AMR-TV
introductory slide deck

as of March 2025

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Installation

Requirements:

- Basic familiarity with a command line interface
- Basic familiarity with Github
- Docker

Other than that, two simple steps:

1) Clone the repo and adaptagrams submodule:

```
$ git clone git@github.com:ivansg44/AMR-TV.git amr-tv --recurse-submodules
```

2) Build the docker image:

`$ docker-compose build` (may take a long time)

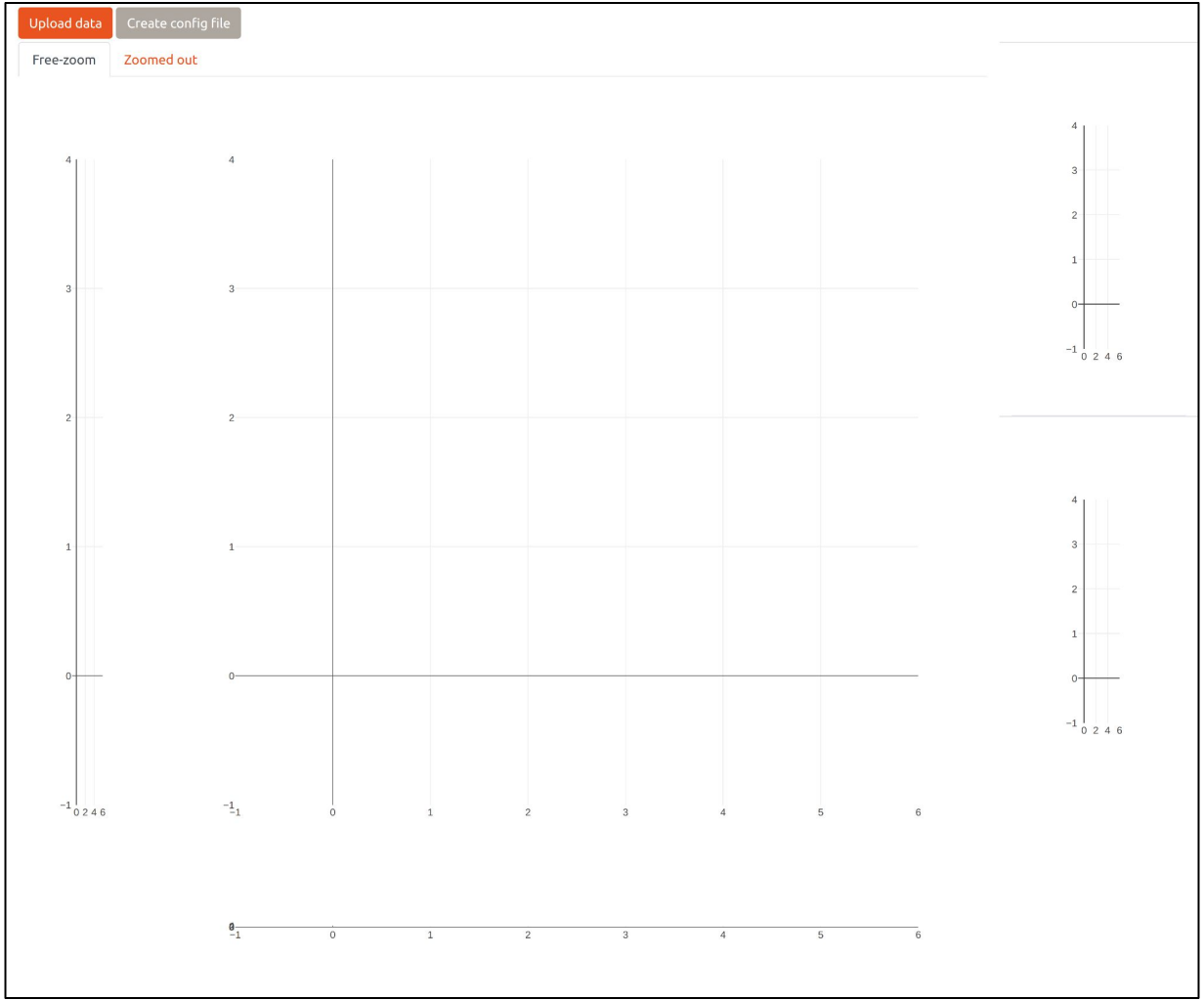
Launching the application

Pretty simple:

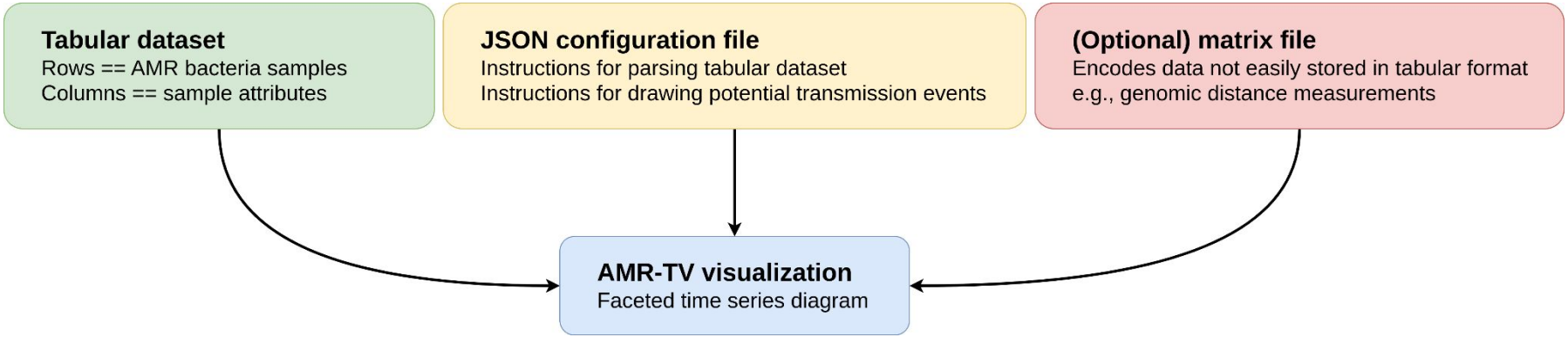
```
$ docker-compose up
```

AMR-TV will be available at http://0.0.0.0:8050/

(see next slide for what launch page should like)


Upload data
Create config file
Free-zoom
Zoomed out

Input data overview



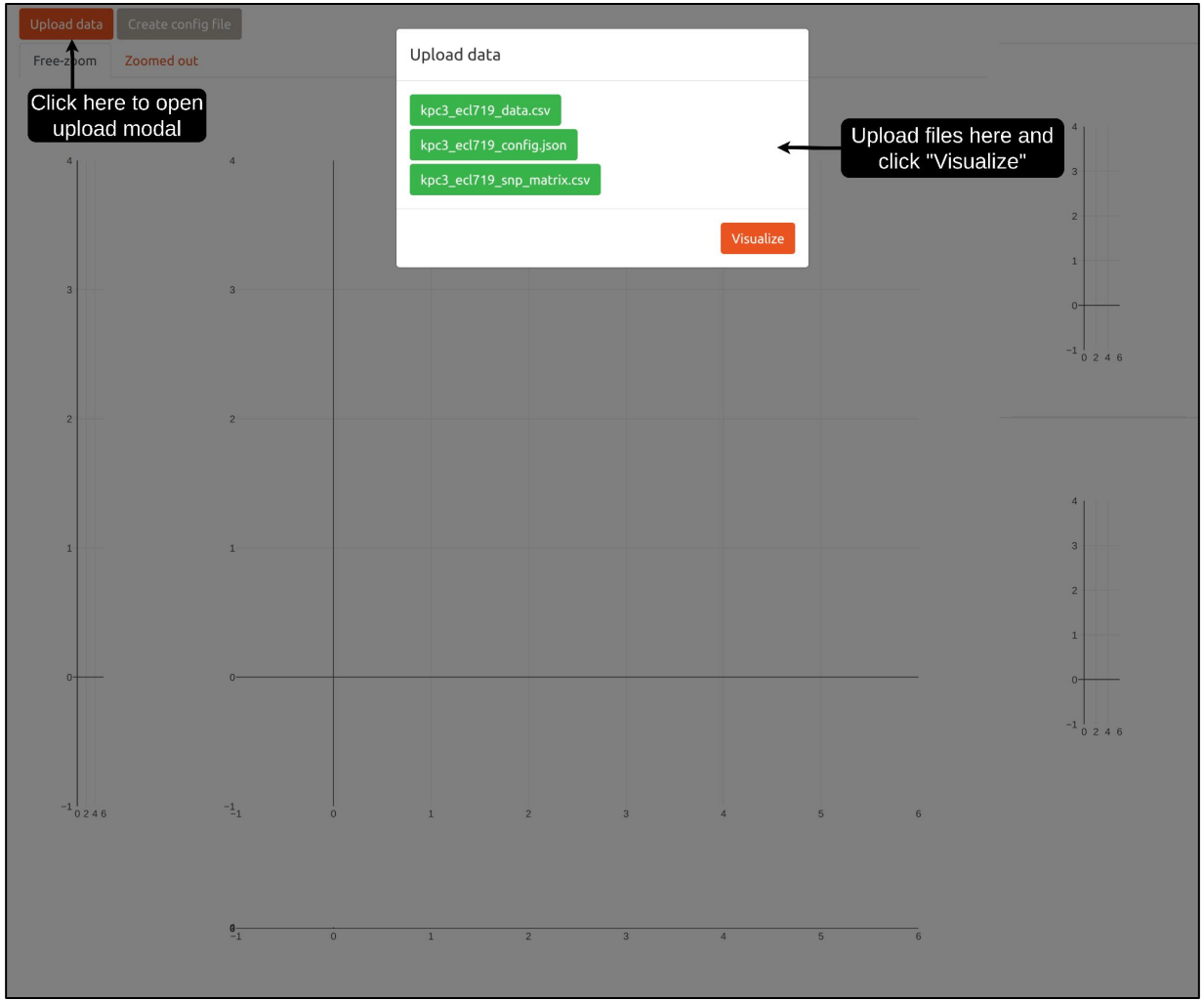
Example data files are available in the `kpc3_data/` folder of the AMR-TV repo

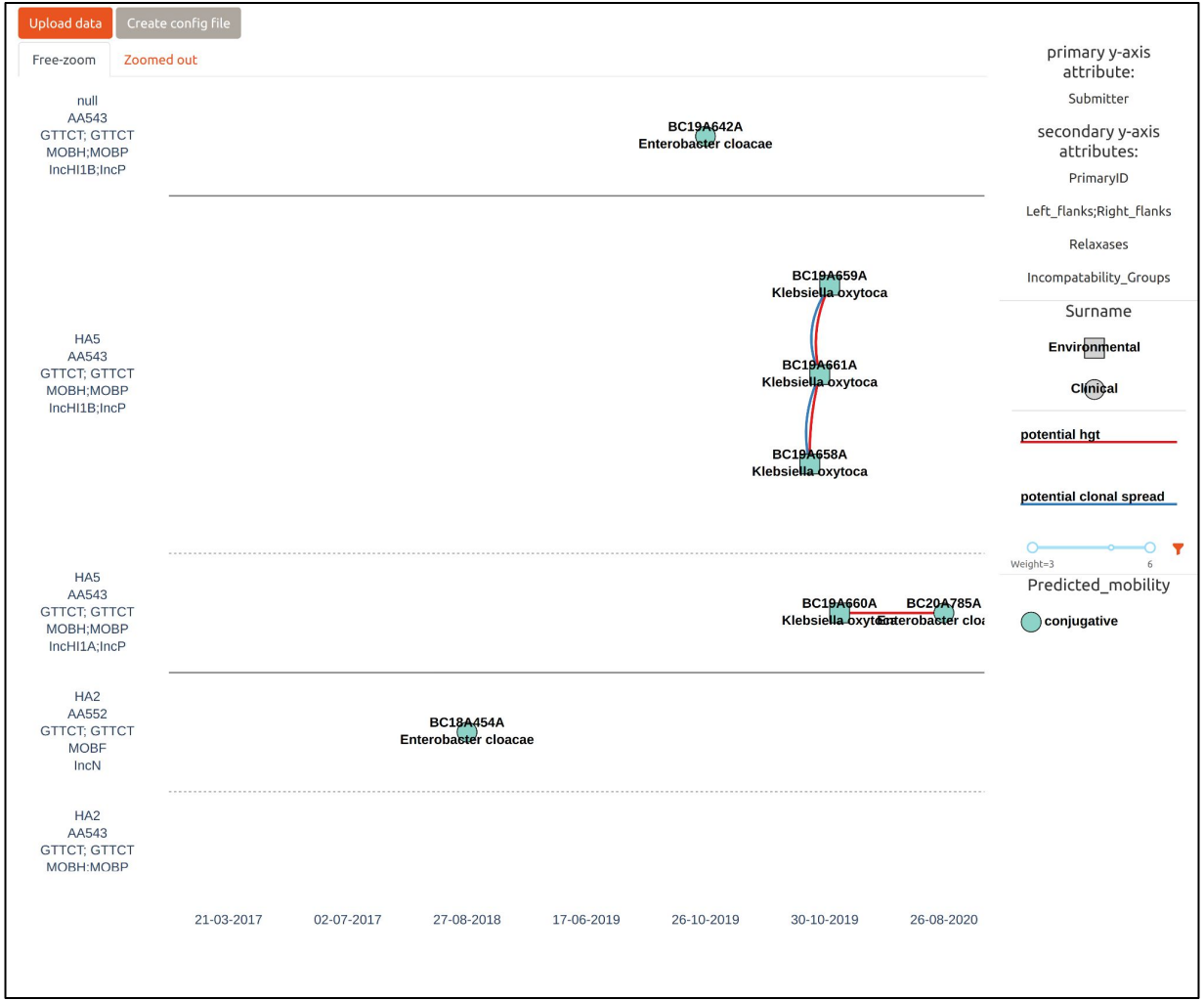
- These files describe KPC bacteria sampled across British Columbia, Canada

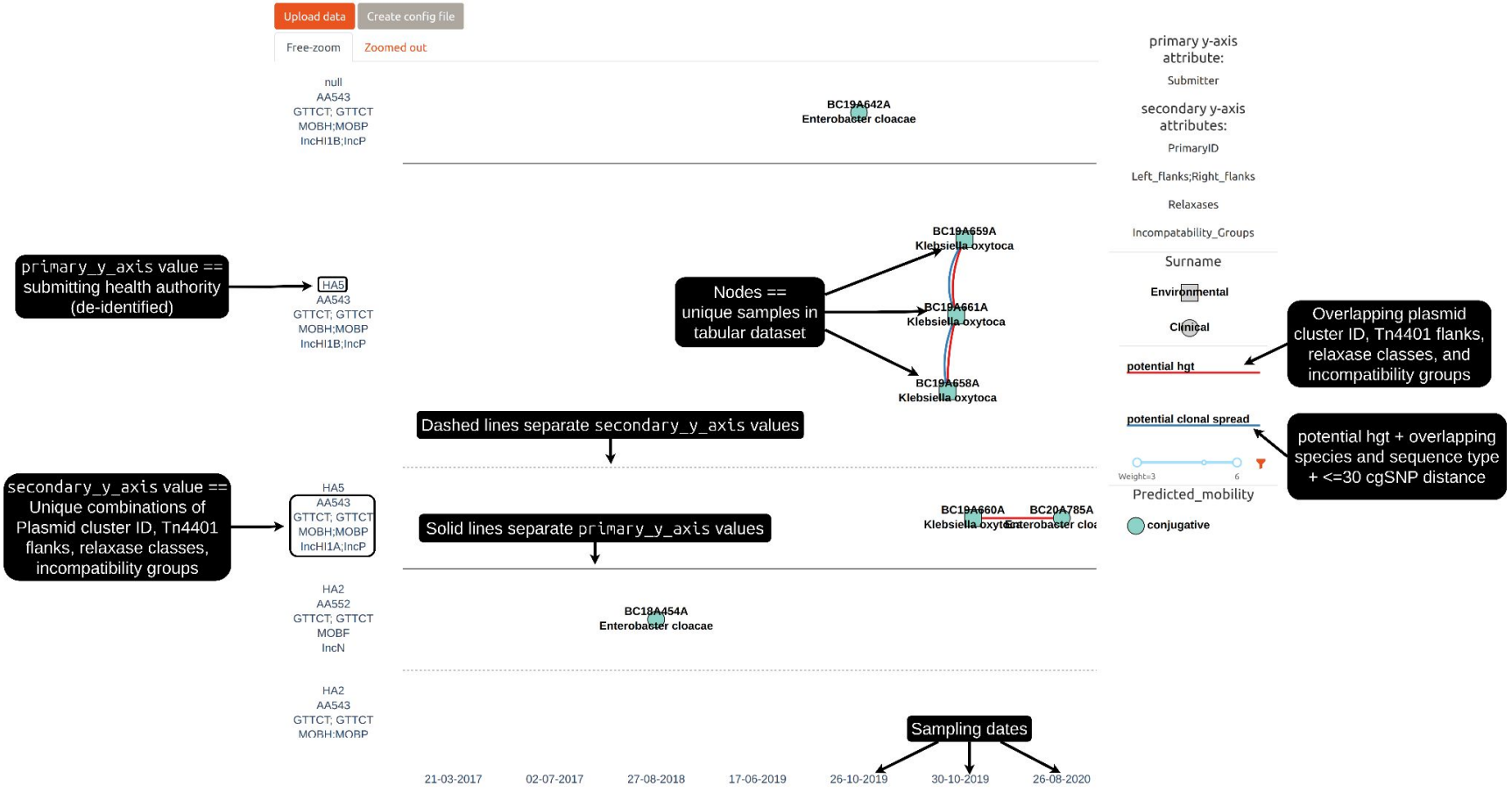
Inputted together:

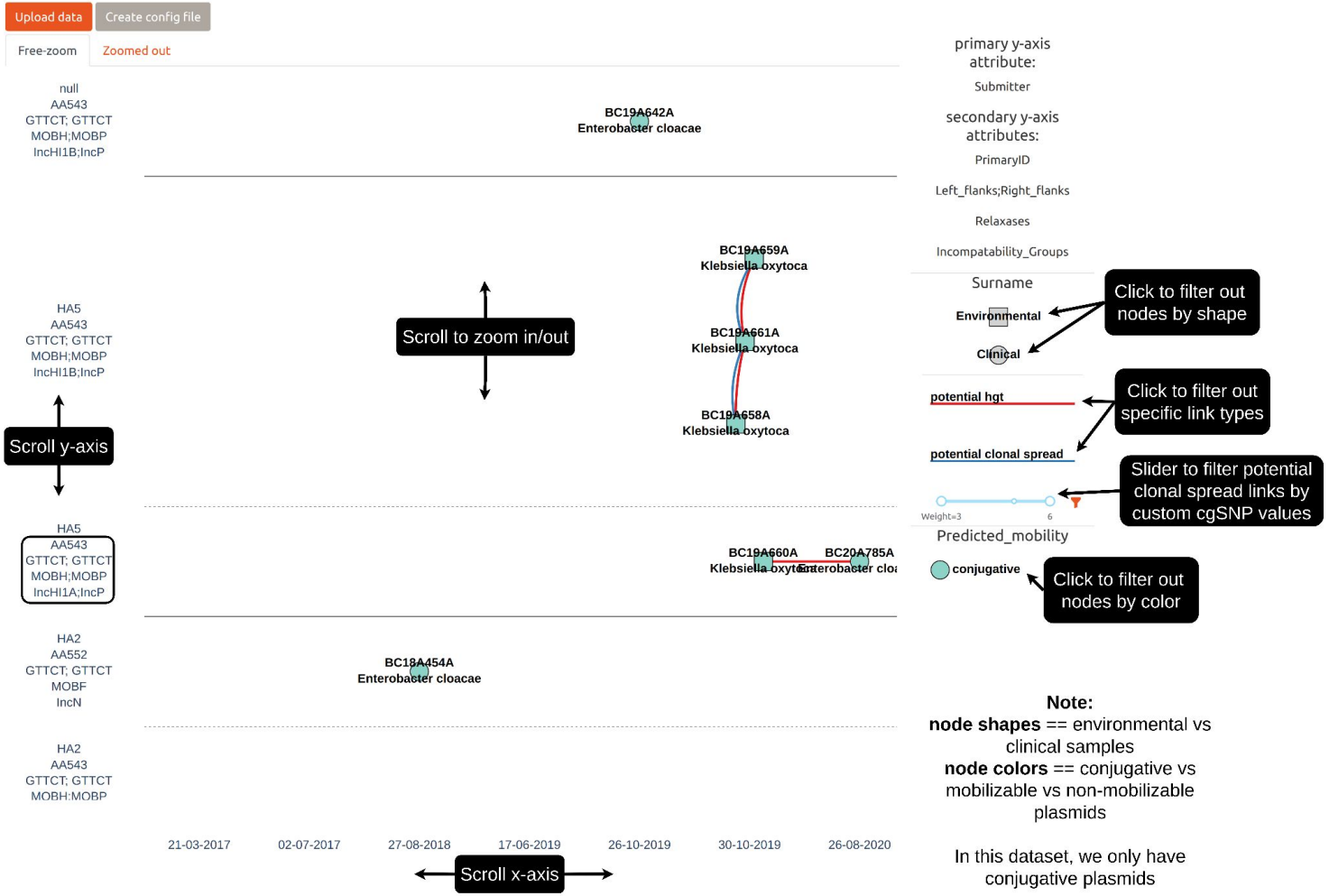
- `kpc3_data.csv`, `kpc3_config.json`
  - Large dataset of KPC bacteria across multiple MLST
- `kpc3_{MLST}_data.csv`, `kpc3_{MLST}_config.json`, `kpc3_{MLST}_snp_matrix.csv`
  - Several smaller datasets for KPC bacteria with a specific MLST

Uploading KPC3 ecl719 data


Upload data
Create config file
Free-zoom
Zoomed out
Click here to open upload modal
Upload data
kpc3_ecl719_data.csv
kpc3_ecl719_config.json
kpc3_ecl719_snp_matrix.csv
Visualize
Upload files here and click "Visualize"


Upload data
Create config file
Free-zoom
Zoomed out
null
AA543
GTTCT; GTTCT
MOBH;MOBP
IncHI1B;IncP
BC19A642A
Enterobacter cloacae
HA5
AA543
GTTCT; GTTCT
MOBH;MOBP
IncHI1B;IncP
BC19A659A
Klebsiella oxytoca
BC19A661A
Klebsiella oxytoca
BC19A658A
Klebsiella oxytoca
HA5
AA543
GTTCT; GTTCT
MOBH;MOBP
IncHI1A;IncP
BC19A660A
BC20A785A
HA2
AA552
GTTCT; GTTCT
MOBF
IncN
BC18A454A
Enterobacter cloacae
HA2
AA543
GTTCT; GTTCT
MOBH:MOBP
21-03-2017
02-07-2017
27-08-2018
17-06-2019
26-10-2019
30-10-2019
26-08-2020
primary y-axis attribute:
Submitter
secondary y-axis attributes:
PrimaryID
Left_flanks;Right_flanks
Relaxases
Incompatability_Groups
Surname
Environmental
Clinical
potential hgt
potential clonal spread
Weight=3
6
Predicted_mobility
conjugative

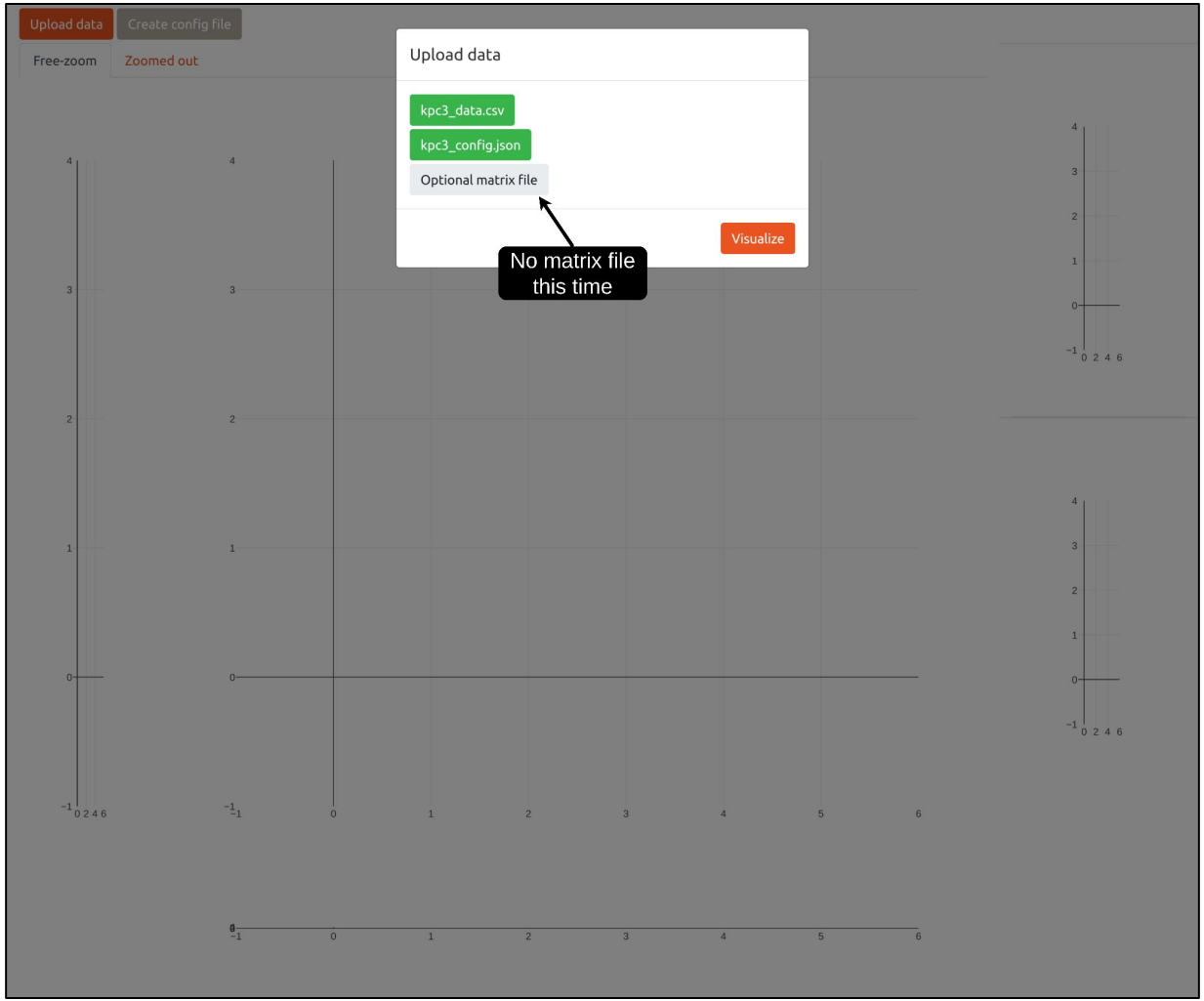

Upload data
Create config file
Free-zoom
Zoomed out
null
AA543
GTTCT; GTTCT
MOBH;MOBP
IncHI1B;IncP
BC19A642A
Enterobacter cloacae
primary y-axis attribute:
Submitter
secondary y-axis attributes:
PrimaryID
Left_flanks;Right_flanks
Relaxases
Incompatability_Groups
Surname
Environmental
Clinical
primary_y_axis value == submitting health authority (de-identified)
HA5
AA543
GTTCT; GTTCT
MOBH;MOBP
IncHI1B;IncP
Nodes == unique samples in tabular dataset
BC19A659A
Klebsiella oxytoca
BC19A661A
Klebsiella oxytoca
BC19A658A
Klebsiella oxytoca
Overlapping plasmid cluster ID, Tn4401 flanks, relaxase classes, and incompatibility groups
potential hgt
potential clonal spread
potential hgt + overlapping species and sequence type + <=30 cgSNP distance
Weight=3
6
Predicted_mobility
conjugative
Dashed lines separate secondary_y_axis values
secondary_y_axis value == Unique combinations of Plasmid cluster ID, Tn4401 flanks, relaxase classes, incompatibility groups
HA5
AA543
GTTCT; GTTCT
MOBH;MOBP
IncHI1A;IncP
Solid lines separate primary_y_axis values
BC19A660A
BC20A785A
HA2
AA552
GTTCT; GTTCT
MOBF
IncN
BC18A454A
Enterobacter cloacae
HA2
AA543
GTTCT; GTTCT
MOBH;MOBP
Sampling dates
21-03-2017
02-07-2017
27-08-2018
17-06-2019
26-10-2019
30-10-2019
26-08-2020

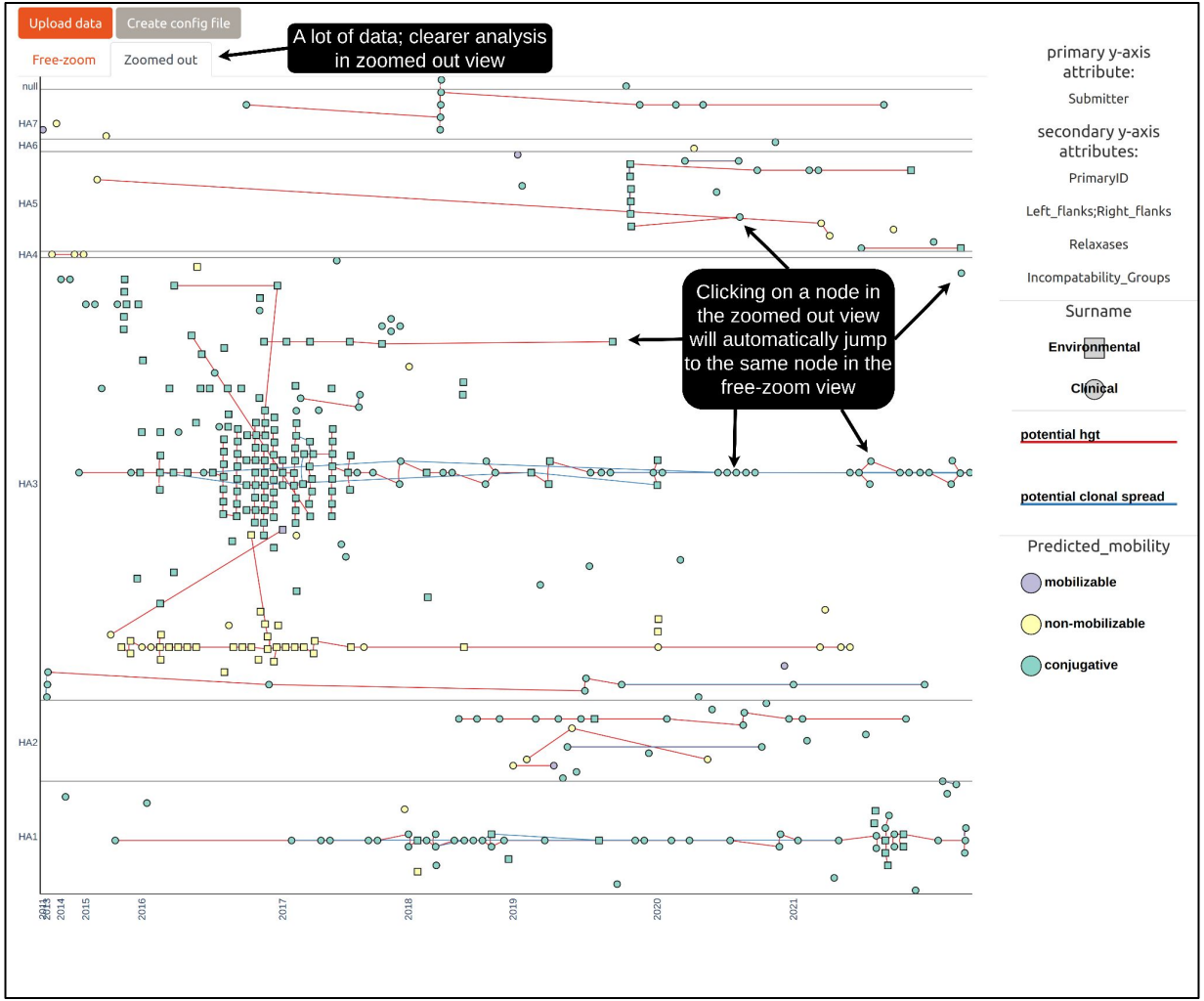


Note:
node shapes == environmental vs clinical samples
node colors == conjugative vs mobilizable vs non-mobilizable plasmids

In this dataset, we only have conjugative plasmids

Uploading multi-MLST KPC3 data


Upload data
Create config file
Free-zoom
Zoomed out
Upload data
kpc3_data.csv
kpc3_config.json
Optional matrix file
Visualize
No matrix file this time


Upload data
Create config file
Free-zoom
Zoomed out
A lot of data; clearer analysis in zoomed out view
Clicking on a node in the zoomed out view will automatically jump to the same node in the free-zoom view
null
HA7
HA6
HA5
HA4
HA3
HA2
HA1
2013
2014
2015
2016
2017
2018
2019
2020
2021
primary y-axis attribute:
Submitter
secondary y-axis attributes:
PrimaryID
Left_flanks;Right_flanks
Relaxases
Incompatability_Groups
Surname
Environmental
Clinical
potential hgt
potential clonal spread
Predicted_mobility
mobilizable
non-mobilizable
conjugative

Generating config files

Standardized JSON vocabulary

You can use the “create config file” modal to help generate a config file

- Requires an existing tabular dataset to generate the correct vocabulary

Multiple “Help” buttons to guide you through the process