

QUICK START GUIDE



HALviz: Healthcare
Associated Visualization
Tool

v.1.0.0

Budi Permana

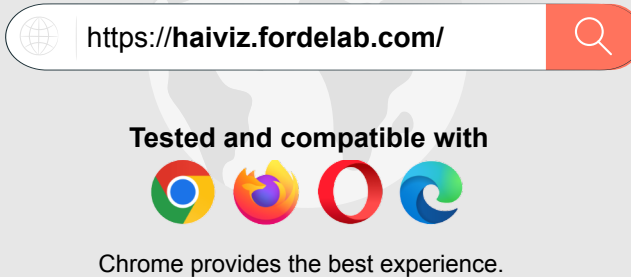
v.2024.01.15

Using HALviz

• Use it online

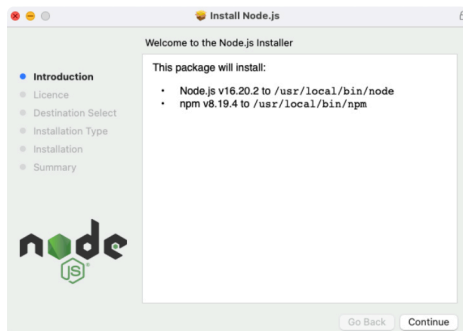
HALviz is deployed at <https://haiviz.fordelab.com> for online use. Users can visit the web page using modern browsers (e.g., Google Chrome, Firefox, Microsoft Edge), drag and drop the input files, and instantly create visualisation dashboard.

All visualisation processes are performed locally in the user's browser with no data uploaded to the server, ensuring the safety of private data



• Self host or use it offline

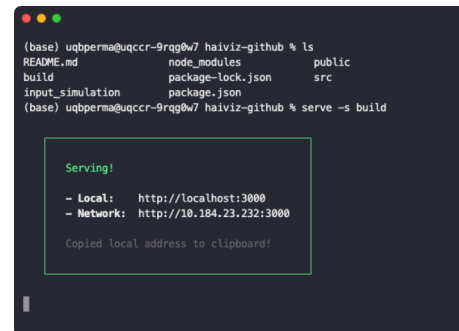
Users also can use HALviz offline by serving it through a static file server, such as, but not limited to `serve` Node.js package.



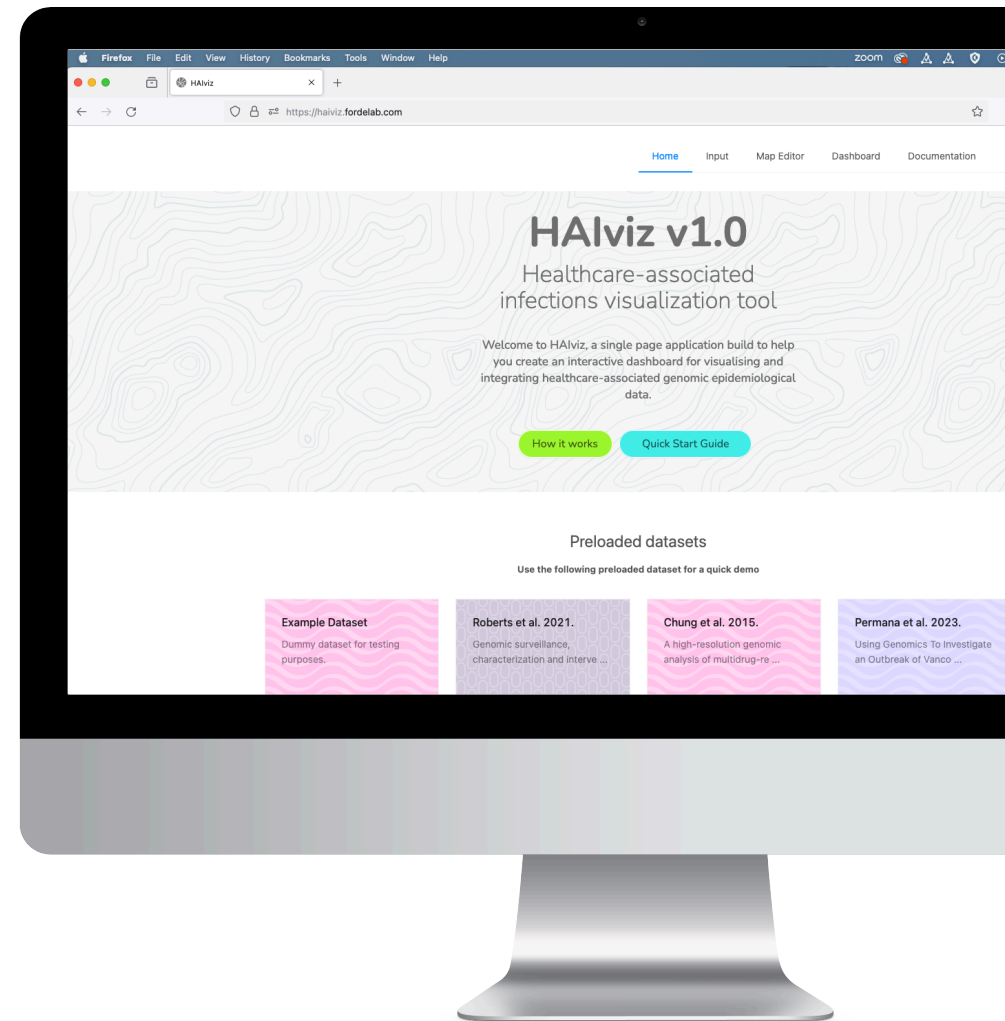
1. Install Node.js



2. Install `serve` Node.js package



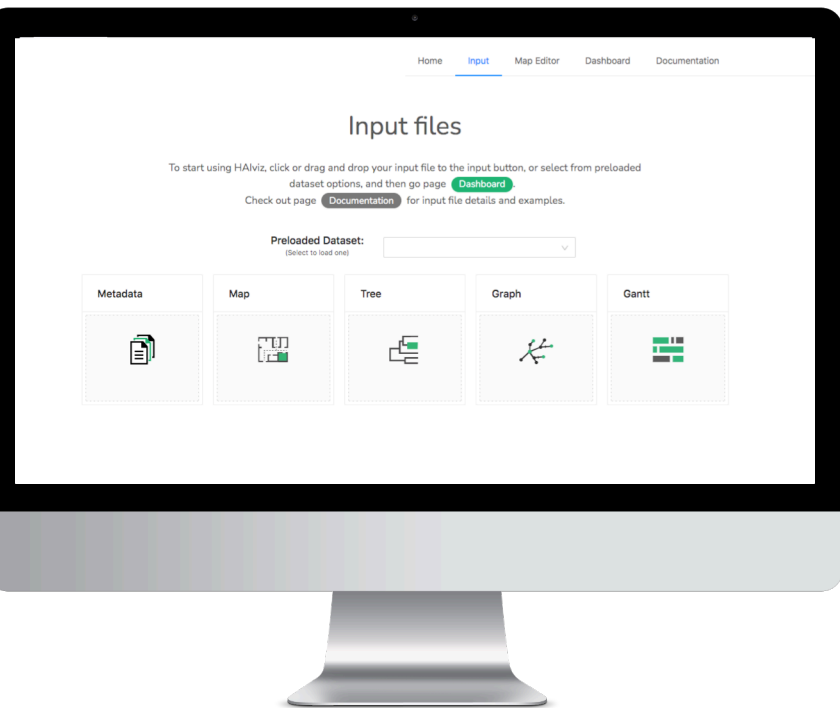
3. Serve the build directory



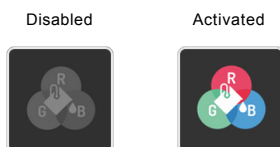
HALviz is a single page application (SPA) visualisation tool that runs on the browser. Users can visualise and explore data by loading their input files or setting up preloaded datasets (can do it on the offline mode only).



Input Files



HALviz is showing page *Input*. Users can click the file input loader or drag and drop the files into the input area. Input file will be parsed and validated, if file is valid, the window's icon in side-menu in page *Dashboard* will be **activated**.



Window's icon

Metadata

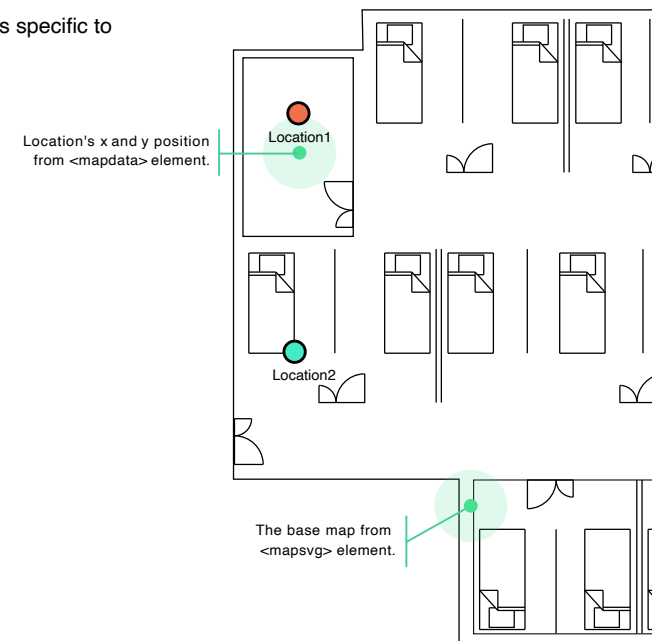
A table contains information about the isolates or samples, written in CSV format. No duplicated records in column **id** and all dates must be written in **ISO 8601 format (YYYY-MM-DD)**.

| Mandatory columns (fixed header) | | | Other columns (optional, user-defined header) | | Color columns (optional, [column]:color) | |
|-------------------------------------|------------|-----------|--|-------------|---|---------------|
| id | date | location | species | source | location:color | species:color |
| Isolate1 | 2019-12-20 | Location1 | Species1 | Patient | blue | #9e0142 |
| Isolate2 | 2019-12-21 | Location2 | Species2 | Environment | lightgreen | #c12949 |

Local map

An XML file contains SVG element and location indexes. This file is specific to HALviz and can be created in page *Map Editor*.

```
<?xml version="1.0" encoding="UTF-8"?>
<haivizmap>
  <mapsvg>
    <svg
      xmlns="http://www.w3.org/2000/svg"
      id="haiviz-localmap-svg"
      width="1000" height="1000"
      viewBox="0 0 1000 1000" >
      <!-- The JPEG/PNG is embedded as
            the SVG element here-->
    </svg>
  </mapsvg>
  <mapdata>
    <location name="Location1" x="100" y="150"/>
    <location name="Location2" x="100" y="350"/>
  </mapdata>
</haivizmap>
```



Example of SVG attributes from a JPGE base image of 1000x1000px.

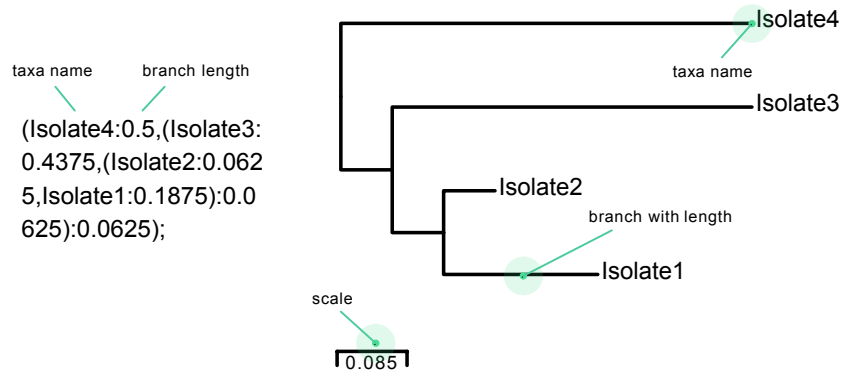


Input Files

(cont.)

Phylogenetic tree

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



Network (graph)

A text file describing a graph object written in DOT language (<https://graphviz.org/doc/info/lang.html>).

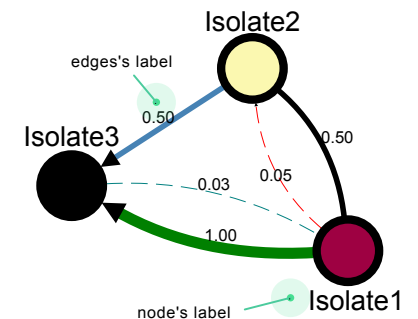
Using igraph R package you can export a network object into DOT format file with this following code:

`write_graph(YourGraphObject, "myGraphInDOT.gv", format = "dot").`

```

graph LR
    0((0)) -- "0.05" --> 1((1))
    1 -- "0.5" --> 0
    0 -- "1.00" --> 2((2))
    2 -- "0.03" --> 0
    1 -- "0.5" --> 2
    2 -- "0.05" --> 1
    style 0 fill:#000,stroke:#fff,stroke-width:2px
    style 1 fill:#fff,stroke:#000,stroke-width:2px
    style 2 fill:#f00,stroke:#000,stroke-width:2px
    
```

Labels in the code: digraph {, node, edge, node's attribute, edges's attributes.



Movement timeline

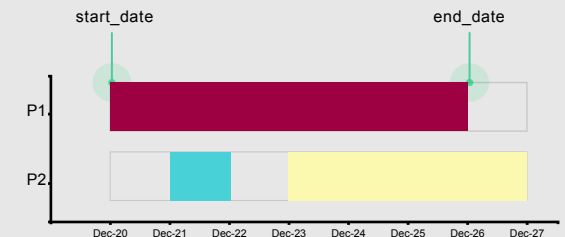
A table file describing an individual movements (e.g. patient) from time to time at a single or multiple locations, written in CSV

format. Column dates cannot empty and must written in **ISO 8601**

format (YYYY-MM-DD), and column *start_date* must be less than or

equal to column *end_date*.

| Mandatory headers and columns (Fixed header name) | | | | Optional |
|---|------------|------------|-----------|----------------|
| pid | start_date | end_date | location | 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 |



Dashboard Interface

Visualisation menu

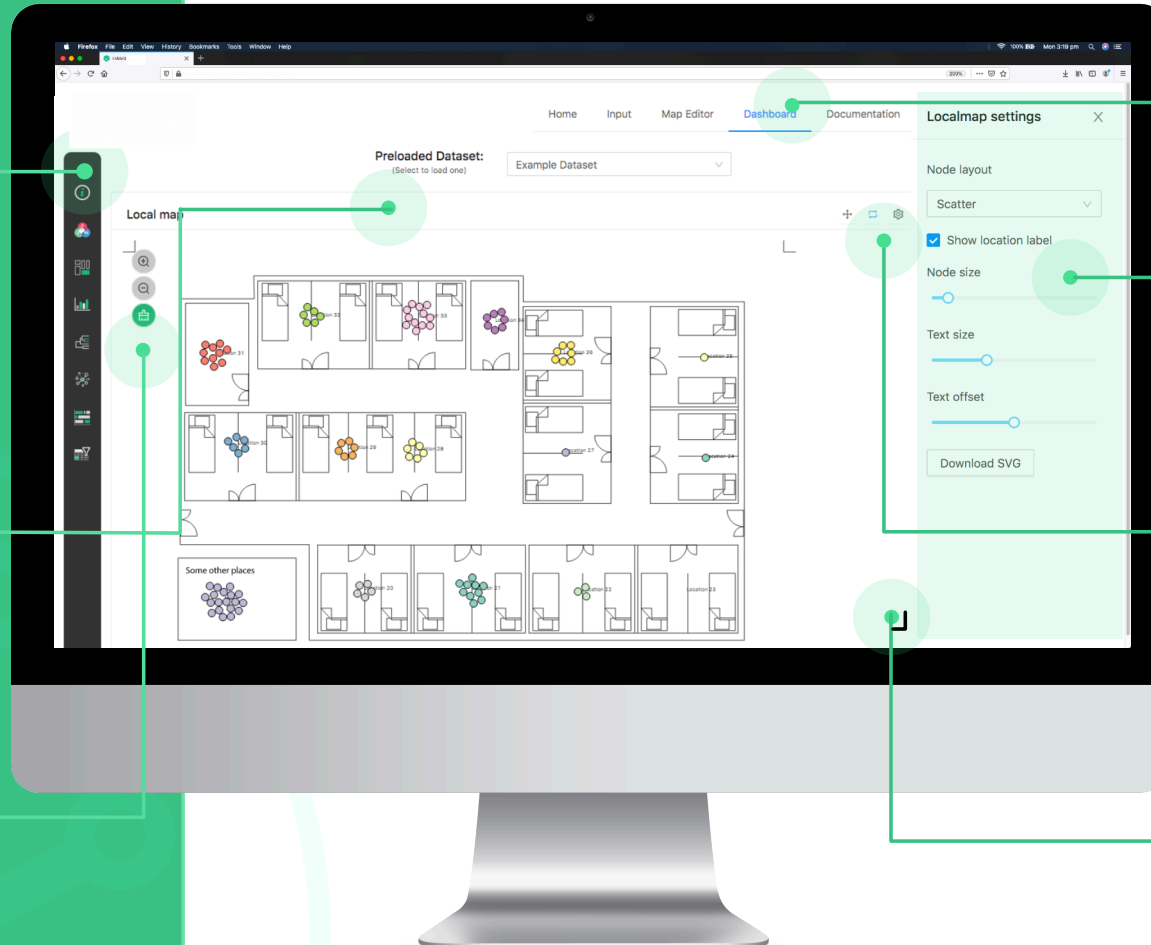
Host all visualisation windows. Each icon will be activated as soon as visualisation from your input file is ready. Click on the icon to display the window.

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.



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.

HALviz is showing page Dashboard with map window displayed. Coloured nodes (circles) represent isolates clustered based in their location. Users can click, mouseover, zoom, pan, change the node layout, node size, location text size and download the the visualisation result.



Creating local map

HALviz is showing page *Map Editor*. Users can start creating the map by loading an JPEG or PNG image. When the image file is loaded, users can add, rename, update or remove a location. A final map can be download for HALviz use.

- (!)
- For a map to be downloadable, at least one map location must be added.
 - Try open the downloaded Map (*haivizMap.xml*) in a text editor, you even can change the coordinates manually.
 - The x and y coordinates follow the input base map image (e.g. x=0 and y=0 will be the very top-left of the image).

Location labeller

Let you enter and update the name of a location.

Zoom controller

Let you zoom in and zoom out the map.

Location logger

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


Location marker

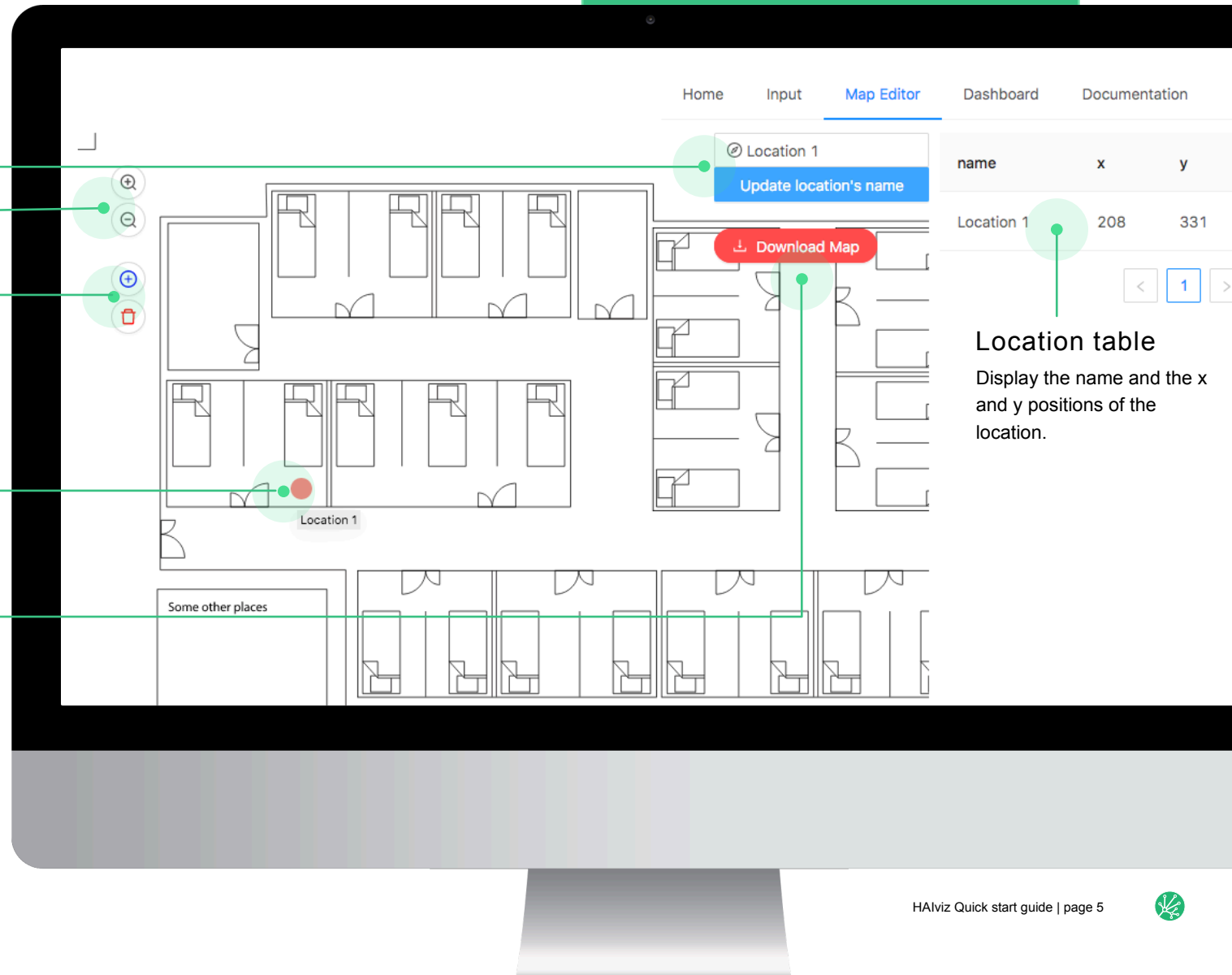
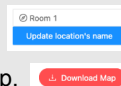
To remove or update location name, users can click or drag to select the marker. Mouse over the circle will display the location label.

Map downloader

Let you download the map for later usage or load the map directly to HALviz.

Five quick steps:

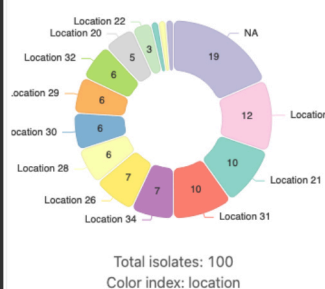
1. Add a location marker. 
2. Move the marker to the desired coordinate.
3. Set the label for the marker.
4. Click the 'Update location's name' to update.
5. Repeat steps 1 to 4, then click Download Map.



Preloaded Dataset:
(Select to load one)

Example Dataset

Piechart



Colour



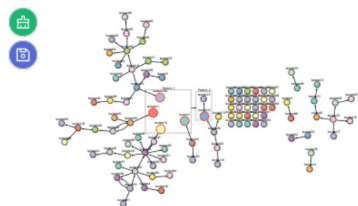
Map



Treemap



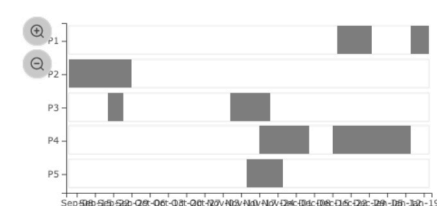
Network



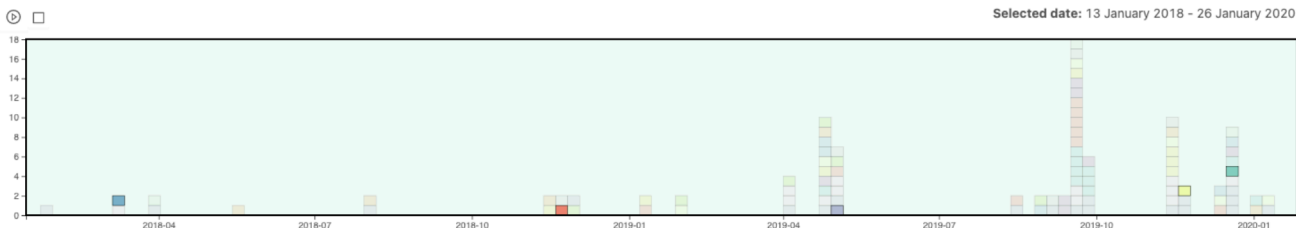
Phylogenetic tree



Gantt Chart



Epidemic Curve



Table

Row/s selected: 5 [Reset Selection](#) [Display Selected Row/s](#)

| <input checked="" type="checkbox"/> | ID | Date | Location | isolate_species | isolate_sourceType | isolate_sourceName | profile_1 | profile_2 | profile_3 |
|-------------------------------------|------------|------------|-------------|-----------------|--------------------|--------------------|-----------|-----------|-----------|
| <input checked="" type="checkbox"/> | Isolate1 | 2019-12-20 | Location 21 | Species1 | Patient | P1 | Sp1 ST 17 | ResGeneE | NA |
| <input checked="" type="checkbox"/> | Isolate10 | 2019-11-20 | Location 28 | Species1 | Patient | P4 | Sp1 ST 20 | ResGeneE | NA |
| <input checked="" type="checkbox"/> | Isolate100 | 2019-05-01 | NA | Species2 | Others | NA | Sp2 ST 17 | ResGeneE | NA |
| <input checked="" type="checkbox"/> | Isolate11 | 2018-11-19 | Location 31 | Species1 | Environment | Env5 | Sp1 NF | ResGeneB | NA |
| <input checked="" type="checkbox"/> | Isolate12 | 2018-03-10 | Location 30 | Species1 | Environment | Env6 | Sp1 ST 17 | ResGeneA | NA |

Interaction And Integration

• HALviz is showing the integrated and interactive visualisation windows in page *Dashboard* created from an example dataset.

• To demonstrate integration functionality, five isolates were selected from the table window and were highlighted in the other active windows.

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

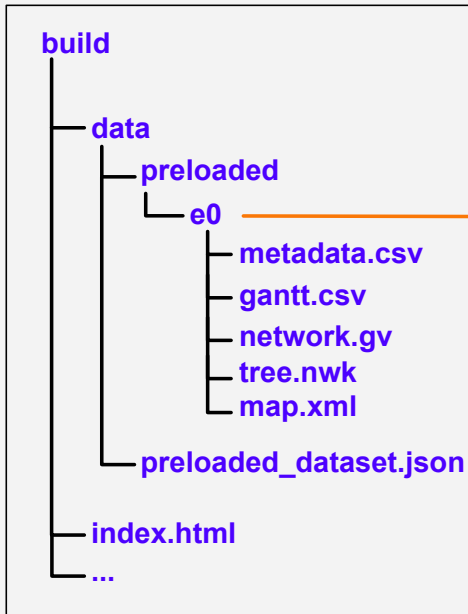
• Image produced by HALviz can be saved to an SVG format, enabling quick and flexible editing for report and publication.



Setting up preloaded dataset

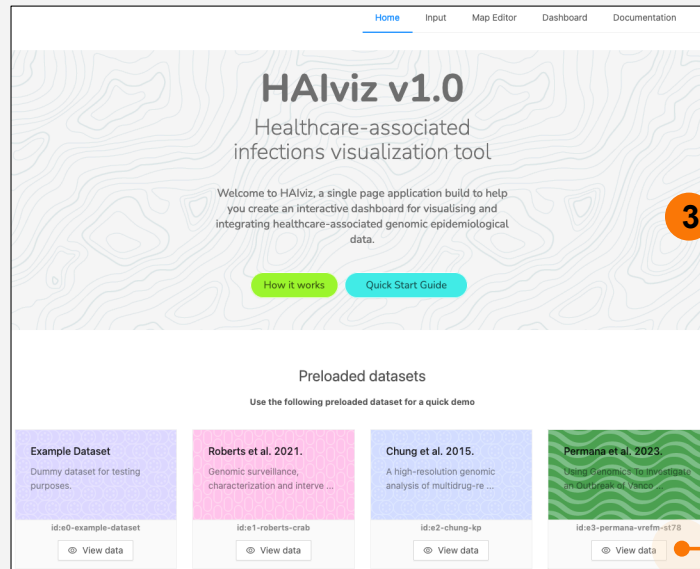
When users self-host or use HALviz offline, they can set up multiple preloaded datasets. This feature allows users to 'permanently' link their input files to HALviz, avoiding the need to manually re-inputting their input files.

Example of directory tree of HALviz build directory



1 Create a directory in the *preloaded* directory then add the input files.

2 Update the *preloaded_dataset.json* file



3 Datasets is listed in HALviz Home, Input, and Dashboard page.

Click View data (in page Home) or select from the preloaded dataset dropdown button (in page Input or Dashboard) to load the all input files to HALviz.

Example of preloaded_dataset.json file

```
{
  "data_list": [
    {
      "id": "e0-example-dataset",
      "name": "Example Dataset",
      "description": "Dummy dataset for testing purposes.",
      "metadata": "./data/preloaded/e0/metadata.csv",
      "map": "./data/preloaded/e0/map.xml",
      "tree": "./data/preloaded/e0/tree.nwk",
      "network": "./data/preloaded/e0/network.gv",
      "gantt": "./data/preloaded/e0/gantt.csv"
    }
  ],
  "description": ["This JSON file describes the preloaded datasets."]
}
```

An example R script to programatically setup the preloaded datasets is given in the `input_simulation` directory in HALviz repository : `setup_preloaded_dataset.R`.



THANK YOU

for reading this guide

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

```
"@nivo/pie": "^0.61.1",
"antd": "^4.2.0",
"babel-polyfill": "6.26.0",
"cytoscape": "^3.17.0",
"cytoscape-cose-bilkent": "^4.1.0",
"cytoscape-fcose": "^2.2.0",
"cytoscape-spread": "^3.0.0",
"cytoscape-svg": "^0.3.1",
"d3": "^5.16.0",
"d3-array": "^2.4.0",
"d3-color": "^1.4.1",
"d3-delaunay": "^5.2.1",
"d3-fetch": "1.1.0",
"d3-scale-chromatic": "1.2.0",
"dotparser": "^0.4.0",
"export-to-csv": "^0.2.1",
"immutable": "3.8.2",
"install": "^0.13.0",
"jscrambler": "^5.5.18",
"jspdf": "^2.5.1",
"lodash": "^4.17.15",
"moment": "^2.25.3",
"moment-range": "^4.0.2",
"npm": "^6.14.9",
"phylocanvas": "^2.8.1",
"phylocanvas-plugin-export-svg": "^1.0.0",
"phylocanvas-plugin-scalebar": "^1.1.1",
"prop-types": "15.6.1",
"react": "^16.13.1",
"react-app-polyfill": "^2.0.0",
"react-color": "^2.17.3",
"react-dom": "^16.13.1",
"react-faux-dom": "4.1.0",
"react-file-drop": "^0.2.8",
"react-grid-layout": "0.16.6",
"react-measure": "1.4.7",
"react-pdf": "^4.2.0",
"react-player": "^2.7.2",
"react-redux": "5.0.7",
"react-router": "^5.1.2",
"react-router-dom": "^5.1.2",
"react-scripts": "2.0.0",
"recompose": "0.26.0",
"redux": "3.7.2",
"redux-immutable": "4.0.0",
"redux-promise": "0.5.3",
"reselect": "3.0.1",
"resize-observer-polyfill": "^1.5.1",
"svgsaver": "0.9.0",
"uuid": "^8.0.0",
"xml-formatter": "^2.0.1",
"xml-js": "^1.6.11"
```



HALviz
Healthcare-Associated
Infections Visualization Tool



React-Grid
Layout

