

# HOWTO: Build and visualize a neighbor-joining tree from Gigwa SNP data, all online

Step 1: Exporting SNP data from <https://gigwa.southgreen.fr>

The screenshot shows the Gigwa web interface. On the left, there are filters for variant types, sequences, position, and variant IDs. The main area displays a list of SNPs with columns for ID, chromosome, position, and alleles. An 'Export format' dialog box is open, showing 'FASTA' as the selected format. The 'Exported individuals' section is set to 'Group 1'. The 'Export metadata' checkbox is checked, and a list of metadata fields is visible: Status, Comments, Variety name, GroupK9, Country, Region, and Region\_T. The 'Keep files on server' checkbox is also checked. An 'Export' button is at the bottom of the dialog.

- Tips:
- Make sure you select the individuals that you want to appear in the tree (no more, no less)
  - Select the FASTA (pseudo-alignment) export format, and check the “Keep files on server” box
  - In order to be able to color tree nodes using metadata, export some too

Export will result in the display of this blue box: (don't close it, don't close the browser tab either!)


The screenshot shows the same Gigwa web interface as before, but with a blue notification box overlaid. The box contains the following text: 'Export file will be available at this URL for 48h: DIVRICE\_3k10M\_extended\_\_project1\_\_2023-09-14\_\_1239variants\_\_FASTA.zip'. Below the URL are two buttons: 'Send exported data to Galaxy' and 'Send tsv file(s) to Taxonium metadata color configurator'.

## Step 2: Feeding a Galaxy instance with the obtained FASTA file

You will want to work with a Galaxy instance that contains the RapidNJ software (for example <https://usegalaxy.fr/>, <https://usegalaxy.eu/> or <https://usegalaxy.org/>). Two options here:

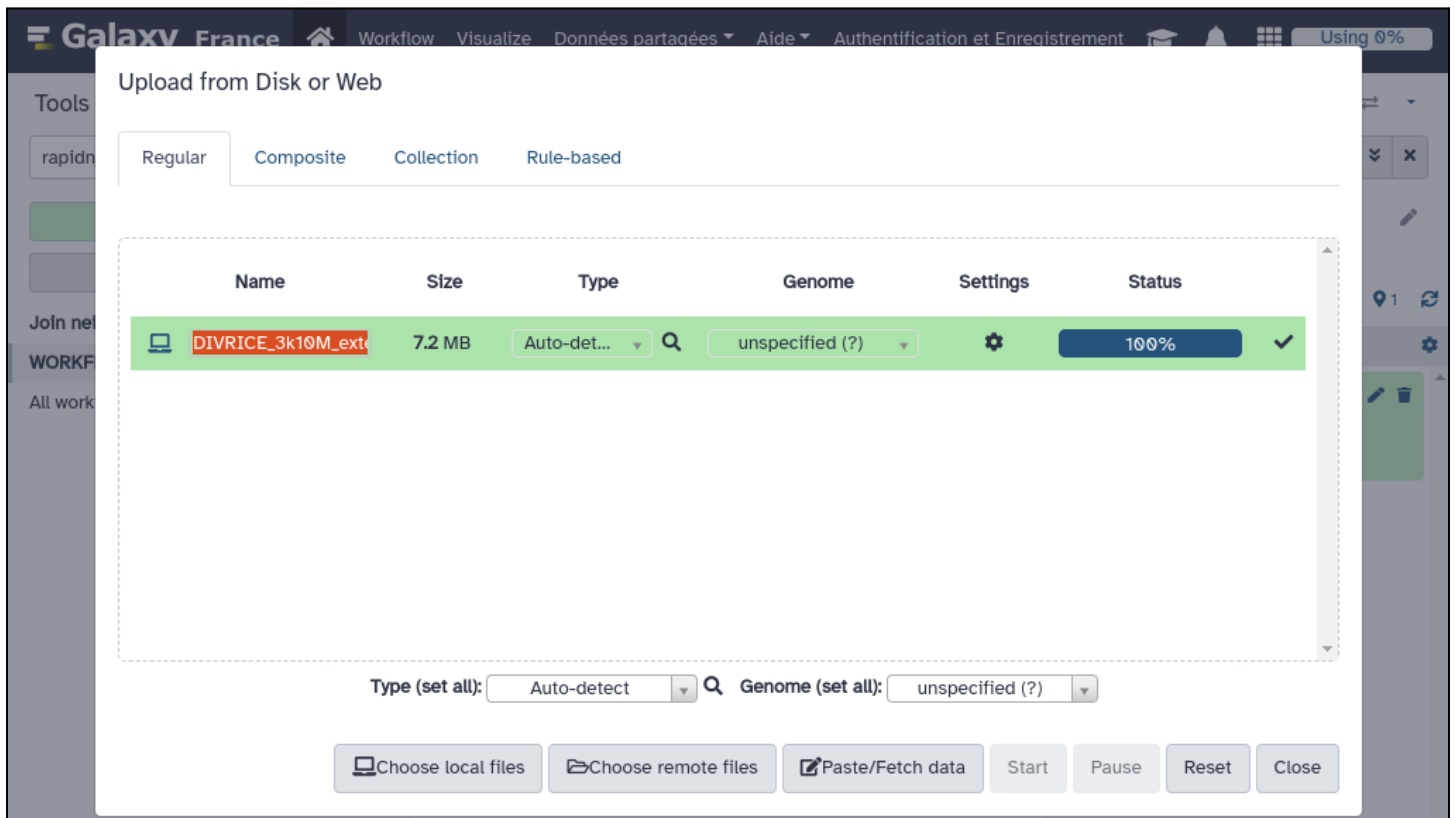
1/ “Hardcore” method, for advanced users, who don’t even need a screenshot ;-)

If you are familiar with Galaxy, have an account on a suitable instance, and know how to obtain an API key, you may:

- Provide Gigwa with the instance URL using this icon 
- Click on the “Send exported data to Galaxy” button in the blue export box
- Paste your API key

=> exported files will be directly sent to a history named “<https://gigwa-gigwa.southgreen.fr/>”

2/ “Simple” method, not requiring a Galaxy account:



- Download and unzip the export file whose link appears in the blue export box
- In a different browser tab, open the Galaxy instance of your choice and click “Upload data” (top-left corner)
- Click “Choose local files”, select the exported FASTA file, click Start then Close
- On the right-hand side panel, an area representing that file will appear as part of the current history (list auto-managed by Galaxy, that grows while new files are generated as you do things with existing ones)

## Step 3: Building the neighbor-joining tree with rapid NJ

Once the fasta file shows in green in the history it means it’s ready to use (upload job is done). Then:

- In the “Search tools” textbox type “rapidnj” then click on lookup result “Join neighbors rapidly with RapidNJ”
- The RapidNJ parameter configuration page appears in the middle: we want a Newick tree as output, built using Jukes-Cantor evolution model (unless you prefer Kimura), with DNA as “Input alignment type”. Click “Run Tool”
- A new file will be added to the history. Its background color will evolve as follows: grey for “in the waiting queue”, orange for “being processed”, green for “successfully generated”.

Galaxy France

Workflow Visualize Données partagées Aide Authentification et Enregistrement Using 0%

Tools

rapidnj

Upload Data

Show Sections

Join neighbors rapidly with RapidNJ

WORKFLOWS

All workflows

Join neighbors rapidly with RapidNJ (Galaxy Version 2.3.2)

Run Tool

Tool Parameters

Input to construct or reconstruct trees \*

1: DIVRICE\_3k10M...

Output format \*

Phylogenetic tree in newick format

(--output-format)

Evolution model \*

Jukes-Cantor

Specifies which sequence evolution method to use when computing distance estimates from multiple alignments, using Kimura's model by default. (--evolution-model)

Samples to use for computing bootstrap - optional

The output tree will be annotated with bootstrap values (--bootstrap)

Input alignment type \*

DNA

(--alignment-type)

Adjust for negative branch lengths.

No

(--no-negative-length)

Run Tool

History

Rechercher des données

Unnamed history

7.54 MB

1 : DIVRICE\_3k10M\_extended\_1239variants\_3025Individuals.fasta

When tree calculation is complete, history contents will look as follows when selecting the new file:

2 : Join neighbors on data 1: C alculated distances

1 line

format nhx, génome de référence ?

0.00% 0.03% 0.07% 0.10% 0.13%  
0.17% 0.20% 0.23% 0.26% 0.30%  
0.33% 0.36% 0.40% 0.43% 0.46%

1 : DIVRICE\_3k10M\_extended\_1239variants\_3025Individuals.fasta

Download the tree by clicking on its floppy disk icon.

#### Step 4: Configuring node colors accounting for metadata (may be done while step 3 is running)


Go back to the Gigwa export page and click on the “Send tsv file(s) to Taxonium metadata color configurator” button:

## Taxonium metadata color configurator

Metadata column:

Select field values:

- admix
- cA (Aus)
- cB (Bas)
- GJ-adm
- GJ-sbtrp
- GJ-tmp
- GJ-trp
- XI-1A
- XI-1B
- XI-2
- XI-3
- XI-adm

Pick a color: 

Newick tree URL (optional, for direct display)

URL of Taxonium instance to work with

Open in separate window


Choose the metadata column you want to use for coloring, then select values (in batch if needed) and pick colors (don't forget to click Save to validate a color selection). Those settings are persisted in your web browser's local-storage and will automatically be reloaded if you provide this interface with the same metadata again. Open Taxonium by clicking the button at the bottom of the page.

#### Step 5: Providing Taxonium with tree and metadata files, and launching visualization


## Taxonium

Welcome to Taxonium, a tool for exploring large trees

Input files

 DIVRICE\_3k10M\_extended\_3025individuals\_metadata.tsv (113.57 KB)

The left-most column in your metadata must be the name of the taxon.

 Galaxy2-[Join\_neighbors\_on\_data\_1\_Calculated\_distances].nhx (114.99 KB)

Ladderize tree

Now you need to select 2 files for upload:

- The .tsv metadata file you found in the zip archive downloaded from Gigwa (format: Metadata TSV)
- The .nhx tree file you built with RapidNJ and downloaded from Galaxy (format: Newick tree)

Once this is done, click “Launch Tanoxium” and you will be able to visualize your tree with pre-configured colors:

