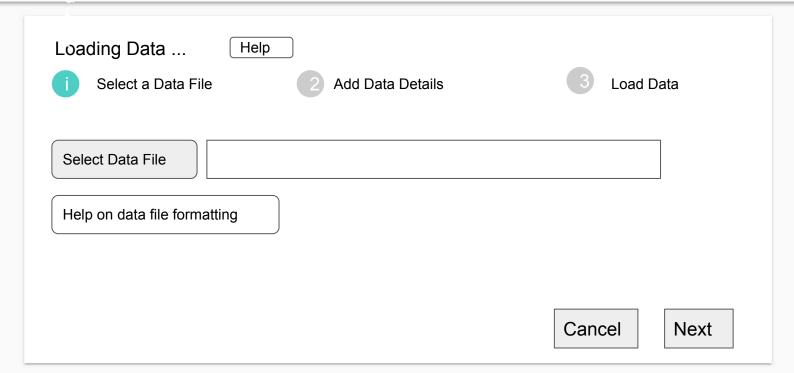
VISUALIZATION

TRANSCRIPTS

DATA HUBS

VIEW MY DATA

**PYTHON** 



### File to Import: donor.all\_projects.xena

- Genomic data: numbers in a rectangle (e.g. expression)
- Phenotypic data: categories or non-genomic in a rectangle (e.g. age, mutation status: 'wt' or 'mutant')

More data types ...

File preview

Help

100.00	sampleID	_age_at_diagnosis	_cohort	_gender
	DO1000	61	ICGC	female
	DO10004	75	ICGC	female
	DO1001	41	ICGC	female
	DO10012	71	ICGC	female

Show more...

BACK

CANCEL

**NEXT** 

#### File to Import: donor.all\_projects.xena

- Genomic data: numbers in a rectangle (e.g. expression)
- Phenotypic data: categories or non-genomic in a rectangle (e.g. age, mutation status: 'wt' or 'mutant')
- Segmented data: (e.g. segmented copy number data)
- Positional data: (e.g. positional mutation data)

Help

Less data types ...

File preview

sampleID	_age_at_diagnosis	_cohort	_gender
DO1000	61	ICGC	female
DO10004	75	ICGC	female
DO1001	41	ICGC	female
DO10012	71	ICGC	female

Show more...

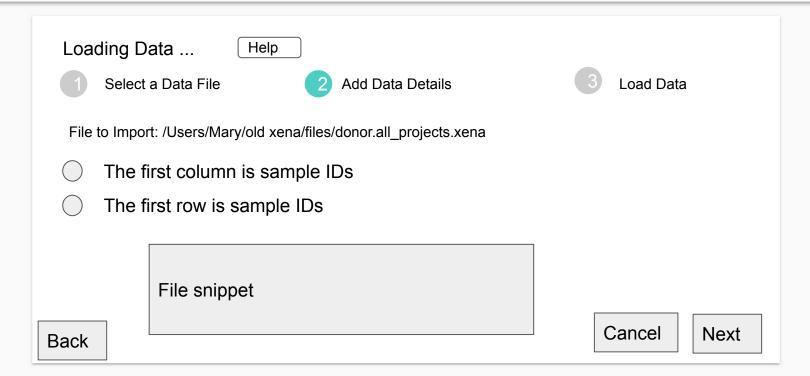


VISUALIZATION

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DATA HUBS

VIEW MY DATA





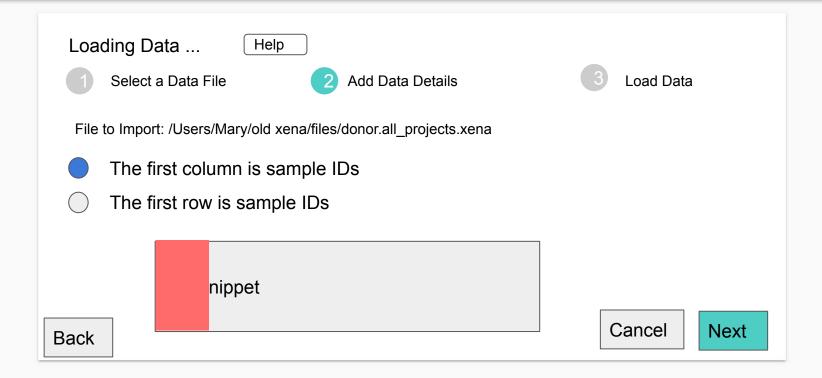
VISUALIZATION

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VIEW MY DATA

**PYTHON** 





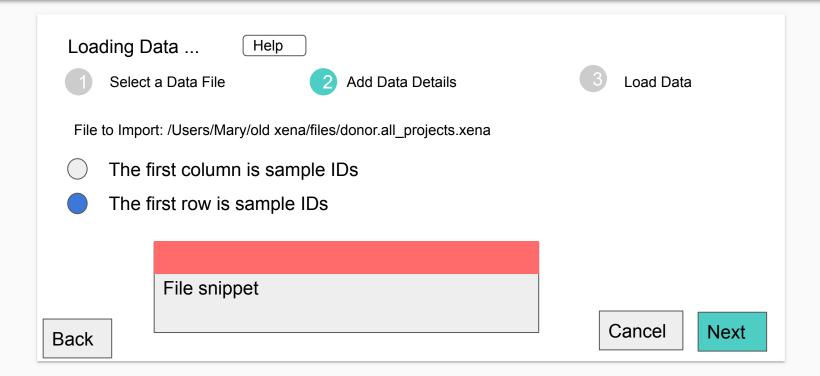


TRANSCRIPTS

DATA HUBS

VIEW MY DATA

PYTHON





VISUALIZATION

DATA HUBS

VIEW MY DATA

HELP

# Loading Data ... Help Select a Data File Add Data Details Load Data File to Import: /Users/Mary/old xena/files/donor.all\_projects.xena These are the first data on these samples. I have loaded other data on these samples and want to connect to it. There is other public data in Xena on these samples (e.g. TCGA) and want to connect to it. File snippet Cancel Next Back



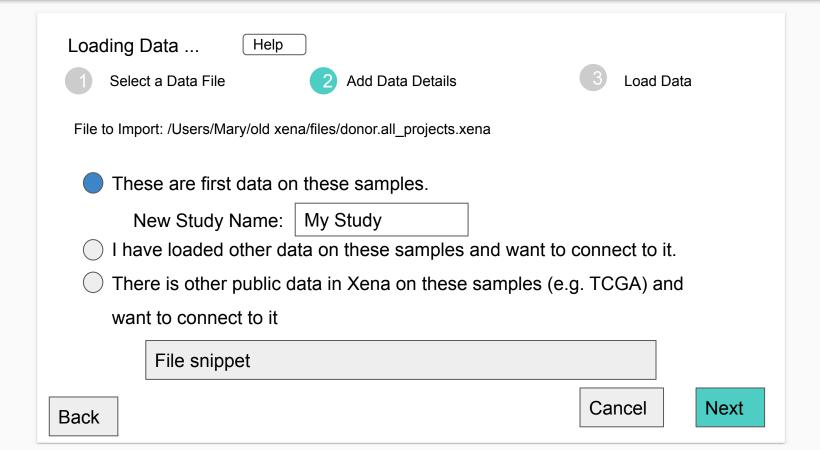


TRANSCRIPTS

DATA HUBS

VIEW MY DATA

PYTHON





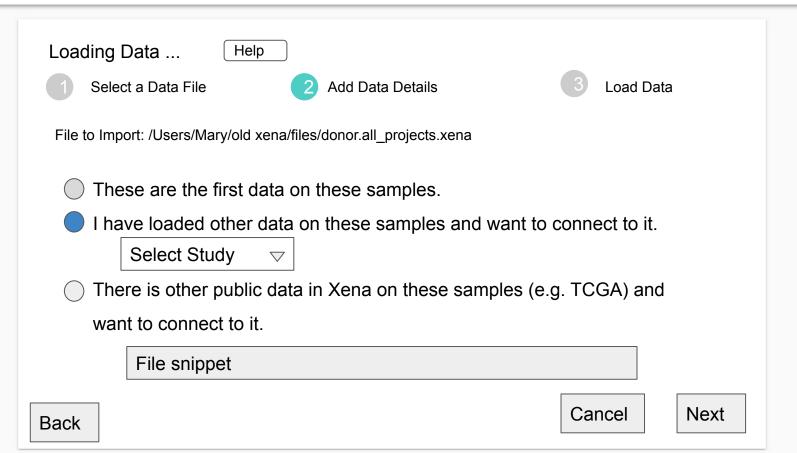
DATA SETS VISUA

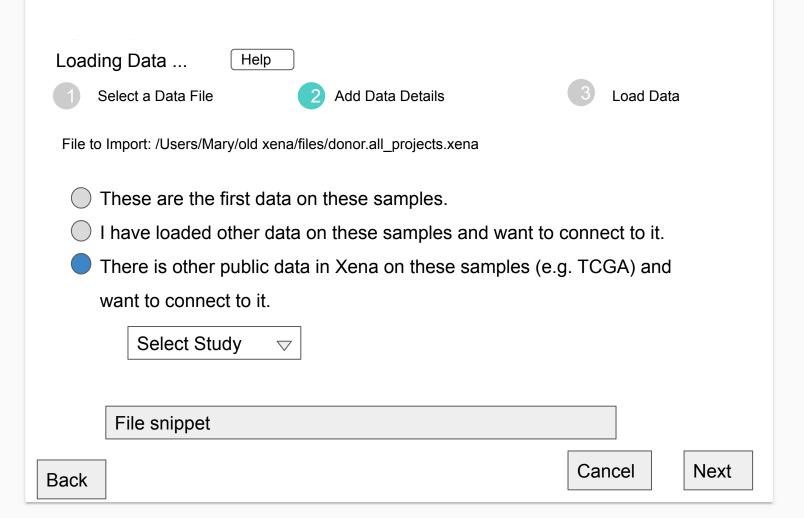
TRANSCRIPTS

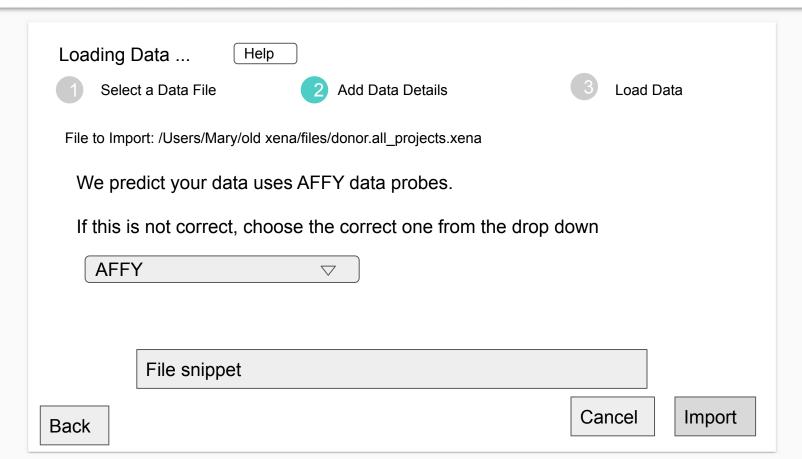
DATA HUBS

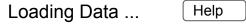
VIEW MY DATA

PYTHON











Select a Data File



Add Data Details



Load Data

File to Import: /Users/Mary/old xena/files/donor.all\_projects.xena

We don't recognize the identifiers in your data. Sorry!

[Let us know which identifiers you're using](mailto:genome-cancer@soe.ucsc.edu) so we can better support you in the future

File snippet

Back

Cancel

Import



VISUALIZATION

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DATA HUBS

VIEW MY DATA

PYTHON

HELP

# Loading Data ... Help Add Data Details Select a Data File Load Data File to Import: /Users/Mary/old xena/files/donor.all\_projects.xena Which reference genome was used to create this file? hg18/GRCh36 hg19/GRCh37 hg38/GRCh38 File snippet Cancel **Import** Back



VISUALIZATION

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DATA HUBS

VIEW MY DATA

HELP

# Loading Data ... Help Add Data Details Select a Data File Load Data File to Import: /Users/Mary/old xena/files/donor.all\_projects.xena Which reference genome was used to create this file? hg18/GRCh36 hg19/GRCh37 hg38/GRCh38 File snippet Cancel **Import** Back



VISUALIZATION

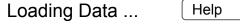
TRANSCRIPTS

DATA HUBS

VIEW MY DATA

**PYTHON** 

HELP



Select a Data File

2

2 Add Data Details

3

Load Data

Loading file ...

Back

Cancel



VISUALIZATION

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VIEW MY DATA

PYTHON

HELP

### Loading Data ... Help



Select a Data File

2

Add Data Details

3

Load Data

Loading file ...

Error messages

File snippet

Example of correct file format for segmented or mutation

Back

Reload file

**Edit Data Details** 

Cancel

### Loading Data ... Help



Select a Data File



Add Data Details



Load Data

Loading file ...

There was an unexpected error:

<java error>

Please [contact](mailto:genome-cancer@soe.ucsc.edu) the Xena team for help

Back

Reload file

**Edit Data Details** 

Cancel



VISUALIZATION

**TRANSCRIPTS** 

DATA HUBS

VIEW MY DATA

**PYTHON** 

HELP

#### Loading Data ... Help

Select a Data File

Add Data Details

Load Data

Loading file ...

Success!

Finish

Load more data

View data