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

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

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!)

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:
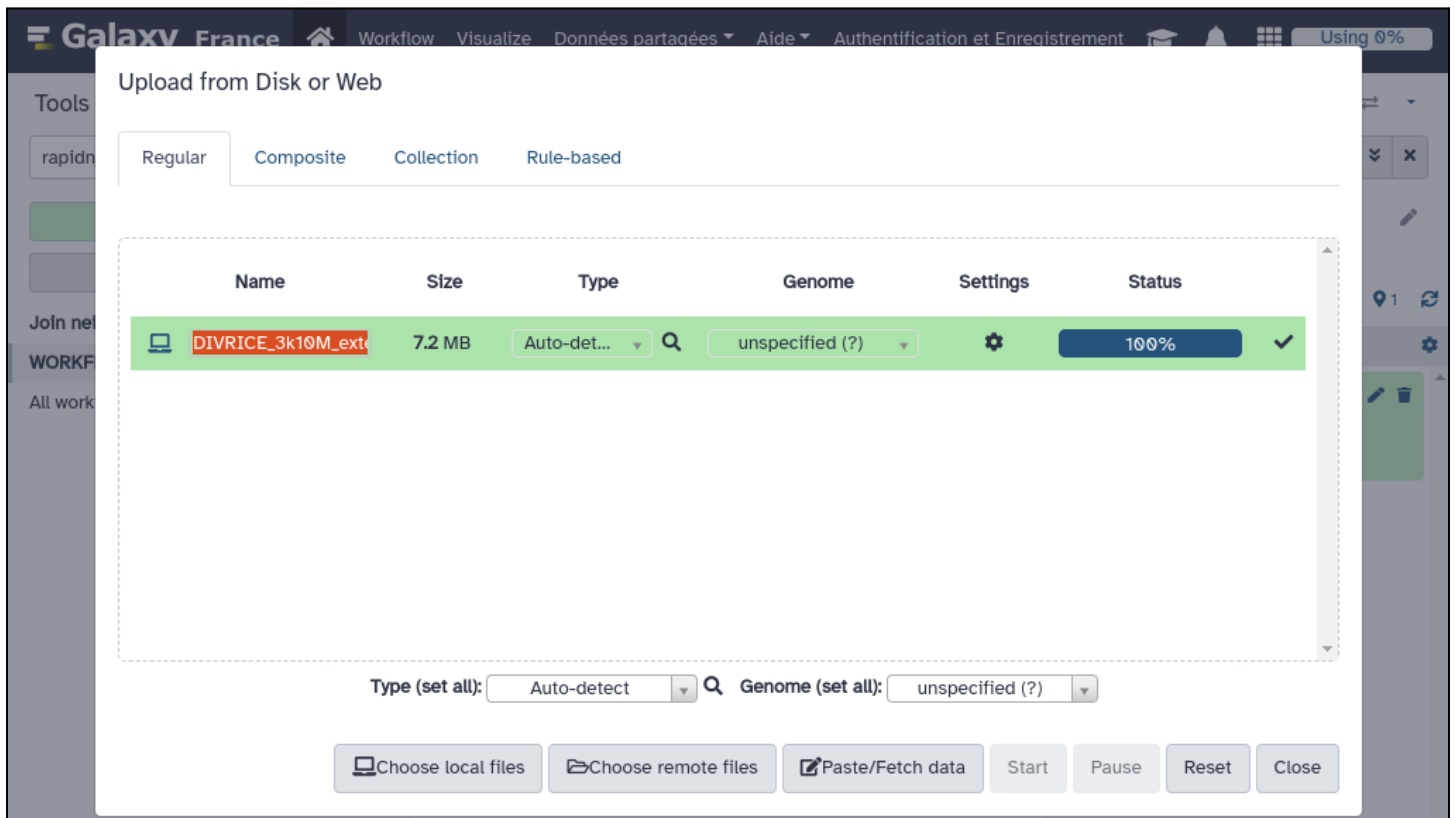
- Download and unzip the export file whose link appears in the blue export box
- In a different browser tab, open the Galaxy instance of your choice and click "Upload data" (top-left corner)
- Click "Choose local files", select the exported FASTA file, click Start then Close
- On the right-hand side 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".

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

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:

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

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: