

Web Load Wireframes

Local Xena Hub

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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.

Help

CLOSE

Local Xena Hub

[Load Data](#)[Help](#)

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

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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)

Loading Data ...

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Select a Data File

2

Add Data Details

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Load Data

[Select Data File](#)[Help on data file formatting](#)[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')

[More data types ...](#)

File preview

Help

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

[Show more...](#)

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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

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File to Import: /Users/Mary/old xena/files/donor.all_projects.xena

☐

The first column is sample IDs

☐

The first row is sample IDs

File snippet

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The first column is sample IDs



The first row is sample IDs

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The first column is sample IDs



The first row is sample IDs

File snippet

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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

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File to Import: /Users/Mary/old xena/files/donor.all_projects.xena

☒ These are first data on these samples.

New Study Name:

☐ 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

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- ☐ These are the first data on these samples.
- ☒ I have loaded other data on these samples and want to connect to it.



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- ☐ 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.

Select Study



File snippet

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File to Import: /Users/Mary/old xena/files/donor.all_projects.xena

We predict your data uses AFFY data probes.

If this is not correct, choose the correct one from the drop down

AFFY



File snippet

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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

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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

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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

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Loading file ...

Error messages

File snippet

Example of correct file format for segmented or mutation

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Loading file ...

There was an unexpected error:

<java error>

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

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Loading file ...

Success!

[Finish](#)[Load more data](#)[View data](#)