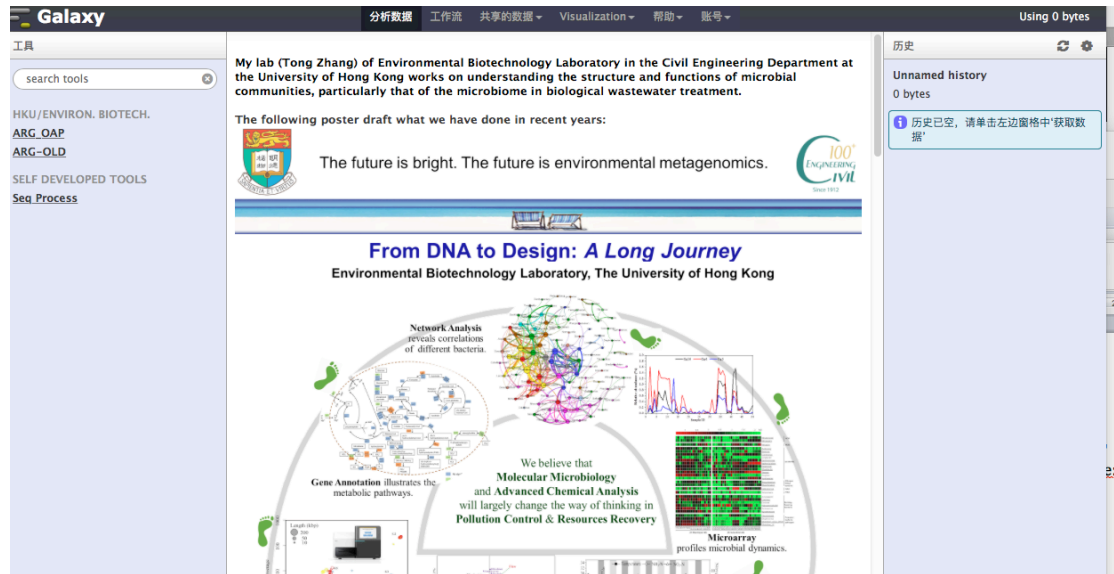
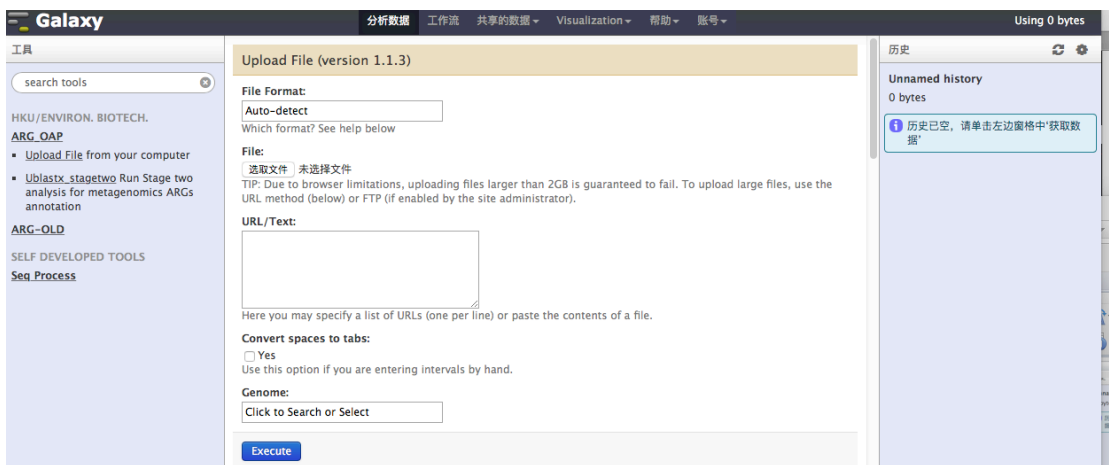


Using ARG_OAP to assign ARGs to type and subtype levels

1. Go to <http://smile.hku.hk/SARGs/>



2. Click **ARG-OAP** -> **Upload Files** to upload files generated by Ublastx_stage_one: **extracted.fa** and **meta_data_online.txt** into ARG_OAP separately.



After uploading it would be like this on the history panel:



3. Click **Ublastx_stagetwo** to run the second step to assign ARGs into type and

subtype level.

Galaxy

分析数据 工作流 共享的数据 Visualization 帮助 账号

Using 87.5 KB

工具

search tools

HKU/ENVIRON. BIOTECH.

ARG_OAP

- Upload File from your computer
- Ublastx_stagetwo Run Stage two analysis for metagenomics ARGs annotation

ARG-OLD

SELF DEVELOPED TOOLS

Seq Process

Ublastx_stagetwo (version 1.2)

Source Fasta File:
1: extracted.fa

Meta-data file:
2: meta_data_online.txt
The meta data file generated by stage one result

Column in Metadata:
3
The column in meta data file used to classify samples into groups for PcoA

blastx alignment length cut-off:
25
Hit Length of amino acid in blastx

blastx alignment evalue cut-off:
1e-07
Evaluate cut-off to in filter blastx result

blastx alignment identity:
60
Identity cut-off to filter blastx result

Execute

历史

Unnamed history
87.5 KB

2: meta_data_online.txt

1: extracted.fa

For **Source Fasta File**: choose the uploaded extracted.fa

Meta-data file: choose the uploaded meta_data_online.txt

Users can choose the parameters for the similarity search and the column number in the meta_data_online file to be the classification category for PcoA plotting colors.

Click **Execute** to perform the analysis.

4. After the step finished, there are four output files on the history panel and user can download them:

Galaxy

分析数据 工作流 共享的数据 Visualization 帮助 账号

Using 2.6 MB

工具

search tools

HKU/ENVIRON. BIOTECH.

ARG_OAP

- Upload File from your computer
- Ublastx_stagetwo Run Stage two analysis for metagenomics ARGs annotation

ARG-OLD

SELF DEVELOPED TOOLS

Seq Process

The following job has been successfully added to the queue:

23: PcoA figure of samples for ARGs abundance matrix normalization against 16S reads number

24: PcoA figure of samples for ARGs abundance matrix normalization against cell number

25: Subtype, type, and merged subtype and environmental samples ARGs abundance matrix, ARG abundance normalized against 16S reads number

26: Subtype, type, and merged subtype and environmental samples ARGs abundance matrix, ARG abundance normalized against cell number

You can check the status of queued jobs and view the resulting data by refreshing the History pane. When the job has been run the status will change from 'running' to 'finished' if completed successfully or 'error' if problems were encountered.

历史

Unnamed history
2.6 MB

26: Subtype, type, and merged subtype and environmental samples ARGs abundance matrix, ARG abundance normalized against cell number

25: Subtype, type, and merged subtype and environmental samples ARGs abundance matrix, ARG abundance normalized against 16S reads number

24: PcoA figure of samples for ARGs abundance matrix normalization against cell number

23: PcoA figure of samples for ARGs abundance matrix normalization against 16S reads number

2: meta_data_online.txt

1: extracted.fa

The four output files are the final results for ARGs identification results:

Files 1, 2 are the PcoA figure for samples of environmental samples from ocean sediment, drinking water system, sewage treatment system and livestock for ARGs abundance matrix normalized by 16S reads number and cell number separately.

File 3, 4 are the mother tables for subtype, type and subtype of user samples and environmental samples ARGs abundance of normalization on 16S reads number and cell number separately.

