Please Enter your Data

AS a CSV or TSV file (see example)

Choisir un fichier | Aucun fichier choisi

OR directly by filling the following field:

```
#ExampleID;Spoligotype;24-loci MIRU-VNTR
1;477777777413071;25432622364361436126136
2;477606317413071;21342513353261436126136
3;770777777777671;
4;777777404760771;
5;nnnnnnonnnnooooooonnnnnonnnnnoooonnonnonnnnnn;254-2622351394232212B3327
6;1111111111111111111111111110000010111110111;
7;nnnnnnonnnnooooooonnnnnonnnnnoooonnonnonnnnnn;
```

The file can contain a header (beginning with "#" symbol) then one strain per line with no spaces or empty lines.
Please note that genotyping data format corresponds to **SITVIT2 nomenclature**.
A maximum of 5000 characters is allowed. No limit is set when using the **command line tool**.

Select a model (algorithm):

☑ Binary rules ☐ Decision tree ☐ Evolutionary algorithm ☐ MIRU-VNTR based lineage (RuleTB)

Select other option(s):

☑ Curated Clade ☑ SNP-based Lineage ☑ Spoligotype International Type (SIT) ☑ Country distribution

Select a delimiter: ◉ semicolon ○ comma ○ tabulation

Reset   Submit

Users can enter their data as a CSV or TSV (delimited by semicolons, commas, or tabulations). Semicolons are used by default.

Missing data are allowed by entering a dot (".") for the 43 spacers spoligo or a dash ("-") for 24-loci MIRU.

Users can then choose the methods of their choice to predict MTBC families from their input data.

Supplemental options will allow users to get information on "curated clades" (from SITVIT2 database), potential correspondence to SNP-based lineages, SIT numbers, and country distribution from spoligotypes (according to SITVIT2).