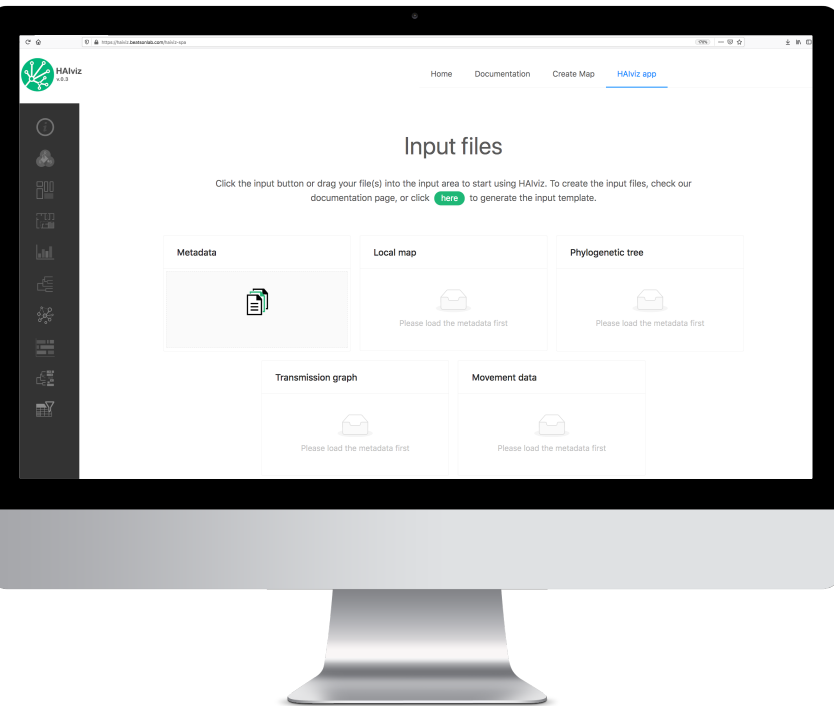# QUICK START GUIDE

HAIviz v.0.3

Budi Permana

v.2021.01.01

Input Files

HAIviz is showing input files loader. Users can click the file loader or drag and drop the files into the area. Input file will be parsed and validated, if file is valid, visualisation widow(s) will be activated, otherwise HAIviz will throw an error message. An active window is indicated by a colourful icon.

Disabled **Activated**

Icon of colour-key menu

● Metadata

A table contains information about the isolates, written in CSV format. Critical requirements including: mandatory headers, no duplicated records in column **isolate_name** and all dates must written in **ISO 8601** format (YYYY-MM-DD).

		Mandatory headers and columns							Optional		
isolate_name	isolate_species	isolate_colDate	isolate_colLocation	isolate_sourceType	isolate_sourceName	profile_1	profile_2	profile_3	profile_1:color	profile_2:color	profile_3:color
Isolate1	Species1	2019-12-20	Location1	Patient	P1	Clade 1	ST 1	vanA	blue	#9e0142	#fea
Isolate2	Species2	2019-12-21	Location2	Environment	P2	Clade 2	ST 2	vanB	lightgreen	#c12949	#fea2

● Local map

An XML file contains SVG element and location indexes. This file is specific to HAIviz and can be easily created on HAIviz map editor tool (page 4).

```xml
<?xml version="1.0" encoding="UTF-8"?>
<haivimap>
    <mapsvg>
        <svg
        version="1.1"
        xmlns="http://www.w3.org/2000/svg"
        xmlns:xlink="http://www.w3.org/1999/xlink"
        x="0px" y="0px"
        width="900px" height="500px">
        <!--SVG elements here-->
        </svg>
    </mapsvg>
    <mapdata>
        <location name="Location1" x="100" y="150"/>
        <location name="Location2" x="100" y="350"/>
    </mapdata>
</haivimap>
```
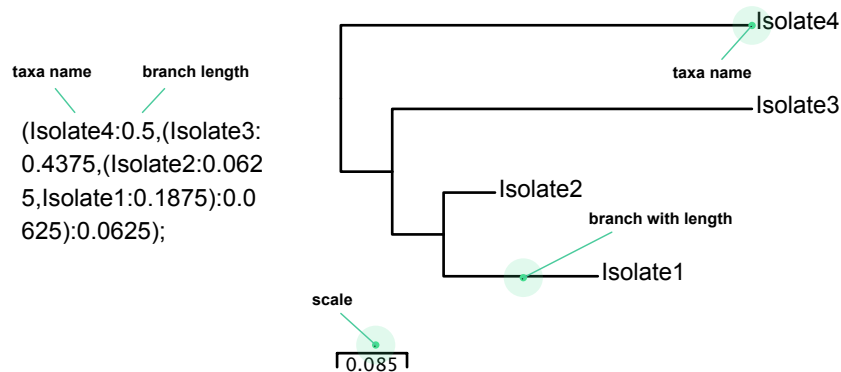
Location's x and y position from <mapdata> element.
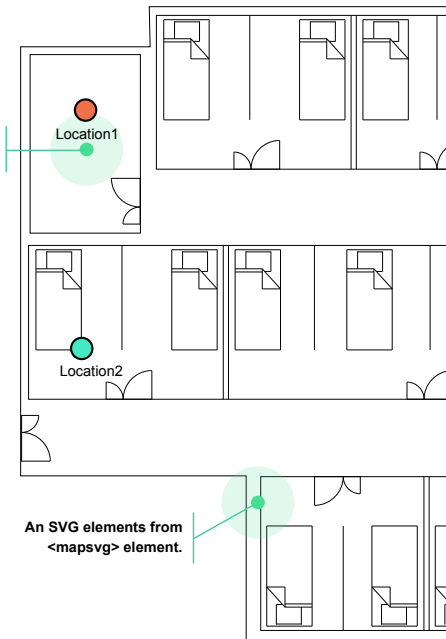
An SVG elements from <mapsvg> element.

Example of recommended SVG attributes for HAIviz map editor.
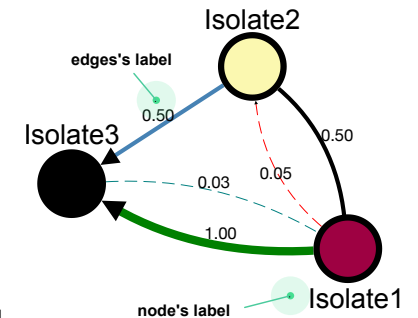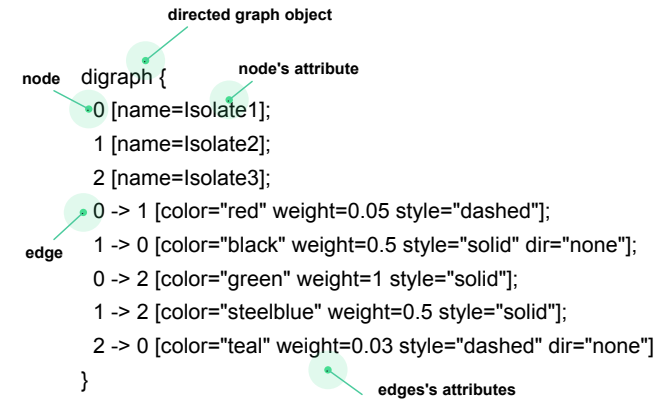
Input Files

● Phylogenetic tree

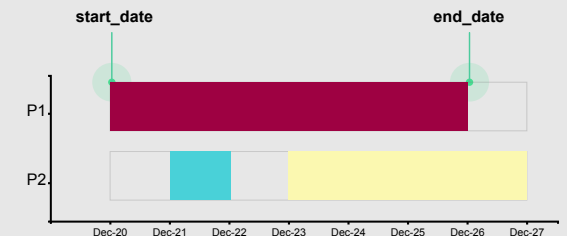A Newick formatted phylogenetic tree file with **taxa name** (leaf label) and **branch length**.

taxa name   **branch length**

(Isolate4:0.5,(Isolate3:
0.4375,(Isolate2:0.062
5,Isolate1:0.1875):0.0
625):0.0625);

Isolate4 — **taxa name**

Isolate3

Isolate2

Isolate1 — **branch with length**

scale

0.085

● Transmission graph

A text file describing a graph object written in **DOT** language.

directed graph object

node digraph {   **node's attribute**
    0 [name=Isolate1];
    1 [name=Isolate2];
    2 [name=Isolate3];
    0 -> 1 [color="red" weight=0.05 style="dashed"];
edge   1 -> 0 [color="black" weight=0.5 style="solid" dir="none"];
    0 -> 2 [color="green" weight=1 style="solid"];
    1 -> 2 [color="steelblue" weight=0.5 style="solid"];
    2 -> 0 [color="teal" weight=0.03 style="dashed" dir="none"]
}
                  edges's attributes

Isolate2

edges's label

0.50

Isolate3   0.50

0.03   0.05

1.00

node's label   Isolate1

● Movement timeline

A table file describing an individual movements (e.g. patient) from time to time at a single or multiple locations, written in **CSV** format. Critical requirements including: mandatory headers, dates column cannot be empty and must written in **ISO 8601** format (YYYY-MM-DD), and **start_date** must be **less than or equal to end_date**.

Mandatory headers and columns   **Optional**

source_name	start_date	end_date	location_name	location_color
P1	2019-12-20	2019-12-25	Location1	#9E0142
P2	2019-12-21	2019-12-22	Location2	#49D1D8
P2	2019-12-23	2019-12-26	Location3	#FBF8B0

start_date   **end_date**

P1

P2

Dec-20 Dec-21 Dec-22 Dec-23 Dec-24 Dec-25 Dec-26 Dec-27

Main Interface

https://haiviz.beatsonlab.com/haiviz-spa


Visualisation menu
Host all visualisation windows. Each icon will be activated as soon as visualisation from your input file is ready. Click on the icon to display the window.

Visualisation window
A window container where the interactive graphics are being rendered. The window can be individually moved, resized and closed.

Visualisation controller
Let you change the current state of visualisation display, such as, zoom in, zoom out and clear data selection.
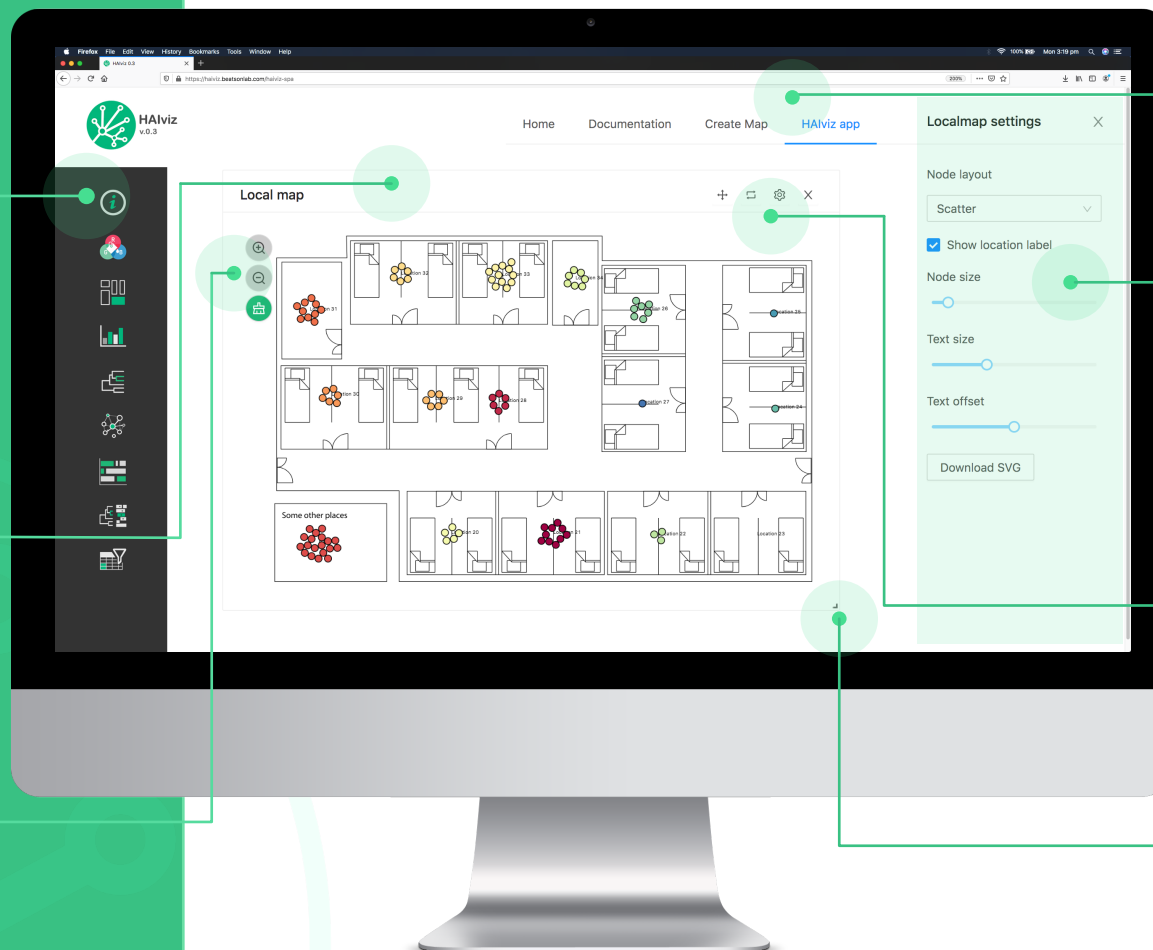
Page navigation
The main application navigation to let you jump between pages.

Window settings
A side drawer provides you additional actions or settings related to the current window.

Window controller
(From left to right) Let you move the window, re-draw visualisation, open additional settings and close the window.

Resize controller
Let you change the current size of your visualisation window.

HAIviz is showing a local map window, its controller and settings. Coloured nodes (circles) represent isolates clustered based in their collection location. Users can click, mouseover, zoom, pan, change the node layout (e.g. to piechart), node size, location text size and download the final visualisation in SVG format.

Creating local map

HAIviz is showing a local map editor page. Users start creating the local map by **loading an SVG** file. To be properly displayed, the SVG file must include attribute of **width and height** in pixel unit (example of recommended attributes is given in page 1). When file is loaded, users can **add, rename, update or remove a location**. A final map can be saved using **download** button or being **directly loaded** to HAIviz if metadata input has been previously loaded.

Location labeller
Let you enter and update the name of a location.

Zoom controller
Let you zoom in and zoom out the map.

Map loader
Let you download the map for later usage or load the map directly to HAIviz.

Location logger
Let you add a new location and remove the selected location.

Location marker
To remove or update location name, users need to click to select the marker. A selected marker is indicated by pink colour.

HAIviz by v.0.3 · Home · Documentation · Create Map · HAIviz app

Location2
Update location's name
Download final map
Load map to HAIviz

Name	x	y
Location1	125	124
Location2	125	309

Location index
Display the name and positions of the locations. Pink cell indicate the selected marker.
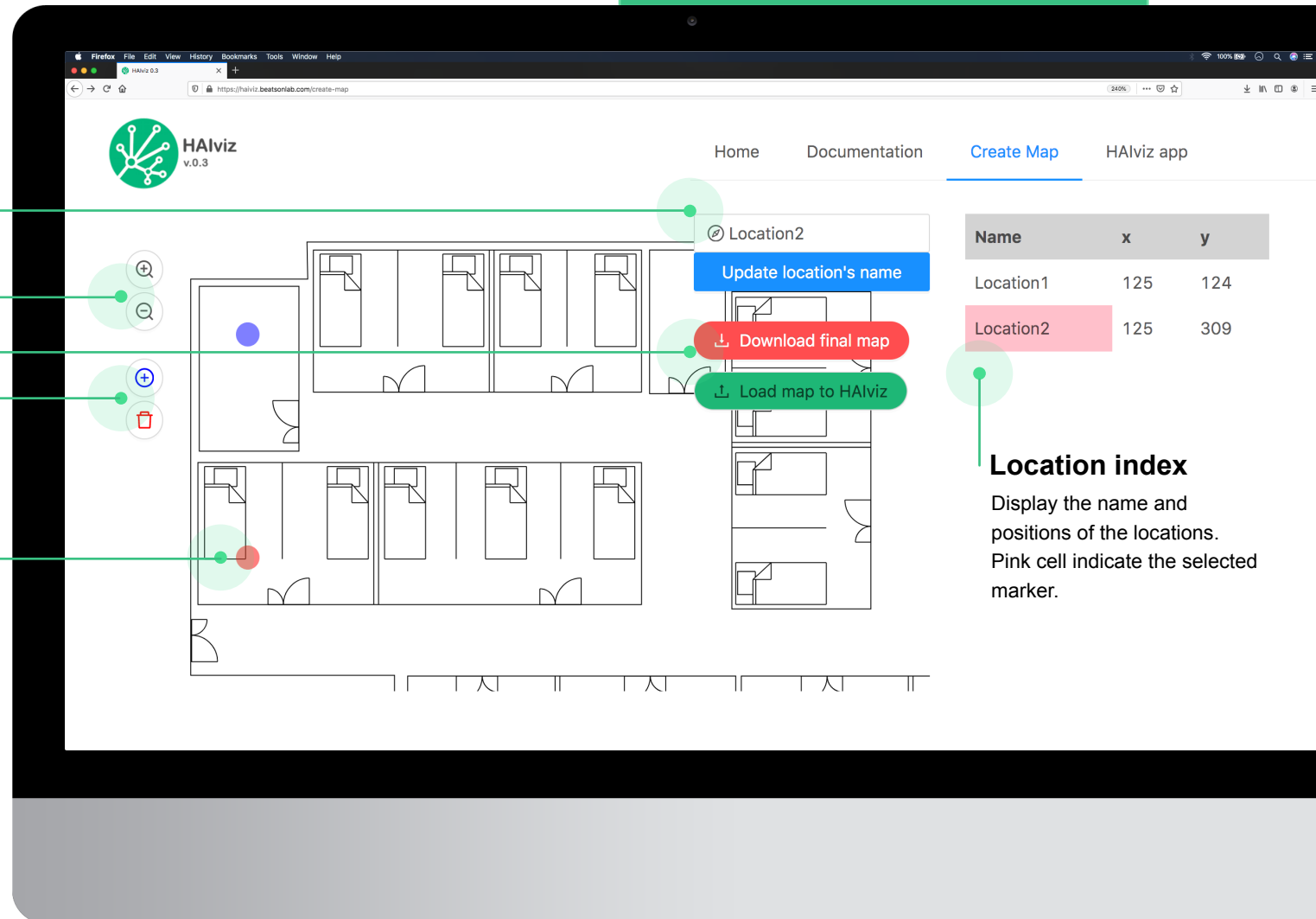
5 quick steps
1. Add a location
2. Move the location marker
3. Click the marker
4. Enter the name and click update name
5. Download final XML map

https://haiviz.beatsonlab.com/create-map

Interaction And Integration

- HAIviz is showing nine integrated and interactive visualisation windows created from an example dataset.
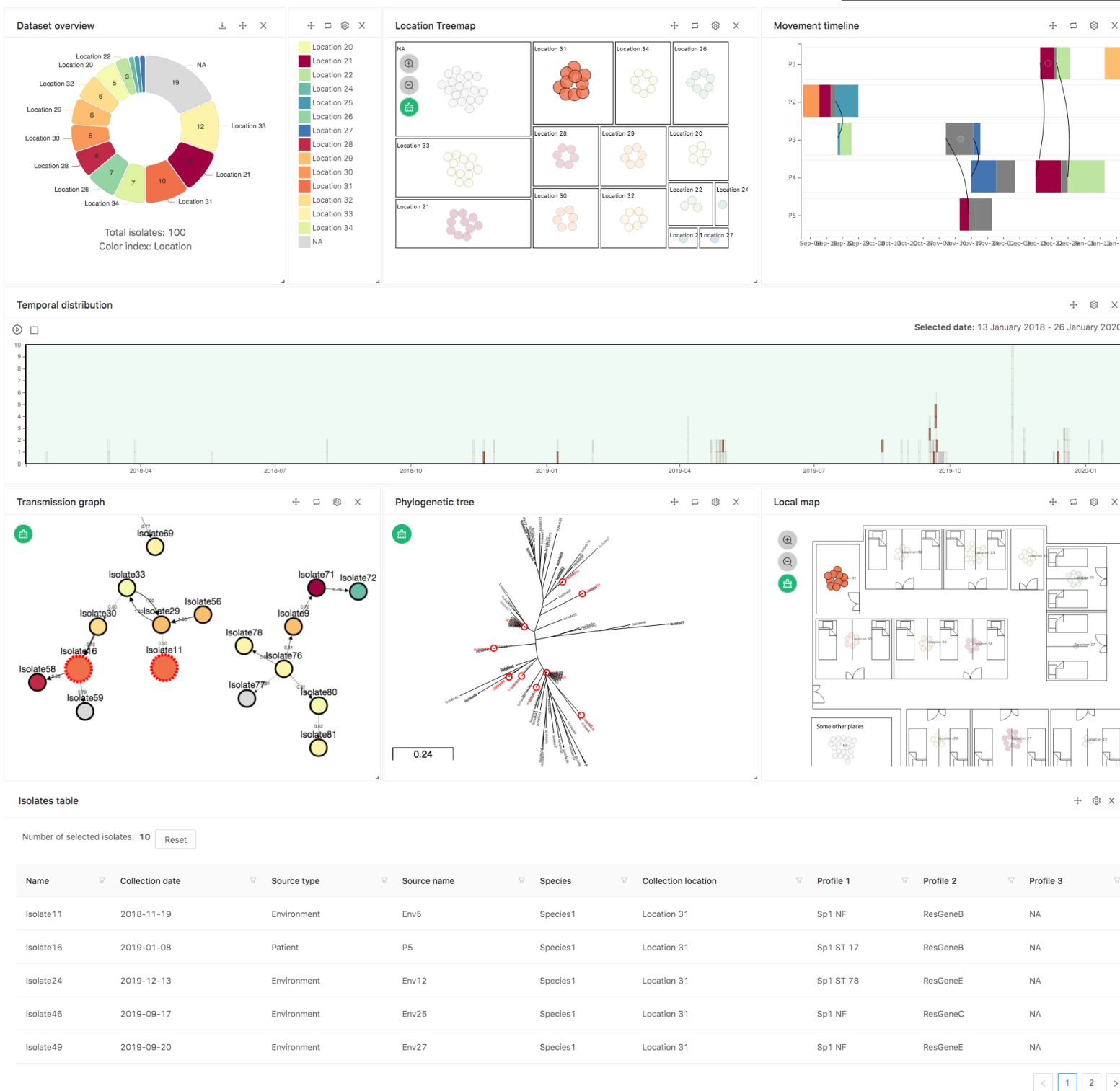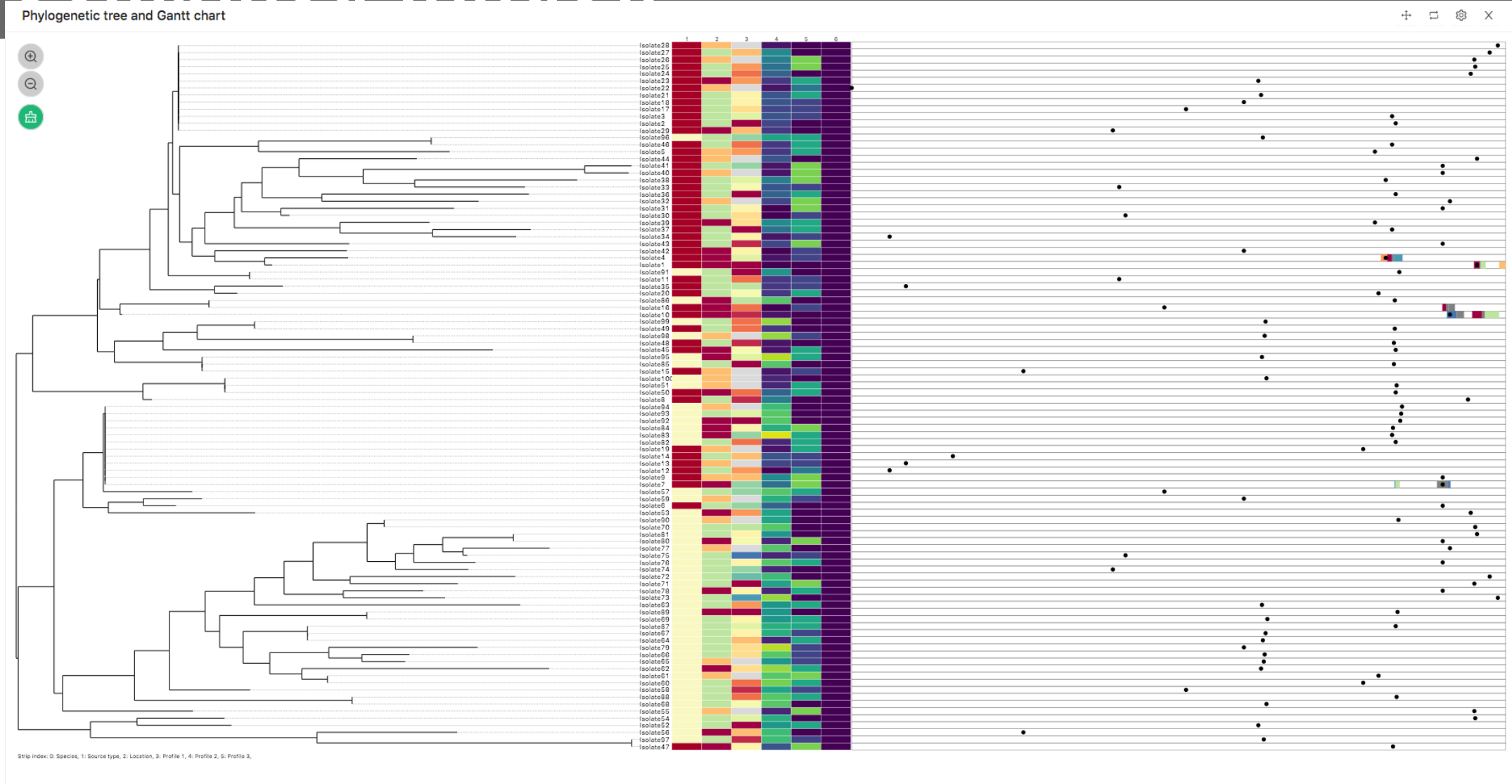
- To demonstrate integration functionality, isolates collected from Location 31 was all selected on location treemap window. This action will highlight all selected isolates on the other windows.

- Selection can also be performed in other windows, including using an interactive brush on temporal distribution window to create animation.

- Isolates table window provides filtering feature to enable users select the isolates based on the table columns. The table is also available to be downloaded as a CSV file.

- All images produced by HAIviz is ready to be saved to an SVG format, enabling quick and flexible editing for report and publication.

Dataset overview

Total isolates: 100
Color index: Location

Location 20, Location 21, Location 22, Location 24, Location 25, Location 26, Location 27, Location 28, Location 29, Location 30, Location 31, Location 32, Location 33, Location 34, NA

Location Treemap

Movement timeline

P1, P2, P3, P4, P5

Sep-08 Sep-22 Sep-29 Oct-13 Oct-20 Oct-27 Nov-03 Nov-17 Nov-24 Dec-01 Dec-15 Dec-22 Dec-29 Jan-12 Jan-19

Temporal distribution

Selected date: 13 January 2018 - 26 January 2020

2018-04 2018-07 2018-10 2019-01 2019-04 2019-07 2019-10 2020-01

Transmission graph

Isolate69, Isolate33, Isolate71, Isolate72, Isolate56, Isolate30, Isolate29, Isolate9, Isolate78, Isolate16, Isolate11, Isolate76, Isolate58, Isolate77, Isolate80, Isolate59, Isolate81

Phylogenetic tree

0.24

Local map

Some other places

Isolates table

Number of selected isolates: 10   Reset

Name	Collection date	Source type	Source name	Species	Collection location	Profile 1	Profile 2	Profile 3
Isolate11	2018-11-19	Environment	Env5	Species1	Location 31	Sp1 NF	ResGeneB	NA
Isolate16	2019-01-08	Patient	P5	Species1	Location 31	Sp1 ST 17	ResGeneB	NA
Isolate24	2019-12-13	Environment	Env12	Species1	Location 31	Sp1 ST 78	ResGeneE	NA
Isolate46	2019-09-17	Environment	Env25	Species1	Location 31	Sp1 NF	ResGeneC	NA
Isolate49	2019-09-20	Environment	Env27	Species1	Location 31	Sp1 NF	ResGeneE	NA

< 1 2 >

Combined window

Phylogenetic tree and Gantt chart

Strip index: 0: Species, 1: Source type, 2: Location, 3: Profile 1, 4: Profile 2, 5: Profile 3,

A window that visualise a combination of phylogenetic tree, colour strips, and movement timeline is available. The strip columns represent colours of isolate species, source type, location, profile 1, 2 and 3, respectively. This colour can be changed interactively on colour key window. This combined window is useful to visualise many information all together in a single image.

THANK YOU

for reading this guide

Thanks to all awesome web frameworks and libraries run on the background, HAIviz is now up and running and available worldwide. The following are some of the core libraries used by HAIviz:

react
react-grid-layout
d3
antd
phylocanvas
phylocanvas-plugin-export-svg
phylocanvas-plugin-scalebar
cytoscape
cytoscape-svg
redux
react-color
@nivo
lodash
moment
moment-range
newickparser
dotparser
export-to-csv
uuid
xml-js
...

HAIviz v.0.3
Healthcare-Associated
Infections Visualization Tool