



Microbes Genotyping

User Guide – version 1.4.0

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1 Introduction and basics

The aim of this site is to facilitate microbes (including pathogenic bacteria) genotyping essentially for epidemiological surveillance purposes. **MicrobesGenotyping** makes data from a genotyping assay easily accessible. The data may be derived *in silico* from whole genome sequence data. Low cost and low resolution typing may be useful as part of routine quality-checking of strain identity, or as a first-line exclusion assay in an outbreak investigation prior to whole genome sequencing.

Typing is sequence-based. Any data which fits in a table, as derived for instance from assays such as polymorphic tandem repeat typing (MLVA for Multiple Loci VNTR analysis) or sequence typing (MLST for Multiple Loci Sequence Typing) or Single Nucleotide Polymorphism (SNP) typing can be managed.

More specific information on individual databases and associated assays can be found on dedicated support websites (links to articles, protocols, primer information).

What is a database ?

A database is an interactive presentation of typing data. **MicrobesGenotyping** can support any numerical data. A database can be queried, viewed or exported. It can be shared with other registered users or made public.

What is a query ?

A query is a comparison of a genotype (a string of allele values) to the genotypes present in a database. A database is selected, then a set of markers representing an assay is chosen, before submitting data from one isolate. The results list the closest genotypes present in the database. The distance between two genotypes is the number of different alleles (categorical or Hamming distance). A Newick format tree can be exported for drawing in dedicated software, as well as the matrix distance or genotyping data for the closest strains.

Whats is a view ?

A View displays all strains present in a database. Fields can be hidden. Lines can be sorted according to field content. The database creator or administrator may have made accessible extra general information on the database on an independent web site, the URL will be indicated.

What is a CSV file ?

A CSV file (comma-separated values) stores tabular data in a plain-text form. Each record contains a number of fields, separated by a comma ("," most used format or ";" french-style format).

2 Getting started

2.1 Creating an account

2.1.1 Difference between guests and users

Guests (no account required) can query, view and export public databases. In addition a logged-in user can create, import, query, view and manage databases, including sharing them with other users, or making them public.

2.1.2 Create an account

To create an account, click on the "Sign Up" button in the home page menu bar, and follow the instructions. Registration is free. If the account creation is successful, you will be redirected to the "Edit Profile" page and you will receive an email.

2.1.3 Login

Account owners can click on “Log In” and fill the login form with their credentials.

2.2 Editing account information

Click on username in the “users” menu (Figure 1).

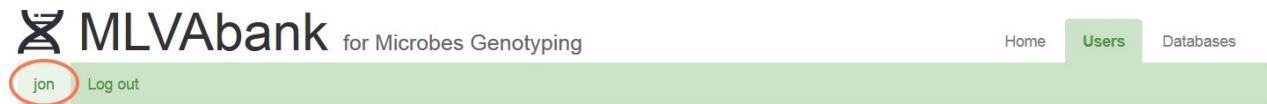


Figure 1: Accessing the profile page

The left-end form manages login credentials (email, password) and the right-end is optional profile information. Forms need to be saved separately.

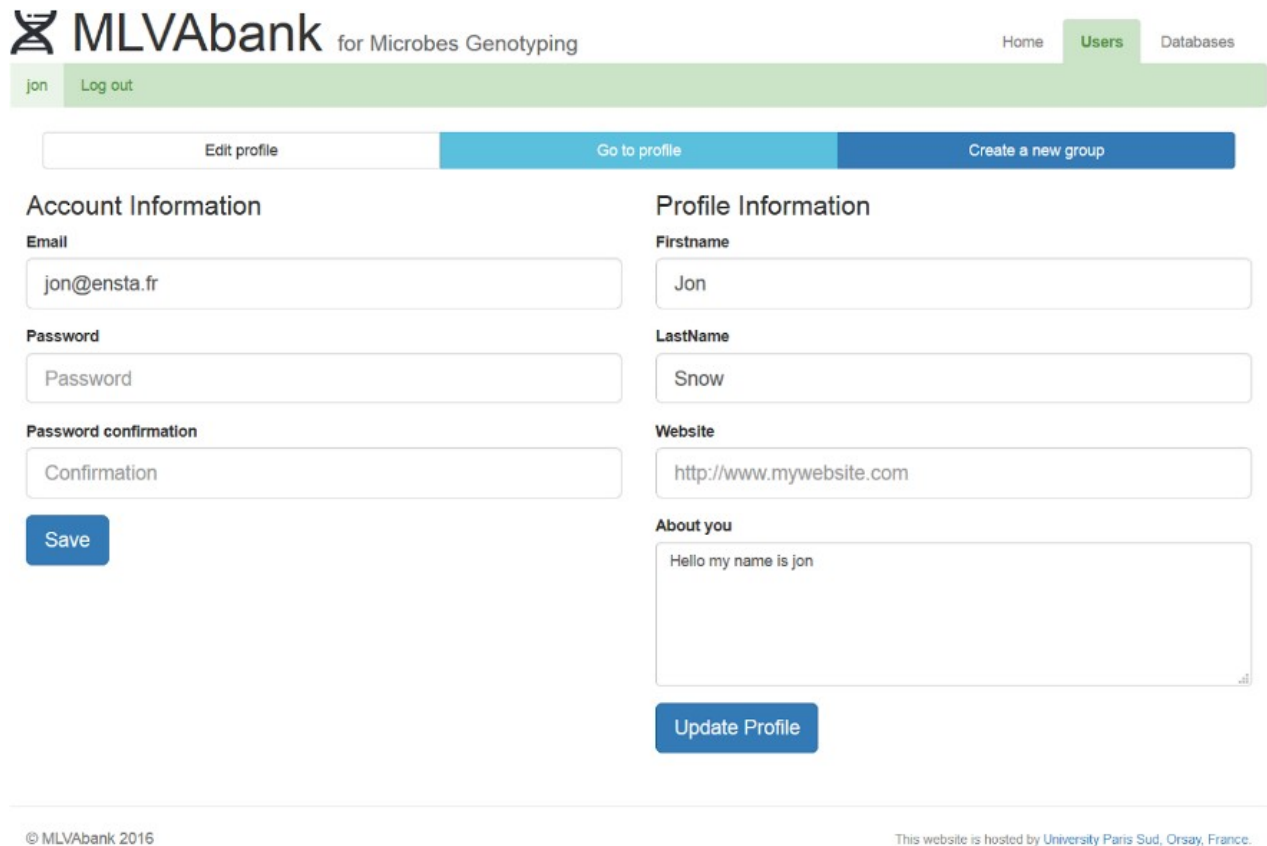


Figure 2: Editing account and profile information

2.3 Creating a group

To create a group, click on username in the users menu (Figure 1) and then on the “create a new group” tab. Provide name, description and choose the members of this group (Figure 3; the creator is automatically included but can be removed). Alternatively, a group can be created while importing a database.

Create a new group

Name (spaces will be removed, please use dashes)

Description of the group

Members of this group

Figure 3: Creating a new group

2.4 Editing a group

Members of a group are allowed to edit the group. Access the editing page by clicking on “my databases” in the database menu and then on “edit” next to the group name. Name and description can be changed, users can be added and removed (Figure 4).

Members of this group

xjon an
antonin
brendan

Figure 4: Editing group members

2.5 Join a group

New members can be added by a current member.

2.6 Forgotten password

Click on “Forgotten password” on the login page and fill the form with the email associated with the account. The password will be reset and an email with the new password will be sent.

3 Managing databases

3.1 Creating databases

Log-in, select “Databases > Create New Database”. Choose a CSV file to upload. It is not possible to use different delimiters (for instance tab and “,”) in the same CSV file. Press “Submit” to create the database. It may take a while if there are a lot of data. Fields can be used to create hyperlinks (contact e-mail address, URL link to publication or sequence file, etc.).

Tip: export data from a public database to obtain an example CSV file.

Create a new database

General information

1 **Database Name**
Burkholderia

Database Support Website
Database Support Website

Database Description

2 **Database Type**
Personal

Is that database public ?

3 **Database Content**

Upload a CSV File
Parcourir... Burkholderia.csv

Import Panels (2 panels)
 Import Strains (189 strains)

4 **Geolocalisation column**
Use Lon/Lat

Create the new database

Name	Key - Name	Information	MLVA Data	Ignore
key	<input checked="" type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
collection	<input type="radio"/>	<input checked="" type="radio"/>	<input type="radio"/>	<input type="radio"/>
strain	<input type="radio"/>	<input checked="" type="radio"/>	<input type="radio"/>	<input type="radio"/>
species	<input type="radio"/>	<input checked="" type="radio"/>	<input type="radio"/>	<input type="radio"/>
Country	<input type="radio"/>	<input checked="" type="radio"/>	<input type="radio"/>	<input type="radio"/>
Collection Year	<input type="radio"/>	<input checked="" type="radio"/>	<input type="radio"/>	<input type="radio"/>

5

Figure 5: Import form

Indicate (Figure 5):

1. Database name
2. the group can be a pre-existing group or a new group. Select “personal” if the database is not shared within a group.
3. the status (public or not) of the database
4. the geolocalisation information field (cf [Accessing geographic view](#))
5. the type of each field to be imported from the CSV file. One field must be defined as the key and contain a unique identifier for each strain. The other fields can be either metadata (such as geographic origin, host, contact, etc.) or typing data. Fields without type assignment will not be imported.

Note: field names should not contain special characters (such as <, >, /, ...). Link to another site, publication, or email address are defined using parentheses: contact_name(example@email.com). Avoid special character(s) such as “é”, “è”, “i” etc in “contact_name”.

3.2 Browsing databases

Public databases can be viewed, queried and exported with no need to log-in. Login is needed to create databases and access private databases. The databases listed can be sorted by clicking on the header of the column. In “My databases”, toggle (show/hide) database lists, to access the group of interest (Figure 6).

My Databases (toggle)

Your private databases, they are not shared with other users. Click on column headers do sort the databases.

Name	Owner	Creation Date	Strains	Panels
Bartonella	antonin	2016-01-31 17:04:06	396	1
brucella3	antonin	2016-02-07 13:40:22	257	1
brucella3_tmp	antonin	2016-03-03 12:37:56	20	3

My Groups

Your shared databases, sorted by groups. Click the name of the group to toggle the list of databases. Click on column headers do sort the databases.

Brucella [Edit](#)

Members: antonin

Bartonella [Edit](#)

Members: antonin

MLVA Team [Edit](#)

Members: antonin · john

Administrator [Edit](#)

Members: antonin · brendan

Figure 6: Database listing page of a logged user

Each database has its specific header including database name, owner, description and link for more support if available (Figure 7). See the database’s menu to edit, query, view, etc. Show/hide columns for clearer navigation.

MLVAbank for Microbes Genotyping

Home Users **Databases**

Create New Database My Databases Public Databases

Pseudomonas aeruginosa

Owned by public_databases

Query Views Options Panel selection

Columns (click to hide): Key - study - Strain_ID - origin - Source - publication - contact - lon - lat

Strains per page: 100 1 2 3 Go to page: 1

Key	study	Strain_ID	origin	Source	publication	contact	ms77	ms127	ms142	ms172	ms211	ms212	ms213	ms214	ms215	ms216	ms217	ms222	ms223	ms61	ms207	ms208	
001	paeru2#0325	PA01		Larche2012	Christine Pourcel		4	8	7	12	5	9	5	3	4	3	2	2	4	12	7	6	
002	paeru2#0002	PK14		Vu-Thien2007	Christine Pourcel		2	9	1	12	2	4	1	5	2	1	5	2	4	12	5	6	
003	paeru2#0326	TR_S0502224	Paris, France	cf	Vu-Thien2007	Christine Pourcel	2	8	4	10	4	5	3	6	5	2	3	1	3			17	4
004	paeru2#0327	TR_S0502106	Paris, France	cf	Vu-Thien2007	Christine Pourcel	2	8	4	12	8	9	2	2	4	2	4	3	3			5	2
005	paeru2#0328	TR_S0502380	Paris, France	cf	Vu-Thien2007	Christine Pourcel	2	8	3	13	6	9	7	4	2	2	3	4	2			6	3
006	paeru2#0329	TR_S0502644	Paris, France	cf	Vu-Thien2007	Christine Pourcel	2	8	1	11	8	9	5	15	4	3	5	2	2			8	5
007	paeru2#0330	TR_S0502629	Paris, France	cf	Vu-Thien2007	Christine Pourcel	2	8	1	11	8	9	5	15	4	3	5	2	2			8	5
008	paeru2#0331	TR_S0502283	Paris, France	cf	Vu-Thien2007	Christine Pourcel	2	8	3	8	8	6	4	2	1	2	1	1	1			4	3
009	paeru2#0332	TR_S0501374	Paris, France	cf	Vu-Thien2007	Christine Pourcel	2	8	1	11	3	8	5	3	2	3	3	3	6			9	5
010	paeru2#0333	TR_S0501556	Paris, France	cf	Vu-Thien2007	Christine Pourcel	2	8	6	11		3	5	3	2	1	3	1	2			14	4
011	paeru2#0335	TR_S0502533	Paris, France	cf	Vu-Thien2007	Christine Pourcel	2	8	4	8	3	4	5	5	1	2	3	1	3			4	8
012	paeru2#0336	TR_S0501638	Paris, France	cf	Vu-Thien2007	Christine Pourcel	2	8	7	12	3	8	3	4	6	2	3	2	3			9	4
013	paeru2#0337	TR_S0501695	Paris, France	cf	Vu-Thien2007	Christine Pourcel	2	8	7	12	3	8	3	4	6	2	3	2	3			9	4
014	paeru2#0340	TR_S0502351	Paris, France	cf	Vu-Thien2007	Christine Pourcel	2	9	1	11	2	9	5	6	6	2	2	4	3			13	7
015	paeru2#0341	TR_S0502141	Paris, France	cf	Vu-Thien2007	Christine Pourcel	2	9	1	11	2	9	5	6	6	2	2	4	3			13	7
016	paeru2#0342	TR_S0502280	Paris, France	cf	Vu-Thien2007	Christine Pourcel	2	9	1	11	2	9	5	6	6	2	2	4	3			13	7
017	paeru2#0343	TR_S0501876	Paris, France	cf	Vu-Thien2007	Christine Pourcel	2	8	4	12	6	5			2	2	4	4	2			4	7
018	paeru2#0344	TR_S0502232	Paris, France	cf	Vu-Thien2007	Christine Pourcel	2	8	1	11	3	8		3	2	3	3	3	6			9	5

Figure 7: Database viewing

3.3 Modifying and deleting

A database can be edited by its owner via the “Options > Edit” menu (Figures 7 and 8).



Bactérie Owned by brendan Back

Database Name
Bactérie

Database Support Website
http://mlva.dev

Database Description

Database Type
ENSTAlab

Is that database public ?

Edit

Figure 8: Database editing page

Click “Edit” to save changes. A database can be deleted by its owner via the “Options > Delete” menu. Confirmation will be required. Once deleted, all metadata (information fields) and genotyping data are lost.

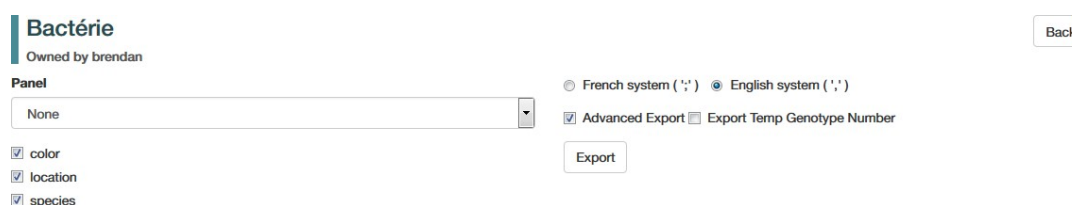
3.4 Exporting and importing via CSV

MicrobesGenotyping does not provide internal data editing tools. Instead, CSV files are used to modify data, including adding or deleting strains. When importing, new fields (metadata or typing data) can be added.

Users able to view a database can export it. Only users belonging to the database-associated group are allowed to import data in the database.

3.4.1 Exporting

To export, select “Views > Export” in the database menu.



Bactérie Owned by brendan Back

Panel
None

French system (',') English system (',')

Advanced Export Export Temp Genotype Number

color
 location
 species

Export

Figure 9: Database export page

The database export page (Figure 9) allows to select information fields to be exported. A data fields selection can be applied by selecting a specific panel (use option “None” to export only a selection of the information fields).

The CSV delimiter can be selected according to local settings. If checked, “Advanced Export” option will add extra lines at the beginning of the file, defining field types and panels. These lines are recognised by **MicrobesGenotyping** and will facilitate subsequent re-import. Press “Export” when done.

For more information on genotype read paragraph [Handling Panels and Genotype numbers](#) Importing.

3.4.2 Importing

To import data in a pre-existing database, select “Options > Import” in the database menu.



Figure 10: Database import page

Choose a CSV file to upload on the database import page (Figure 10). Partial files can be imported, the only column needed is the “key” column that will allow the website to identify the strains.

The geolocalisation column is selected as during the creation step (Creating a database). The “Import genotype number” option in Figure 10 is accessible to the database owner only (cf Handling Panel and Genotype numbers)

3.5 Accessing geographic view

If the database includes geographic location, click on views -> Strains geolocalisation to access the map.

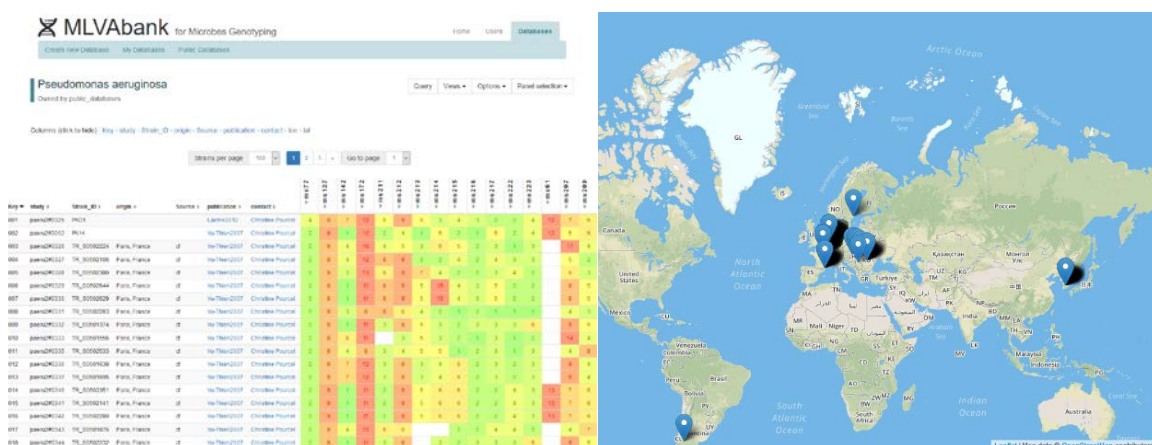


Figure 11: Geolocalisation of strains

Geolocalisation needs to be defined during database creation. It can be done in two ways:

- If there are two fields (columns) named lat and lon, they will be used automatically
- In the absence of lat and lon, select the field containing the geographic information, latitude and longitude will be computed during the creation. Also assign the field to the “information” type.

If there are two columns “lat” and “lon” but information is missing for some strains, option 2 can be used in combination: when “lat” and “lon” information is available, it will be used. If not, the field defined as geographic information field will be used. In a subsequent export, the “lat” and “lon” fields will be filled with the deduced values.

3.6 Querying a database

To query a database, go to its page (e.g. “Databases > Public Databases”) then “Query” in the database’s menu (Figure 12). The query takes into account the panel chosen when viewing the database.

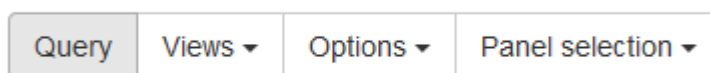


Figure 12: Accessing the query form

The different alleles can be typed individually or the whole genotype can be pasted in the leftmost box. The values will be automatically parsed. Choose the “Maximal distance” between the query and the strains (Hamming distance) (e.g. 2) and the “Maximal number of strains” to be listed in the results page (e.g. 20). The “only one strain per genotype” option allows to show one strain per genotype (the first found). Press Submit.

Figure 13: Submitting a query

Expect a longer processing time if high “Maximal distance” and “Maximal number of strains” output values were selected.

The query result is shown in a way similar to database viewing (Figure 14). Strains can be sorted by clicking on arrows next to column headers and show/hide metadata columns. The geographic origin of matching strains can be displayed if the database contains geolocalisation information. The genotyping data of matching strains can be exported as a CSV as previously shown for the whole database by selecting “Views > Export as CSV”.

Strains per page 100 Go to page 1

Key	study	Strain_ID	origin	Source	publication	contact	lon	lat	Distance to reference	-ms177	-ms127	-ms142	-ms172	-ms211	-ms212	-ms213	-ms214	-ms215	-ms216	-ms217	-ms222	-ms223	-ms207	-ms209									
Reference strain										2	8	5	11	3	9	4	3	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
035	paeru2#0381	TR_S0600035	Paris, France	cf	Vu-Thien2007	Christine Pourcel	2.3522219	48.8566140	0	2	8	5	11	3	9	4	3	2	2	2	2	2	2	2	7	4							
036	paeru2#0382	TR_S0600038	Paris, France	cf	Vu-Thien2007	Christine Pourcel	2.3522219	48.8566140	0	2	8	5	11	3	9	4	3	2	2	2	2	2	2	2	7	4							
037	paeru2#0383	TR_S0600036	Paris, France	cf	Vu-Thien2007	Christine Pourcel	2.3522219	48.8566140	0	2	8	5	11	3	9	4	3	2	2	2	2	2	2	2	7	4							
038	paeru2#0364	TR_S0600379	Paris, France	cf	Vu-Thien2007	Christine Pourcel	2.3522219	48.8566140	0	2	8	5	11	3	9	4	3	2	2	2	2	2	2	2	7	4							
069	paeru2#0396	TR_S0601180	Paris, France	cf	Vu-Thien2007	Christine Pourcel	2.3522219	48.8566140	0	2	8	5	11	3	9	4	3	2	2	2	2	2	2	2	7	4							
086	paeru2#0451	TR_S0601180	Paris, France	cf	Vu-Thien2007	Christine Pourcel	2.3522219	48.8566140	0	2	8	5	11	3	9	4	3	2	2	2	2	2	2	2	7	4							
087	paeru2#0452	TR_S0601287	Paris, France	cf	Vu-Thien2007	Christine Pourcel	2.3522219	48.8566140	0	2	8	5	11	3	9	4	3	2	2	2	2	2	2	2	7	4							
263	paeru2#1017	RO13	Romania	tracheal aspirate	Larche2012	Christine Pourcel	24.9667600	45.9431610	2	2	8	4	11	4	9	4	3	2	2	2	2	2	2	2	6	5							
278	paeru2#1032	PK555	Pecs	blood	Larche2012	Christine Pourcel		2		2	8		11	4	9	4	3	2	2	2	2	2	2	2	6	5							
279	paeru2#1033	PK396	Budapest	blood	Larche2012	Christine Pourcel	19.0402350	47.4979120	2	2	8	4	11	4	9	4	3	2	2	2	2	2	2	2	6	5							
410	paeru2#1358	Pcj6328168	Clamart, France	blood	Larche2012	Christine Pourcel	2.2572890	48.7998150	1	2	8	4	11	3	9	4	3	2	2	2	2	2	2	2									
411	paeru2#1359	Pcj657454	Clamart, France	bronchoalveolar lavage	Larche2012	Christine Pourcel	2.2572890	48.7998150	1	2	8	4	11	3	9	4	3	2	2	2	2	2	2	2									
412	paeru2#1360	Pcj8283027	Clamart, France	blood	Larche2012	Christine Pourcel	2.2572890	48.7998150	1	2	8	4	11	3	9	4	3	2	2	2	2	2	2	2									

Strains per page 100 Go to page 1

Figure 14: Query output page

The distance matrix (categorical distance) can be retrieved by clicking on “Views > Distance Matrix”. To export it to the MEGA format, click on the button “Export to MEGA format” (Figure 15).

Export to MEGA Matrix Format

Export to MEGA Format

Distance Matrix

Key	263	279	035	036	037	038	069	086	087	410	411	412	278	Queried strain
263	0	0	2	2	2	2	2	2	2	1	1	1	1	2
279	0	0	2	2	2	2	2	2	2	1	1	1	1	2
035	2	2	0	0	0	0	0	0	0	1	1	1	2	0
036	2	2	0	0	0	0	0	0	0	1	1	1	2	0
037	2	2	0	0	0	0	0	0	0	1	1	1	2	0
038	2	2	0	0	0	0	0	0	0	1	1	1	2	0
069	2	2	0	0	0	0	0	0	0	1	1	1	2	0
086	2	2	0	0	0	0	0	0	0	1	1	1	2	0
087	2	2	0	0	0	0	0	0	0	1	1	1	2	0
410	1	1	1	1	1	1	1	1	1	0	0	0	2	1
411	1	1	1	1	1	1	1	1	1	0	0	0	2	1
412	1	1	1	1	1	1	1	1	1	0	0	0	2	1
278	0	0	1	1	1	1	1	1	1	1	1	1	0	2
Queried strain	2	2	0	0	0	0	0	0	0	1	1	1	2	0

Figure 15: Distance matrix

A Newick Tree can be obtained by clicking on “Views > Newick Tree”. A representation can be selected from the drop-down menu : Radial, Diagonal, Circular, Rectangular and Hierarchical. Labels can be modified as well from the second drop-down menu.

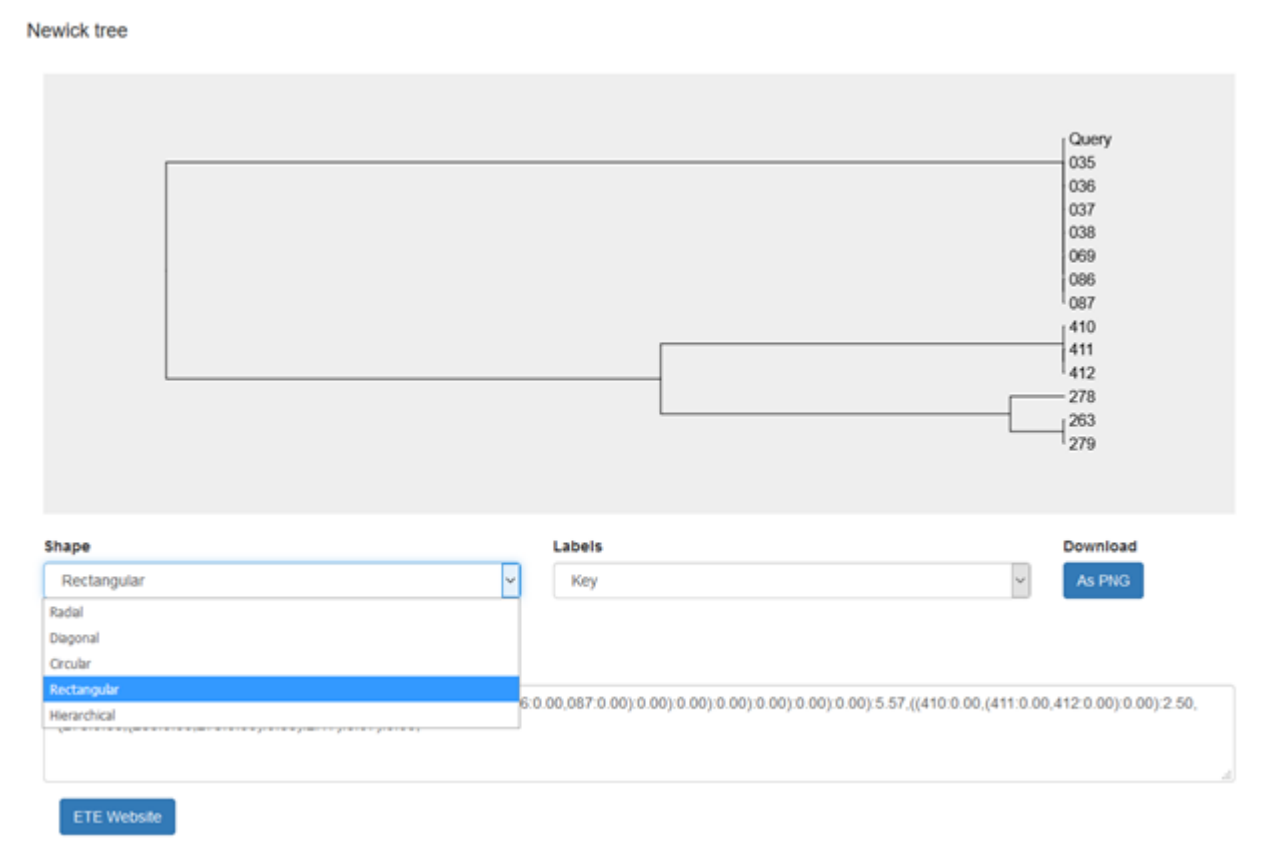


Figure 16: UPGMA tree

A tree can be downloaded as jpeg file with the download button or as Newick format tree code at the bottom. The “ETE website” button is a link to ETE toolkit, a phylogenetic tree viewer.

3.7 Handling Panels and Genotype numbers

3.7.1 Panels

Panels are made to view and query databases more easily. Most importantly, panels can correspond to different types of assays, for instance MLVA, MLST, canSNPs, etc. Select a panel in the “Panel selection” tab from the database’s menu. Members of the database’s group can access the “Handle Panels” menu to add or edit panels.

Handle panels																			
Name	ms 77	ms 127	ms 142	ms 172	ms 211	ms 212	ms 213	ms 214	ms 215	ms 216	ms 217	ms 222	ms 223	ms 61	ms 207	ms 208			
MLVA15Orsay	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	Update	Generate Geno Num	Delete
MLVA16Orsay	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	Update	Generate Geno Num	Delete
MLVA9London	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	Update	Generate Geno Num	Delete
MLVA9Utrecht	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	Update	Generate Geno Num	Delete
New Panel	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	Invert selection	Submit	

Figure 17: Panel editing page

To modify an existing panel, check or uncheck the marker in the corresponding line and press “Update” to validate. A panel name can be changed, given that each panel has a different name. Changes must be validated before editing an other panel.

To delete a panel, click on the “Delete” button of the corresponding line.

To create a panel, edit the last line and press “Submit” to validate, you can inverse the selection by clicking on the “Invert selection” button.

3.7.2 Genotype numbers

To facilitate the quoting of a genotype, genotype numbers may be assigned. It is then common to all strains sharing that particular genotype.

To generate genotype numbers for a particular panel, go to the “Handle Panels” page and click the “Generate Geno Num” button. It will create genotype numbers for every strains.

Genotype numbers can be modified by exporting with the “Advanced Export” option checked, editing, and importing back (cf Exporting and Importing via CSV). It is not necessary to indicate the new genotype number for all strains, as the import tool will spread genotypes to any strain sharing the same genotype.

When exporting a database as a CSV file, genotype numbers that are not yet verified can be exported. After re-importing, the genotype numbers will be verified for all users. Be careful on that option.