Phylogeotool
Reference Manual

EWOUT VANDEN EYNDEN, PIETER LIBIN, KRISTOF THEYS,
ANDEREN, GUY BAELE

Rega Institute

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1 Installation

1.1 Preparations before installation

Java

Download and install the newest Java Development Kit (JDK) from `http://www.oracle.com/technetwork/java/javase/downloads/index.html`. The current version of the tool was build on JDK 1.8.0_31.

Tomcat

Download and install the newest Tomcat version from `http://tomcat.apache.org`.

Github

Download the code from `https://github.com/rega-cev/phylogeotool/`. The project is currently still private. During the trial period you can send an email to ewout.vandeneynden@kuleuven.be with your Github account name to get read rights on the project.

Ant

Download and install the newest Ant version from `http://ant.apache.org/` as we will use it to build our project. The current version of the tool was build with Ant 1.9.4

2 Data preparation

After building the code, different jar files can be found in the dist folder. Their function is explained here.

2.1 DistanceMatrix.jar

Tool to create a distance matrix based on the phylogenetic tree that will be used in the PhyloGeoTool.
DistanceMatrix.jar takes the following input values:

- phylo.tree: Link to the phylogenetic tree to be used in the PhyloGeoTool.

- distance matrix: Link to the location where the distance matrix can be written.

2.2 PreRender.jar

Before any data can be shown to the user, a lot of calculations are done backend. To speed up the process, most of those calculations can be done beforehand.

PreRender.jar is a multithreaded application meaning that it performs best on any Java version > 7. Lower Java versions do not support our implementation of multithreading and will thus fail.

PreRender.jar takes the input files:

- phylo.tree: Link to the phylogenetic tree used in the PhyloGeoTool.

- csvFile: Link to the csv file that connects nodes in the tool to attributes. Note: The id in the csv file has to be the same as the id of the nodes in the tree.

- distance matrix: Link to the distance matrix that was generated from this tree.

- folder xml tree: Link to the folder where this jar can write its resulting tree files.

- folder xml clusters: Link to the folder where this jar can write its resulting cluster files.

- folder xml csv: Link to the folder where this jar can write its resulting csv files.

- folder figtree: Link to the folder where this jar can write its resulting figtree representations.

3 Tool functionality

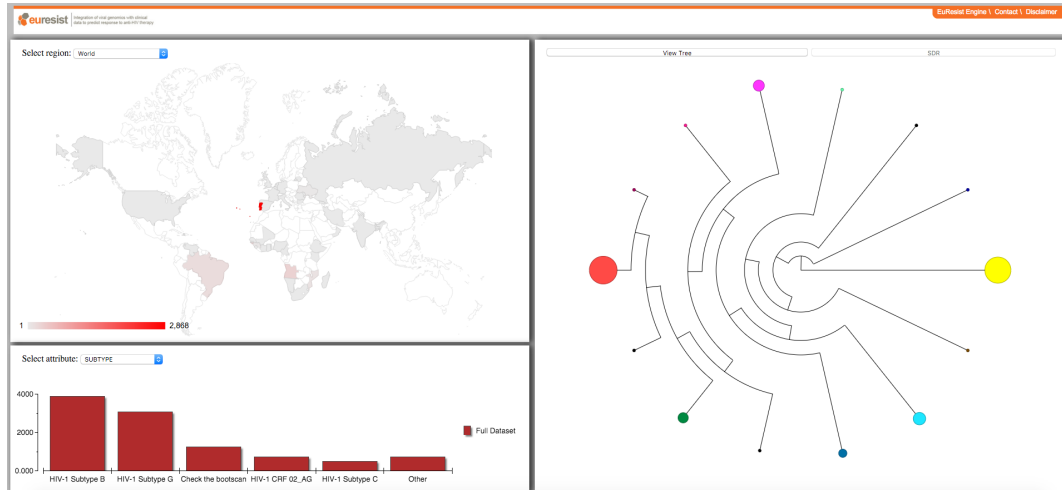## 3.1 Basic functionality

Figure 1: Initial view of the tool

The tool is divided into different area's

- Top left shows a world map where each country is colored darker as more sequences are originating from here. It also contains a drop down box where you can select the region on which you want to zoom in (e.g. Europe, North-America, . . .).

- Bottom left shows a bar chart which shows a certain attribute/characteristic from all sequences currently shown in the circular tree on the right. It also contains a drop down box where you can select the attribute/characteristic that you want to display in the bar chart. The attributes available for representation depend on the attributes given in the csv file.

- On the right, initially, the best clustering of the phylogenetic tree is shown. It also contains a button to visualise the tree in FigTree format.
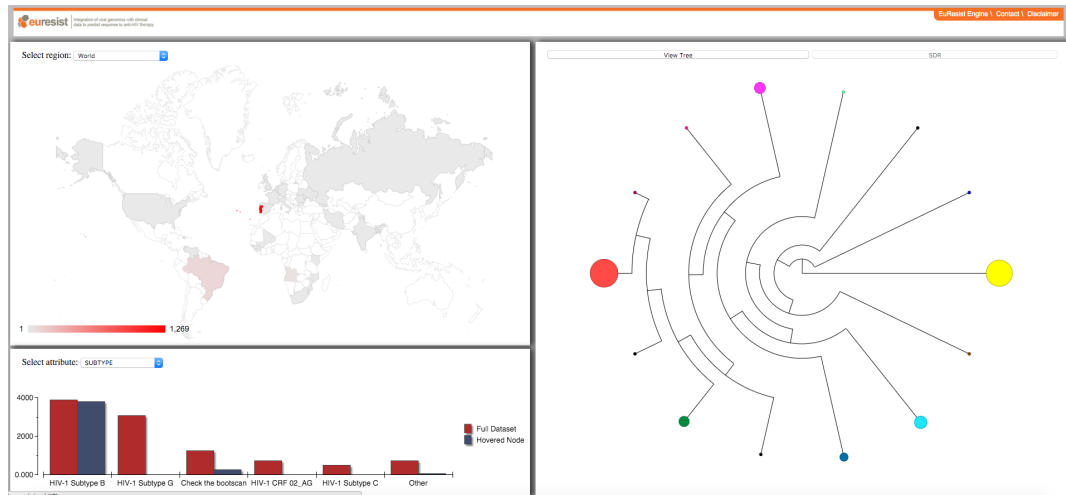
3.1.1 Hover over node in clustered tree

Figure 2: Hovering over a node in the tree

When you hover over a node in the phylogenetic tree, the bar chart on the bottom left and the map on the top left will be updated with data coming specifically from the node you hovered over.

In the bar chart it'll be shown as an extra column that is added next to the already visible column.

On the map it'll be shown as a new country colouring where each country is coloured based on only information coming from the hovered node.
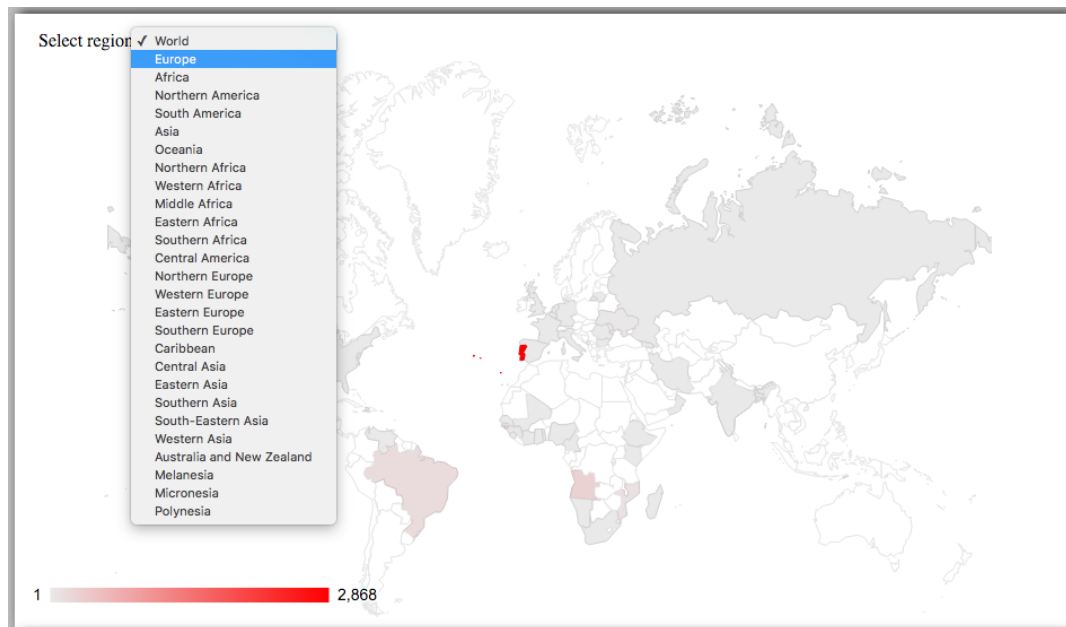
3.1.2 Change region

Figure 3: Change the region in the drop down box

When you change the region by selecting a new value in the drop down box on top of the map (see fig. 3), the world map will update and now only show information originating from this specific region.
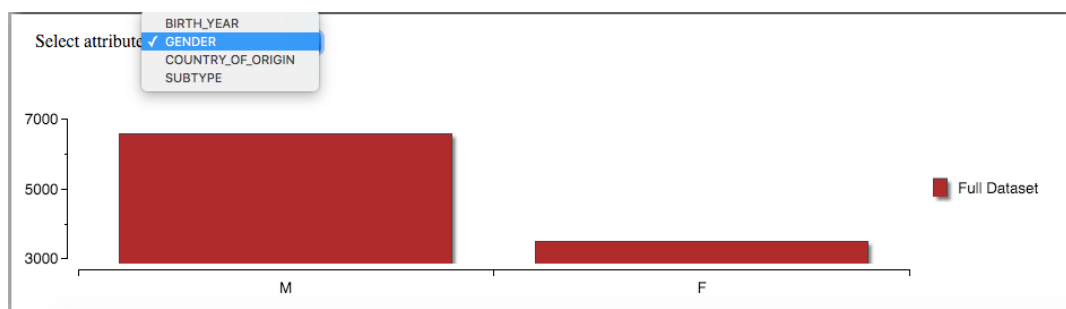
3.1.3 Change attribute

Figure 4: Change the attribute in the drop down box

When you change the attribute by selecting a new value in the drop down box on top of the bar chart (see fig. 4), the chart will update and now only show data for this specific newly selected attribute.
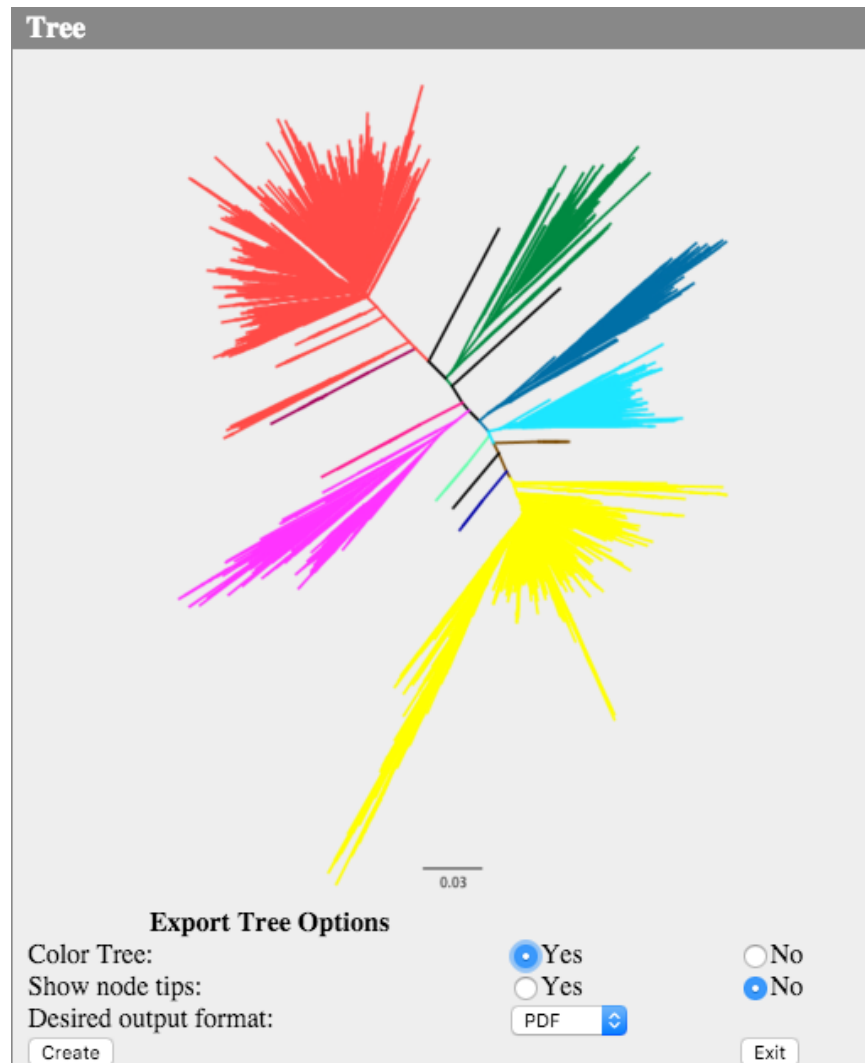
3.1.4   View Tree

Figure 5: Tree visualization in FigTree

When the 'View Tree' button on top of the circular phylogenetic tree representation is clicked, a popup window will appear such as in fig. 5 where the tree is shown as a radial tree such as it is represented in FigTree. The different clusters get different colours. The colours in the radial tree repre-

sentation correspond to the colours in the circular tree representation.
In addition to the visualisation of the tree, export options are available. The
user can select if he/she wants the tree to be coloured, if the node tips should
be shown and in which format the tree will be exported.

3.2   PPlacer

Explanation of the PPlacer here. Not enough relevant data yet. Should be
added here.