

Tips

The following screenshot shows us:

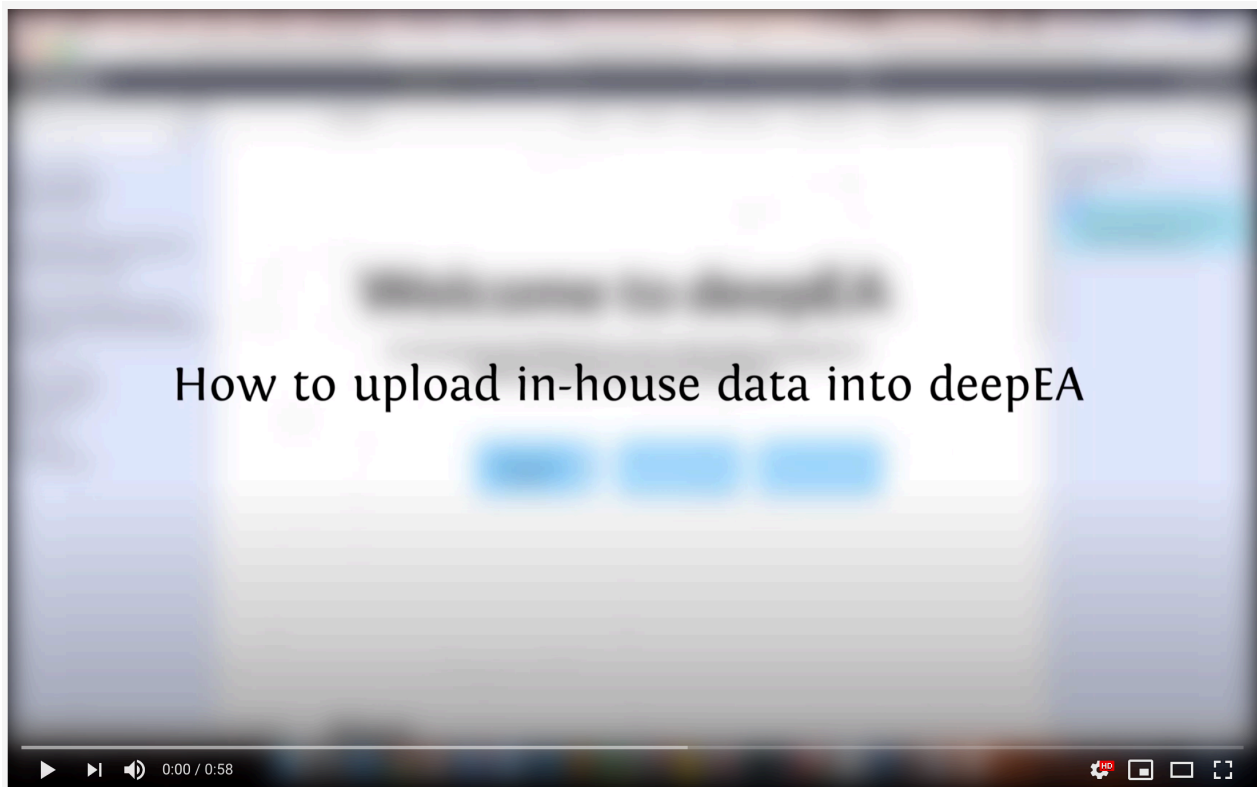
- How to view the data in deepEA
- How to re-run a job
- How to save data to your local disk

The screenshot displays the Galaxy web interface. The main panel shows the 'Obtain Epi-transcriptome Sequencing Reads (Galaxy Version 17.09)' tool. The 'Accession' field is set to 'SRR1508371'. The 'History' panel on the right shows a list of datasets. Three red arrows point to specific elements in the history panel:

1. Click here to view this data (points to the dataset name 'SRR1508371.sra.fastq.gz')
2. Click here to re-run this job (points to the 're-run' button)
3. Click here to save this data to local disk (points to the 'download' button)

Frequently Asked Questions (FAQs)

How to upload in-house data into deepEA local server



How to upload in-house data into deepEA

How to become an admin user

- First, register with email `admin@example.org`, set the password arbitrary.
- Then, login with `admin@example.org`

How to stop deepEA local server

- Press `ctrl + c` (for windows and unix users) or `Cmd + c` (for Mac OS users)

How to re-launch deepEA local server when I exited the docker container

- First, using the following command to check the container ID

```
docker ps -a
```

- Then run the following command

```
docker container start container ID
docker exec -it container ID bash
bash /home/galaxy/run.sh
```

How to mount local disk into deepEA docker container

```
docker run -it -v /your home directory:/home/galaxy/database/files/000 -p
8080:8080 malab/deepEA bash
```

