GraphSNP USER MANUAL

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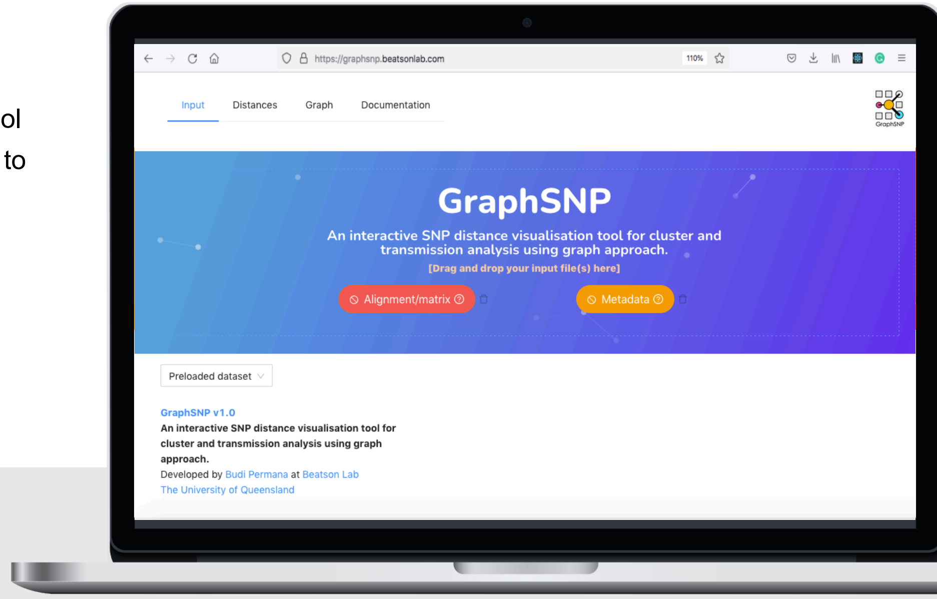
v.2022.09.07

Using GraphSNP

GraphSNP is an interactive visualisation tool running in a web browser that allows users to rapidly generate pairwise SNP distance networks, investigate SNP distance distributions, identify clusters of related organisms, and reconstruct transmission routes.



GraphSNP

An interactive SNP distance visualisation tool for cluster and transmission analysis using graph approach.

[Drag and drop your input file(s) here]

GraphSNP v1.0

An interactive SNP distance visualisation tool for cluster and transmission analysis using graph approach.

Developed by Budi Permana at Beatson Lab

The University of Queensland

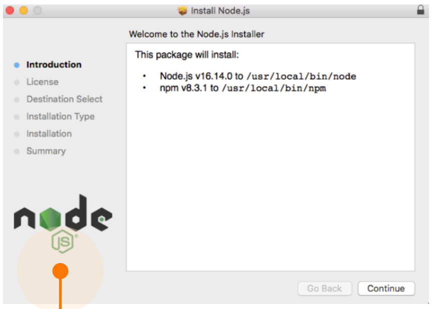
Use it online

GraphSNP is deployed in https://graphsnp.beatsonlab.com for online use. Users can visit the web page using the majority of modern browsers (e.g., Google Chrome, Firefox), drag and drop the input files, and instantly perform interactive data visualization and analysis.

Use it offline

Users also can use GrapSNP offline by serving it through a local HTTP server. GraphSNP SPA can be downloaded from https://github.com/nalarbp/graphsnp/build/.

Example of serving GraphSNP using HTTP-server "*serve*" tool

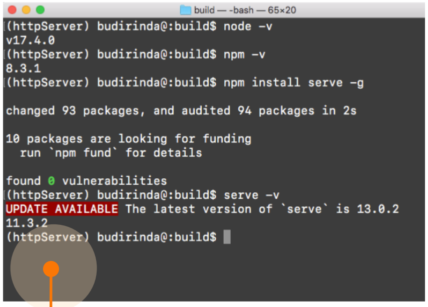


Welcome to the Node.js Installer

This package will install:

- Node.js v16.14.0 to /usr/local/bin/node
- npm v8.3.1 to /usr/local/bin/npm

Install Node.js
(available at https://nodejs.org/en/)



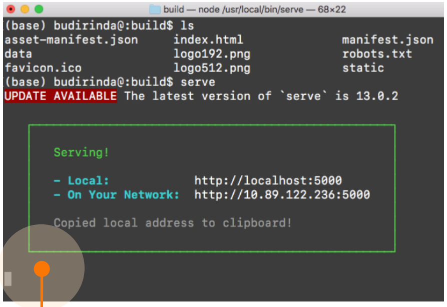
```
(httpServer) budirinda@:build$ node -v
v17.4.0
(httpServer) budirinda@:build$ npm -v
8.3.1
(httpServer) budirinda@:build$ npm install serve -g

changed 93 packages, and audited 94 packages in 2s

10 packages are looking for funding
  run `npm fund` for details

found 0 vulnerabilities
(httpServer) budirinda@:build$ serve -v
UPDATE AVAILABLE The latest version of `serve` is 13.0.2
11.3.2
(httpServer) budirinda@:build$ 
```

Install serve via npm
(npm install serve -g)



```
(base) budirinda@:build$ ls
asset-manifest.json     index.html              manifest.json
data                    logo192.png             robots.txt
favicon.ico             logo512.png             static
(base) budirinda@:build$ serve
UPDATE AVAILABLE The latest version of `serve` is 13.0.2

   ┌──────────────────────────────────────────────────┐
   │                                                  │
   │   Serving!                                       │
   │                                                  │
   │   - Local:            http://localhost:5000      │
   │   - On Your Network:  http://10.89.122.236:5000  │
   │                                                  │
   │   Copied local address to clipboard!             │
   │                                                  │
   └──────────────────────────────────────────────────┘
```

Run the HTTP server
(serve .)

Input Files

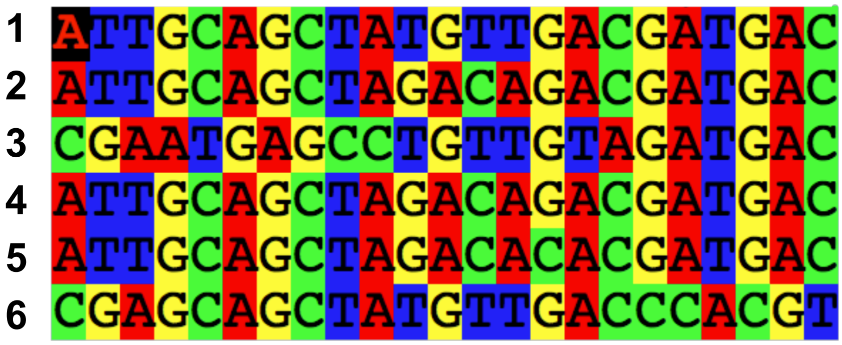
SNPs alignment

A text file containing a minimum of two equal lengths of fasta-formatted non-gap ATGC-exclusive nucleotide sequences (when other caharacters (e.g., N, '-') and or specific models need to be taken into account, users can use distance matrix generated by other tools, instead of alignment).

Example SNPs alignment input *(sample.fasta)*

```
>1
ATTGCAGCTATGTTGACGATGAC
>2
ATTGCAGCTAGACAGACGATGAC
>3
CGAATGAGCCTGTTGTAGATGAC
>4
ATTGCAGCTAGACAGACGATGAC
>5
ATTGCAGCTAGACACACGATGAC
>6
CGAGCAGCTATGTTGACCCACGT
```

Sample ID in fasta header


1 ATTGCAGCTATGTTGACGATGAC
2 ATTGCAGCTAGACAGACGATGAC
3 CGAATGAGCCTGTTGTAGATGAC
4 ATTGCAGCTAGACAGACGATGAC
5 ATTGCAGCTAGACACACGATGAC
6 CGAGCAGCTATGTTGACCCACGT

Pairwise distances matrix

Example of pairwise SNP distances matrix *(sample_matrix.csv)*

dist	1	2	3	4	5	6
1	0	4	12	4	5	9
2	4	0	16	0	1	13
3	12	16	0	16	17	15
4	4	0	16	0	1	13
5	5	1	17	1	0	14
6	9	13	15	13	14	0

Matrix in CSV format

```
dist,1,2,3,4,5,6
1,0,4,12,4,5,9
2,4,0,16,0,1,13
3,12,16,0,16,17,15
4,4,0,16,0,1,13
5,5,1,17,1,0,14
6,9,13,15,13,14,0
```

User can also input the pairwise distances matrix instead of SNP alignment. The symmetric matrix should be written in comma-separated value (CSV) format.

Metadata

A table contains information about the isolates or sample, written in CSV format. Critical requirements including: mandatory headers, no duplicated records in column **sample_id**. Column **collection_day** is required for transmission analysis.

Mandatory column — Mandatory column for transmission analysis — Any additional column — Columns to set the color

sample_id	collection_day	Location	Source	Clade	Gene-A	Source:color	Gene-A:color
1	1	room A	clinical	A	present	#FF8076	Black
2	2	room B	clinical	A	present	#FF8076	Black
3	3	room C	clinical	A	present	#FF8076	Black
4	3	room A	environmental	A	absent	#53DE22	White
5	4	room B	environmental	A	absent	#53DE22	White
6	5	room C	environmental	A	absent	#53DE22	White

Main Interface

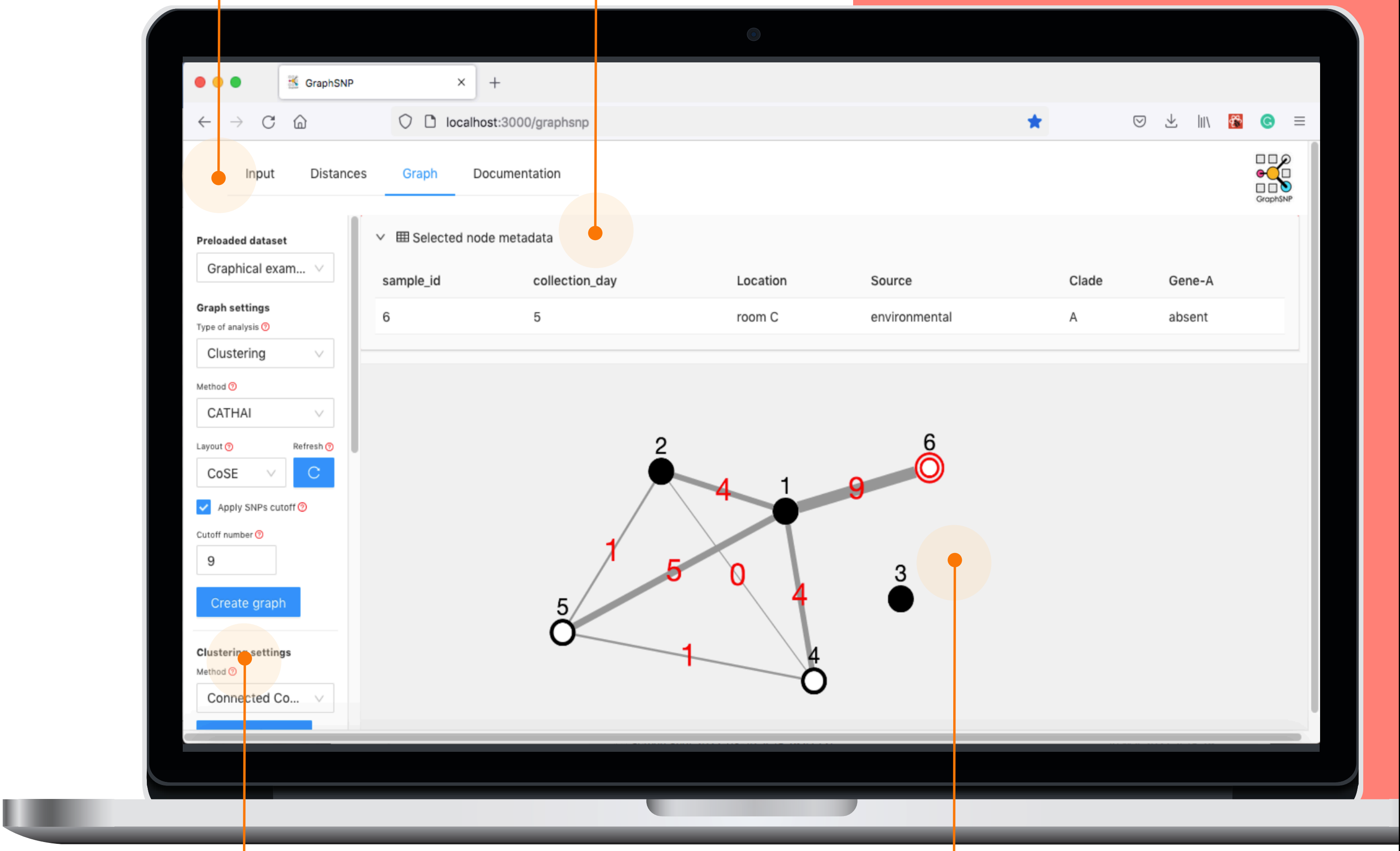
page *Graph*

Page navigation

Navigation menu to let you jump between pages: *Input, Distances, Graph, and Documentation.*

Metadata table

Let you display metadata associated with selected node(s).



GraphSNP

localhost:3000/graphsnp

Input | Distances | Graph | Documentation

Preloaded dataset

Graphical exam...

Graph settings

Type of analysis: Clustering

Method: CATHAI

Layout: CoSE

Refresh

☑ Apply SNPs cutoff

Cutoff number: 9

Create graph

Clustering settings

Method: Connected Co...

Selected node metadata

sample_id	collection_day	Location	Source	Clade	Gene-A
6	5	room C	environmental	A	absent

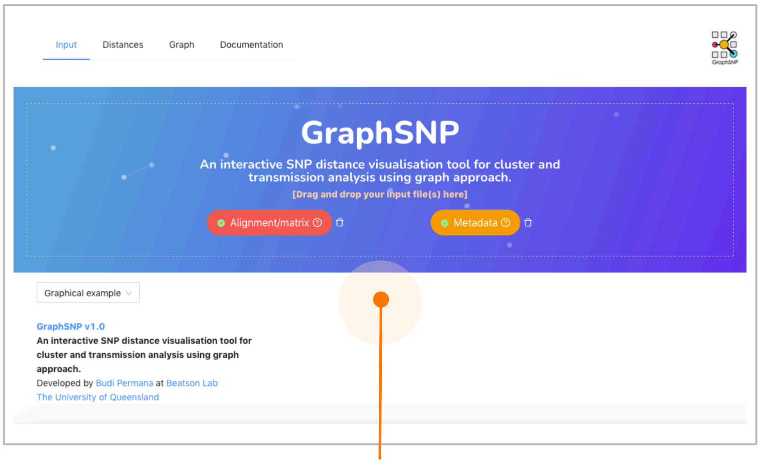
Sidebar settings

A sidebar menu provides you a control to adjust the visualisation.

Graph visualisation window

A window container where the interactive graph is being rendered.

page *Input*



Input | Distances | Graph | Documentation

GraphSNP

An interactive SNP distance visualisation tool for cluster and transmission analysis using graph approach.

[Drag and drop your input file(s) here]

Alignment/matrix | Metadata

Graphical example

GraphSNP v1.0

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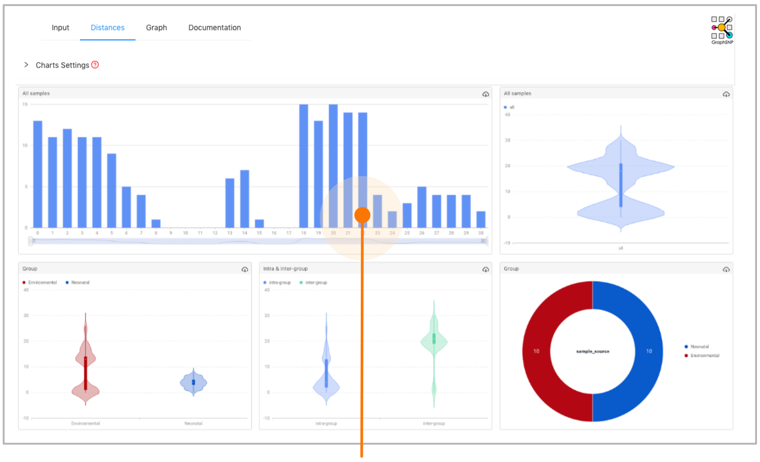
Developed by Budi Permana at Beatson Lab

The University of Queensland

page *Distances*



Input | Distances | Graph | Documentation

Charts Settings

Input placeholder

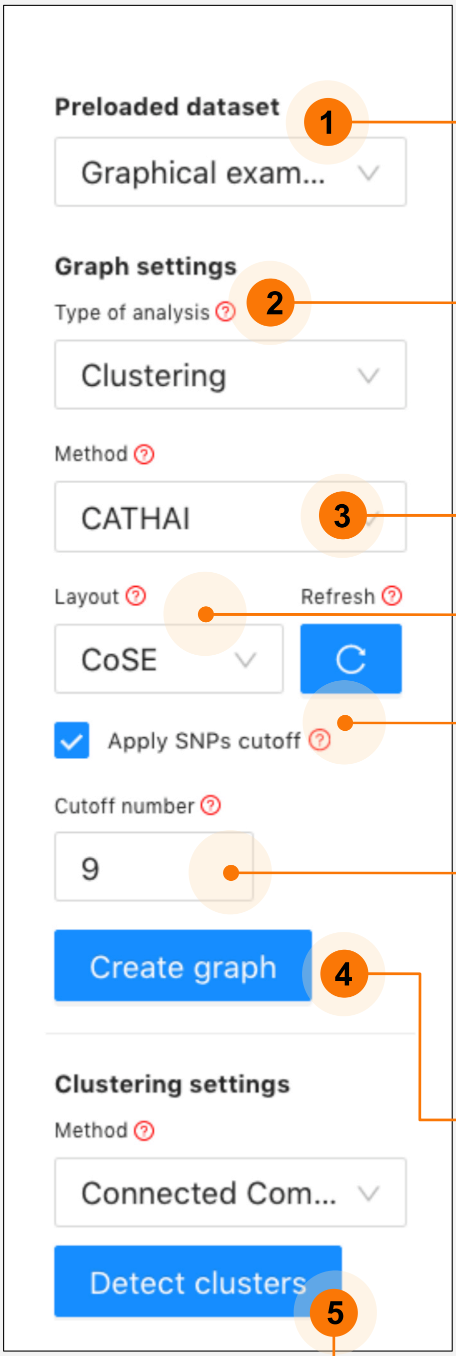
Drag and drop your input files here.

Chart visualisation window

A container where charts showing pairwise distances, like bar chart, is being rendered.

Cluster analysis

Users can perform cluster analysis and visualization by five simple steps: Loading the input files, select clustering as the type of analysis (another type is transmission analaysis), select the clustering method, create the Graph and detect cluster from the Graph.



Preloaded dataset: Graphical exam...

Graph settings

Type of analysis: Clustering

Method: CATHAI

Layout: CoSE

Refresh

☑ Apply SNPs cutoff

Cutoff number: 9

Clustering settings

Method: Connected Com...

1 **Load input files**

2 **Select Clustering**

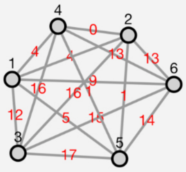
3 **Select reconstruction method**

Select which layout to display the Graph.

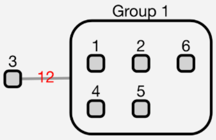
Apply a cutoff number to limit the maximum pairwise distance value to be displayed

Set cut-off value

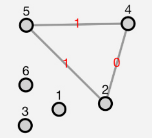
4 **Create Graph**



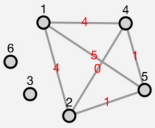
Network: *an undirected Graph based on pairwise distances. Node represents individual isolate. Edge represents distance.*



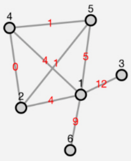
Minimum spanning tree (MST): *MST of single-linkage cluster when a cut-off is applied to the network. Node represents individual or group of isolates. Edges represents a minimum distance.*



Cut-off = 1

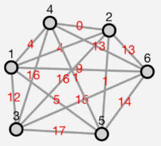


Cut-off = 5



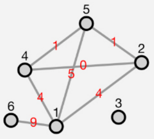
Cut-off = 12

□ Apply SNPs cutoff



No cut-off value was applied, thus all edges were displayed.

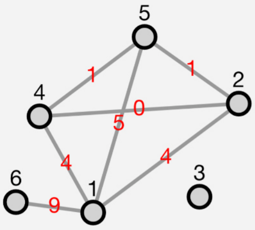
☑ Apply SNPs cutoff



A cut-off of 9 was applied.

5 **Identify cluster**

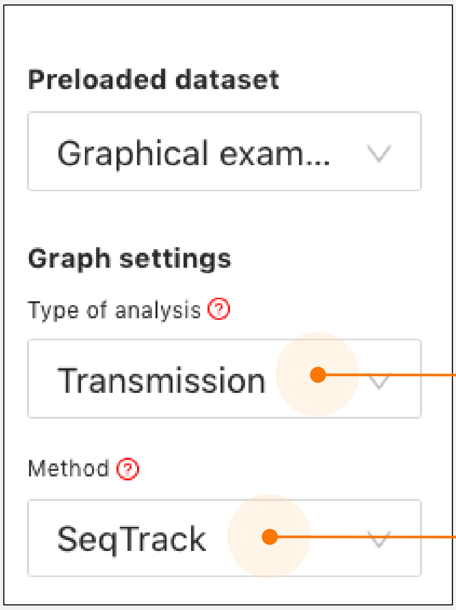
A cluster is defined by a sinlge-linkage clustering approach (e.g., Interconnected nodes are belong to the same cluster).



sample	clusterID
1	1
2	1
4	1
5	1
6	1
3	na

The clustering result can be downloaded as ***a CSV file****.*

Transmission analysis



Preloaded dataset

Graphical exam...

Graph settings

Type of analysis: Transmission

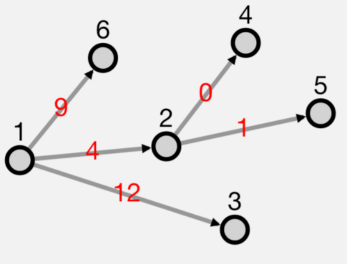
Method: SeqTrack

Performing transmission analysis is similar to cluster analysis. Users only need to select Transmission instead of Clustering. Currenltly, only one method is implemented: SeqTrack [1]

1. Jombart, T., et al., *Reconstructing disease outbreaks from genetic data: a graph approach.* Heredity (Edinb), 2011. **106**(2): p. 383-90.

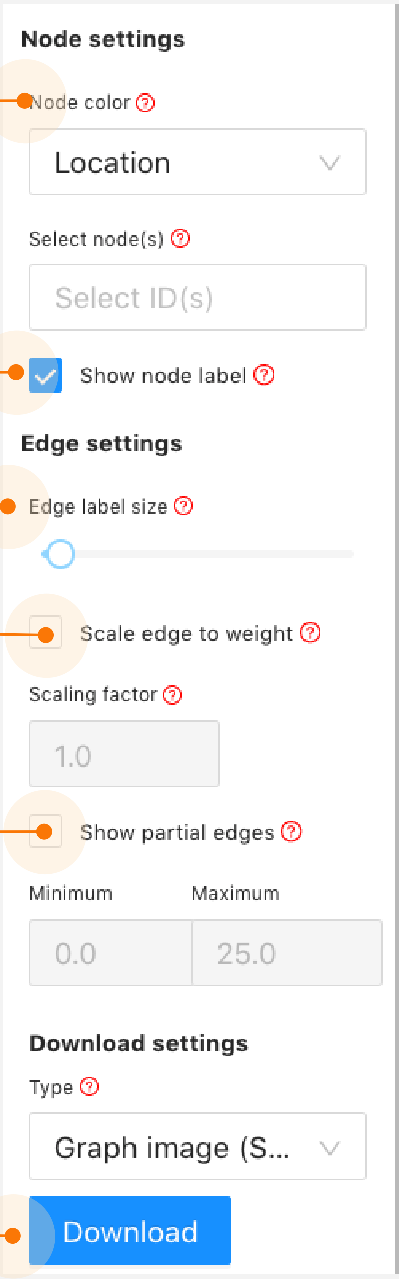
Select Clustering

Select reconstruction method



Most parsimonious transmission tree created using SeqTrack algorithm.

Graph settings



Node settings

Node color: Location

Select node(s): Select ID(s)

☑ Show node label

Edge settings

Edge label size

☐ Scale edge to weight

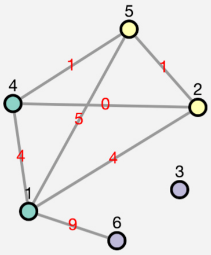
Scaling factor: 1.0

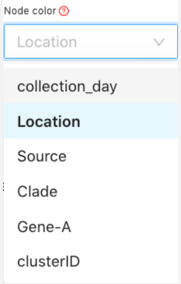
☐ Show partial edges

Minimum: 0.0 Maximum: 25.0

Download settings

Type: Graph image (S...

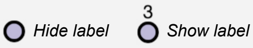


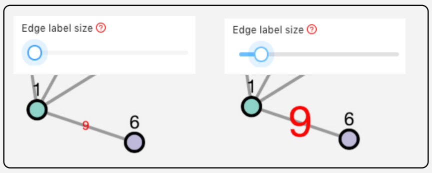


Color nodes by the selected column in metadata or by the clustering result.

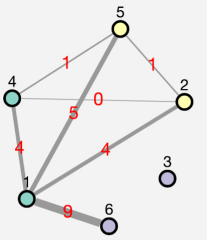
Here, we color the nodes based on Location column in metadata.

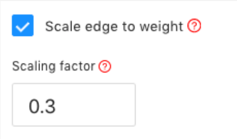
Show or hide node's label.





Change edge label size



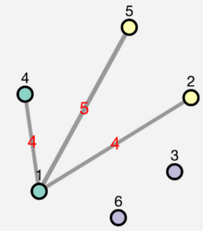


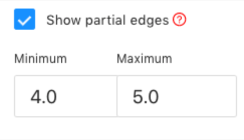
☑ Scale edge to weight

Scaling factor: 0.3

Here, we scale the edges with factor of 0.3

Change the thickness of the edge according to its weight. (e.g., the higher the SNP distance the thicker the line).





☑ Show partial edges

Minimum: 4.0 Maximum: 5.0

Here, only edges with distance 4 and 5 were displayed.

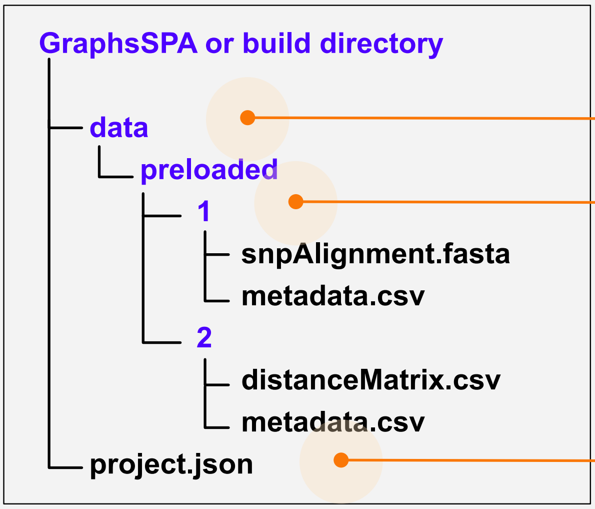
Only show edges which have weight within the specified range (min to max) (Note: It doesn't remove the edges but only hide it to the background)

Download Graph image (SVG) or Graph file (DOT) or clustering result (CSV)

Setting up preloaded dataset

When users use GraphSNP offline, they can set up multiple preloaded datasets. This feature allows users to 'permanently' link their input files to GraphSNP, avoiding the need to re-inputting their input files every time the browser refreshed.

Example of directory tree of GraphSNP preloaded datasets



```
GraphsSPA or build directory
 ├ data
 │  └ preloaded
 │     ├ 1
 │     │  ├ snpAlignment.fasta
 │     │  └ metadata.csv
 │     └ 2
 │        ├ distanceMatrix.csv
 │        └ metadata.csv
 └ project.json
```

1 **Go to directory of *data* in GraphSNP SPA**

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

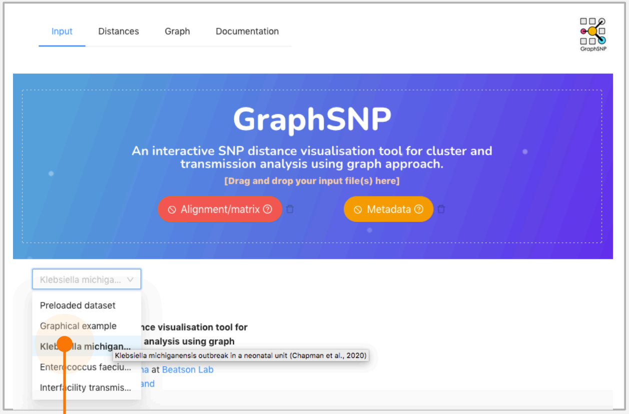
3 **Update project.json file**

Add the dataset ID and input files path to project.json and save the file.

Example project.json content

```
{
  "projects": [
   {
    "id": "1",
    "name": "Dataset 1: Graphical example",
    "matrixOrAlignment": "alignment",
    "snpDistance": "./data/preloaded/1/snpAlignment.fasta",
    "metadata": "./data/preloaded/1/metadata.csv"
   },
   {
    "id": "2",
    "name": "Dataset 2: NCBI Cluster of VREfm ST78",
    "matrixOrAlignment": "matrix",
    "snpDistance": "./data/preloaded/2/distanceMatrix.csv",
    "metadata": "./data/preloaded/2/metadata.csv"
   }
  ],
  "description": "This JSON file describes preloaded datasets to be rendered in the landing page. The path of these files must be written with directory 'public' as the root (e.g. ./data/ means 'data' is inside directory 'public'"
}
```

4 **Datasets is listed in GraphSNP *input* page**



GraphSNP

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[Drag and drop your input file(s) here]

Klebsiella michiganensis outbreak in a neonatal unit (Chapman et al., 2020)

Click the preloaded dataset dropdown button and select dataset of interest and GraphSNP will automatically load the input files.

React Data-Driven Documents

Ant Design Cytoscape

THANK YOU

for reading this manual

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

react
d3
antd
cytoscape
redux
bio-parsers
graphlib-dot
hamming
kruskal-mst
lodash
moment
ve-sequence-utils

GraphSNP