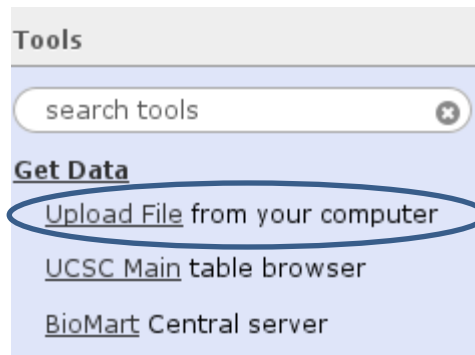


Importing data into Galaxy: Data upload

upload of BAM, bigWig, BED files = your data



Upload File (version 1.1.1.3)

File Format:
Auto-detect
Which format? See help below

File:
Browse... No file selected. *files < 2GB can directly be uploaded*
TIP: Due to browser limitations, uploading files larger than 2GB is guaranteed to fail. To upload large files, use the URL method (below) or FTP (if enabled by the site administrator).

URL/Text:

you can also insert a URL here if that's where your data lies

Here you may specify a list of URLs (one per line) or paste the contents of a file.

Files uploaded via FTP:

File	Size	Date
Your FTP upload directory contains no files.		

This Galaxy server allows you to upload files via FTP. To upload some files, log in to the FTP server at deeptools.ie-freiburg.mpg.de using your Galaxy credentials (email address and password).

Convert spaces to tabs:
☐ Yes
Use this option if you are entering intervals by hand.

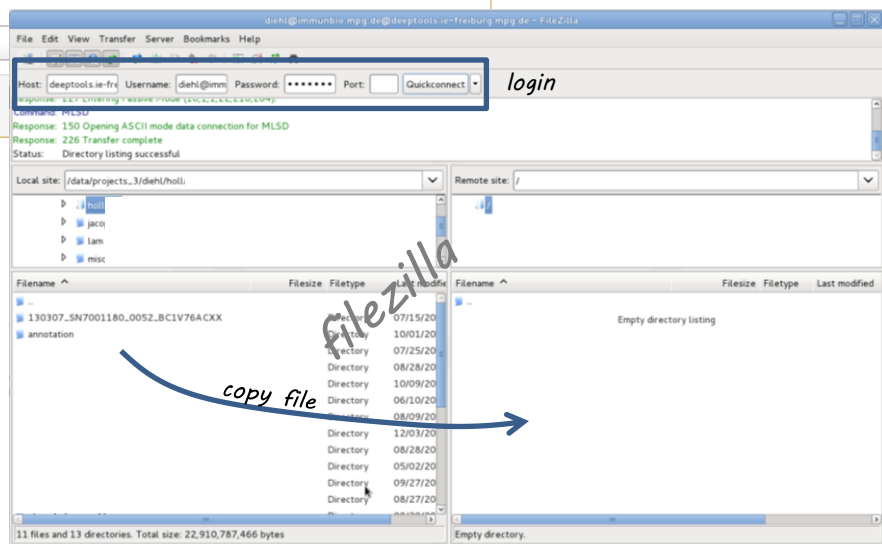
Genome:
----- Additional Species Are Below -----

Execute

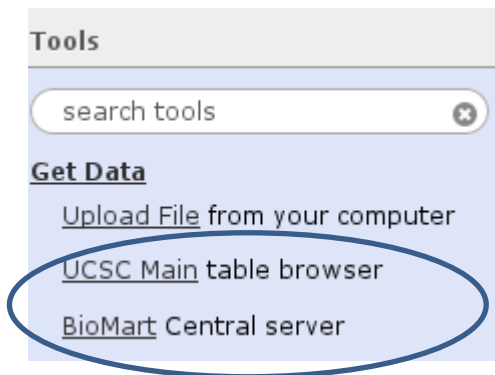
if you're not sure about the data type, leave it up to Galaxy, but it's always good to know before what you're going to upload

for files >2GB you must register with deeptools.ie-freiburg.mpg.de (via "User" → "register") and you'll need an FTP client, e.g. filezilla (<https://filezilla-project.org/>). Login to the FTP client using your deepTools Galaxy user name and password (host: deeptools.ie-freiburg.mpg.de, move the desired file to the remote site and go back to deepTools Galaxy where the file should now appear → hit "execute"

important! specify the reference genome that was used for aligning the reads!



Importing data into Galaxy: Annotation



import of external data sets, e.g. gene lists

UCSC

be aware, that BED files from UCSC will have chromosomes labelled with “chr” while ENSEMBL usually returns just the number – this might lead to incompatibilities, i.e. when working with annotations from UCSC and ENSEMBL, you need to make sure to use the same naming!



here you can always check what kind of table will be returned

choose the info you want, e.g. chromosome, gene start, gene end...