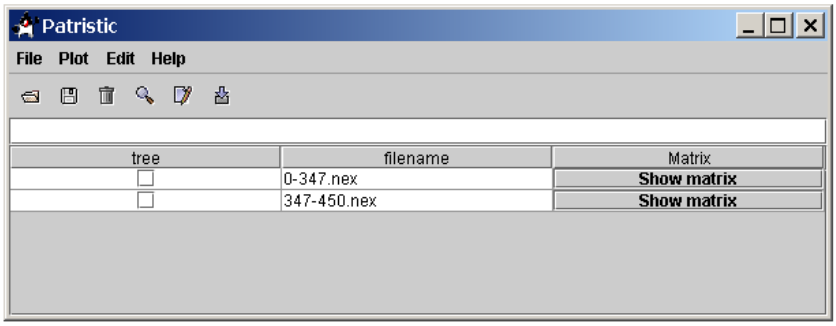
# PATRISTICv1.0

## Introduction:

Patristic is a Java program that uses as input different tree files and computes their patristic distances. Patristic allows saving and editing in different ways those distances. Patristic provides different graphic views of the results as well as the possibility to save them in the CSV format for building graphics using Excel.




## System requirements:

Patristic runs on Windows, Mac and Linux in a graphic mode. Make sure you have a version a Java.

### *Java on windows:*

Patristic requires the Java Runtime Environment downloadable on the sun website. Follow the link J2SE Runtime Environment (JRE).

### *Java on Mac OS X:*

A recent version of Mac OS X should have a Java version already installed otherwise the latest version is downloadable from the Apple website. Follow the link Java 1.4.2.

### *Java on linux:*

Patristic requires the Java Runtime Environment downloadable on the sun website. Follow the link J2SE Runtime Environment (JRE).

## Installation:

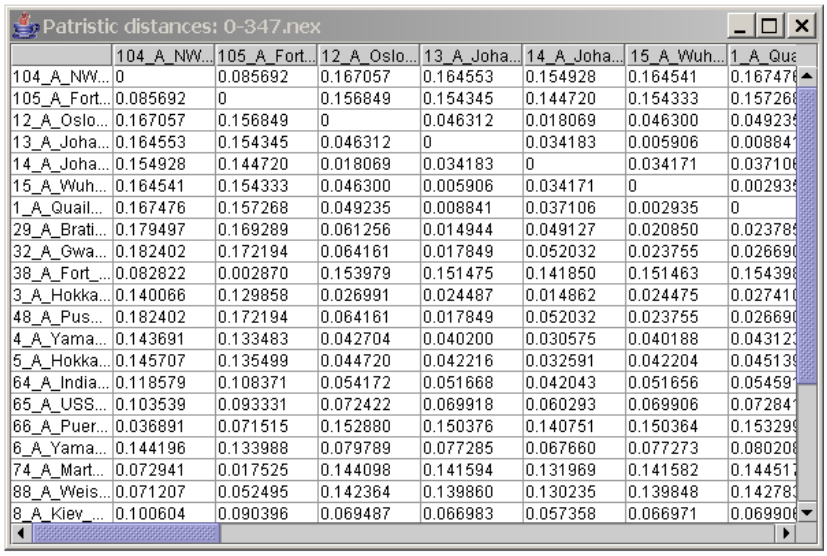
1. Install the Java Runtime Environment if not already present.
2. Download the Patristic zip file.
3. Unzip it wherever you want.
4. Run Patristic.bat (Windows) or Patristic.sh (Linux) in the base directory to run the program.

You can also run the program with the command line: java -jar Patristic.jar.

## Opening a tree:

Once in Patristic, use File | Open tree to open a compatible tree file. Once opened the name of the tree should appear in the table with a clickable button “show matrix” for looking at the matrix distances in a new window. If the tree is made of a lot of taxa, the program will take some time to load and compute the distances from a tree but meanwhile it’s still possible to open another tree or what ever you want to do.

The icon can also be used for opening a tree. A tree can be loaded by copying the tree expression in the text area and confirming with the button . A drag and drop in the same text area will open a tree file (Windows only).




| | 104_A_NW... | 105_A_Fort... | 12_A_Oslo... | 13_A_Joha... | 14_A_Joha... | 15_A_Wuh... | 1_A_Qua |
|---|---|---|---|---|---|---|---|
| 104_A_NW... | 0 | 0.085692 | 0.167057 | 0.164553 | 0.154928 | 0.164541 | 0.16747 |
| 105_A_Fort... | 0.085692 | 0 | 0.156849 | 0.154345 | 0.144720 | 0.154333 | 0.15726 |
| 12_A_Oslo... | 0.167057 | 0.156849 | 0 | 0.046312 | 0.018069 | 0.046300 | 0.04923 |
| 13_A_Joha... | 0.164553 | 0.154345 | 0.046312 | 0 | 0.034183 | 0.005906 | 0.00884 |
| 14_A_Joha... | 0.154928 | 0.144720 | 0.018069 | 0.034183 | 0 | 0.034171 | 0.03710 |
| 15_A_Wuh... | 0.164541 | 0.154333 | 0.046300 | 0.005906 | 0.034171 | 0 | 0.00293 |
| 1_A_Quail... | 0.167476 | 0.157268 | 0.049235 | 0.008841 | 0.037106 | 0.002935 | 0 |
| 29_A_Brati... | 0.179497 | 0.169289 | 0.061256 | 0.014944 | 0.049127 | 0.020850 | 0.02378 |
| 32_A_Gwa... | 0.182402 | 0.172194 | 0.064161 | 0.017849 | 0.052032 | 0.023755 | 0.02669 |
| 38_A_Fort_... | 0.082822 | 0.002870 | 0.153979 | 0.151475 | 0.141850 | 0.151463 | 0.15439 |
| 3_A_Hokka... | 0.140066 | 0.129858 | 0.026991 | 0.024487 | 0.014862 | 0.024475 | 0.02741 |
| 48_A_Pus... | 0.182402 | 0.172194 | 0.064161 | 0.017849 | 0.052032 | 0.023755 | 0.02669 |
| 4_A_Yama... | 0.143691 | 0.133483 | 0.042704 | 0.040200 | 0.030575 | 0.040188 | 0.04312 |
| 5_A_Hokka... | 0.145707 | 0.135499 | 0.044720 | 0.042216 | 0.032591 | 0.042204 | 0.04513 |
| 64_A_India... | 0.118579 | 0.108371 | 0.054172 | 0.051668 | 0.042043 | 0.051656 | 0.05459 |
| 65_A_USS... | 0.103539 | 0.093331 | 0.072422 | 0.069918 | 0.060293 | 0.069906 | 0.07284 |
| 66_A_Puer... | 0.036891 | 0.071515 | 0.152880 | 0.150376 | 0.140751 | 0.150364 | 0.15329 |
| 6_A_Yama... | 0.144196 | 0.133988 | 0.079789 | 0.077285 | 0.067660 | 0.077273 | 0.08020 |
| 74_A_Mart... | 0.072941 | 0.017525 | 0.144098 | 0.141594 | 0.131969 | 0.141582 | 0.14451 |
| 88_A_Weis... | 0.071207 | 0.052495 | 0.142364 | 0.139860 | 0.130235 | 0.139848 | 0.14278 |
| 8_A_Kiev_... | 0.100604 | 0.090396 | 0.069487 | 0.066983 | 0.057358 | 0.066971 | 0.06990 |

## Importing distances:

Once in Patristic, use File | Import | PAUP or DIP or MEGA to load patristic distances already computed.

PAUP can be used for saving patristic distances in different ways:

1. A one line patristic distance file can be loaded from a PAUP file after the command “savedist file=filename format=oneColumn”.
2. The patristic distances with parsimony can also be loaded from the display buffer of PAUP after using the following commands:

Load treefile=tree.nex;
Matrixrep brlens=yes file=mytreefile.nex;

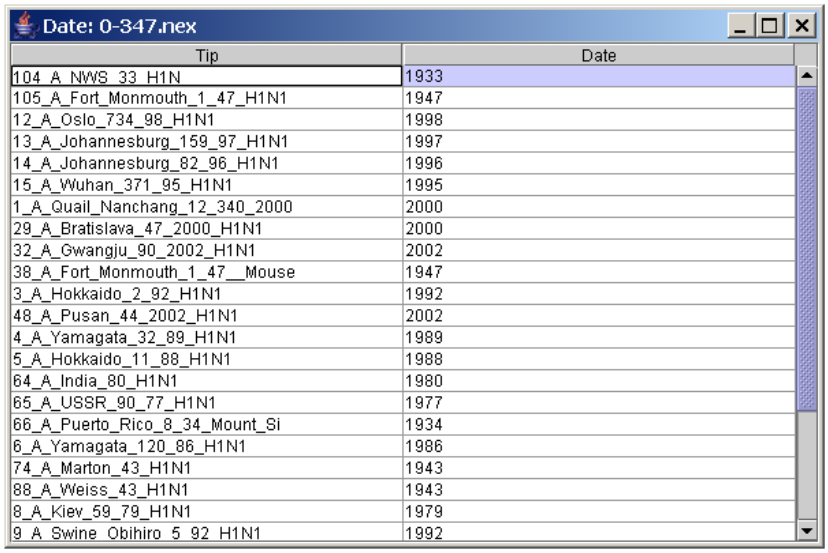
Execute mytreefile.nex;
Hs;
Describetrees 1/ patristic=yes;

The matrix is made of the patristic distances and the adjusted character distances respectively below and above the diagonal (both half matrix can be loaded). This file is a buffer so lots of information can be found in it; a minimum of editing must be done.

- The first line must be the number taxon
- Then the matrix.
- If the previous matrix was not complete because of a large number of taxa a void line should separate the other parts of the matrix.

## Editing time:

Once a tree is opened and its checkbox ticked in the table, the time isolation for each taxon can be edited using Edit | Time, the icon  or by using a file with dates ordered as in the in the tree file (Edit | Load time). This will allow to plot the time against the distances. (Each column edited must be validated by using the return key).




## Saving distances:

Once a tree is opened or the distances are imported the distances can be saved in a Comma-separated text file (CSV), using Save | Matrix or Time or Column or DIP.

The submenu Matrix as well as the icon  will save the distances as an upper hemi-matrix.
The submenu Column will save the distances as follow:

1. First column: first taxon
2. Second column: second taxon
3. Third column: corresponding patristic distance

The submenu Time will save the time like in column plus three columns:

4. Fourth column: first taxon date
5. Fifth column: second taxon date
6. Sixth column: absolute value of the time difference

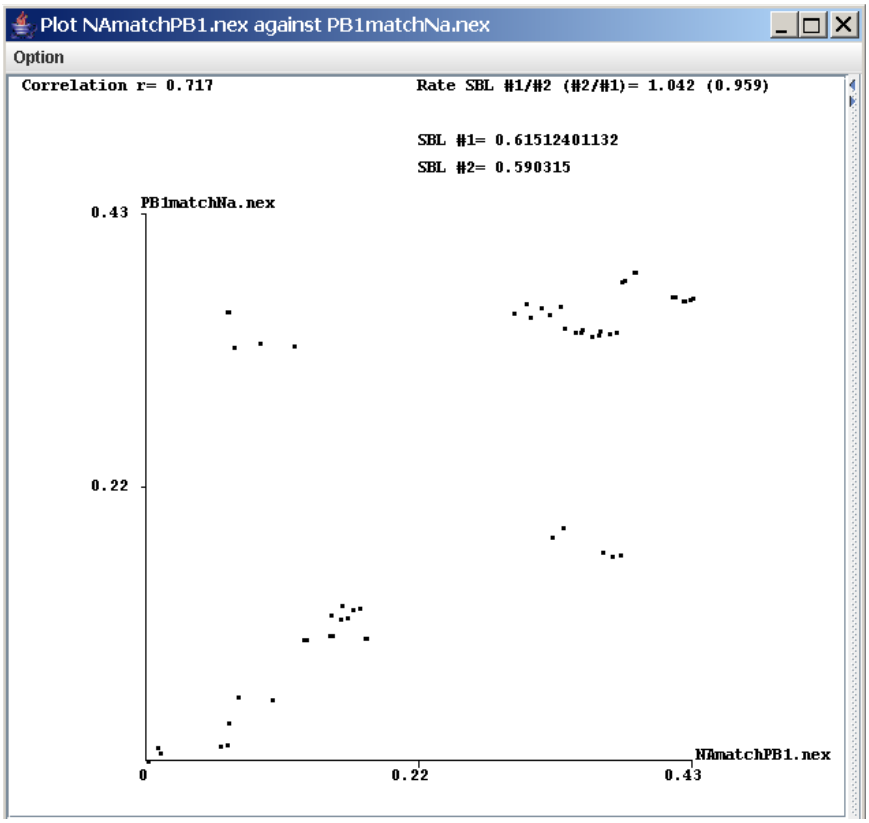
The submenu DIP will save one or several loaded trees in Diplomo's format: DIP.

## Reordering the distances:

Before doing a plot in some cases the distances have to be reordered. To do so, both windows with the matrix can be open and dragging the rows will allow the matching of each cell. Even after the reordering a message can appear, saying "Do you need to reorder?", click no if you are sure of your order. This can happen when the names are different, especially when you have used 2 different programs (programs allow different length names).

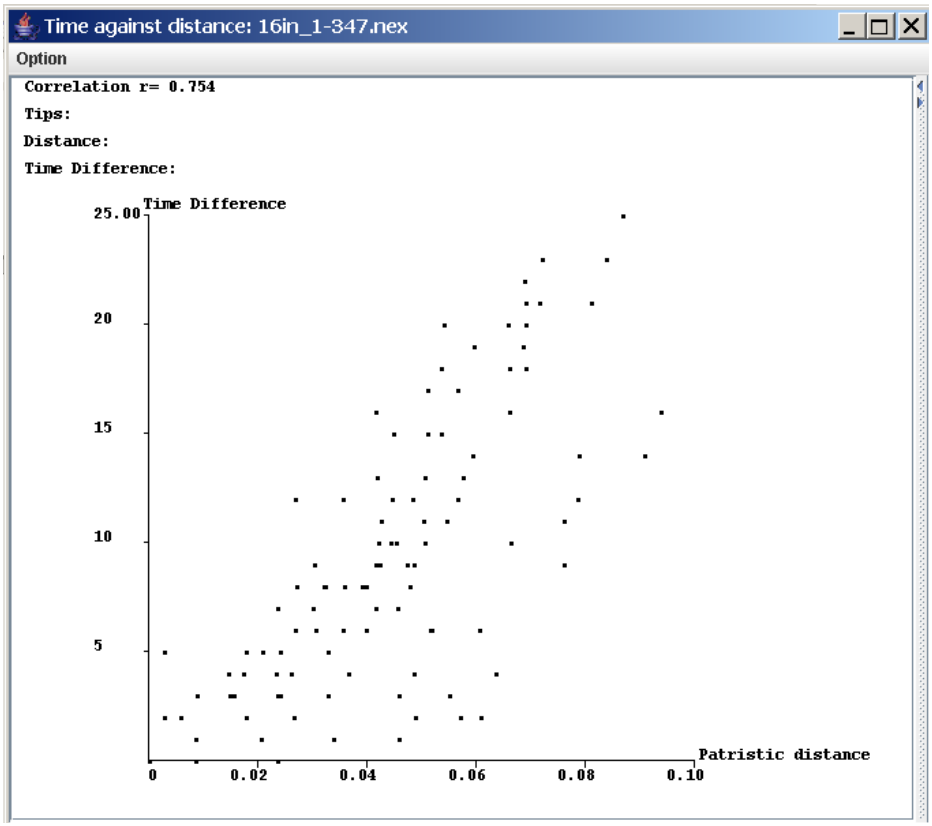
## Distance against distance plot view window:

When at least 2 trees are loaded a plot of their distances can be visualized in a new window using Plot | Dist vs. Dist or the icon  . The advantage of this plot over Excel is the distance and the time difference corresponding to two taxa can visualized by moving the mouse over one of the dot. At the bottom of the list a table contains the names of the taxa, their patristic distances for both trees and statistics about those distances.



## Distance against time plot view window:

When one tree has been loaded and the time has also been edited then a plot of the distances against the time can be visualized using Plot | Dist vs. Time or the icon  . The advantage of this plot over Excel is the distance and the time difference corresponding to two taxa can visualized by moving the mouse over one of the dot. This plot can also be assessed with the correlation coefficient as describe above.




## Plot assessment:

Both types of plot can be assessed statistically for determining its scattering and to identify which pair of distances highly differ from the mean. The formula for determining the mean and the standard deviation is up to the user but should follow some restrictions:

The formula can contain only the following characters: ( ) + - * / x y.

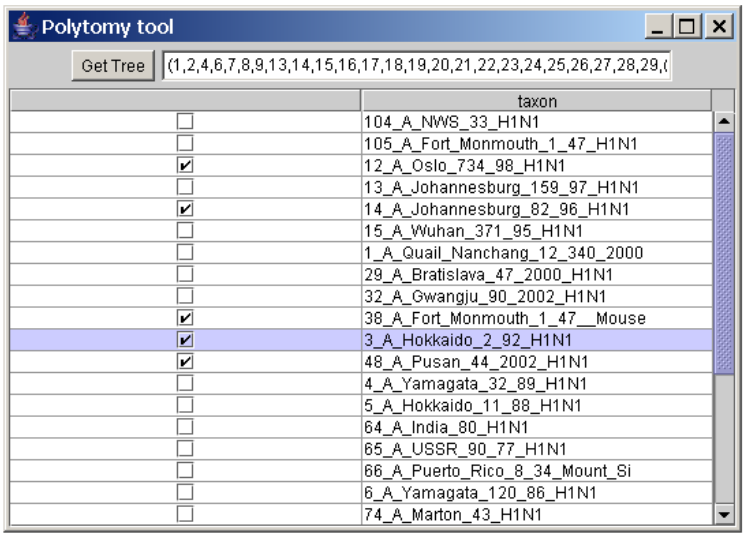
X and Y represent the distances for each tree. The minimum expression could be (x-y) and each calculation has to be between brackets thus the expression x-y would raise an error. ((x-y)*x) and ((x-y)*(x/y)) are correct but not (x-y)*x or (x-y)*(x/y).

The second field which should be comprise between 1 and 3 represents the number of standard deviation which will be used

The plot is assessed with the correlation coefficient r, which is a measure of linear association between variables. The coefficient r is a number between 0 and 1. If there is no relationship between the variables, in our case between patristic distances from two trees, the coefficient tend to 0 but if the more variables correlate the more r tends to 1.

## Other tools:

Polytomy tool: (Edit | Polytomy) program for creating a tree made of two polytomy, used in our case for creating a constraint for T-PTP test in PAUP. Every taxon ticked will in the same polytomy and the non ticked taxa will be in the other polytomy. Click the button Get Tree for getting the tree which can be copied in the clipboard.




## Troubleshooting:

- The applet can't be loaded, a grey rectangle appears instead of the applet and the following message appears at the bottom of the page: "load class: Patristic/PatristicApplet not found". The applet was created with Java 2 SDK 1.4 and you may be using an anterior version of the JRE such as JRE 1.2. Download and install the latest version of the Java RE. This is available for download under http://java.sun.com/j2se/downloads.html. Follow the links for the latest version of J2SE, but you only need to download and install the latest version of JRE.

## Certificate:

Java forbids by default the access to the file system for file protection and privacy, since our applet needs to open and save files when you attempt to load the applet a certificate pops up and say "The security certificate was issued by a company that is not trusted". This only means that the certificate hasn't been purchased from a well-known Certificate Authority (CA) but the certificate is still valid and usable.
No applet with certificate or not can execute process or even manipulate threads outside the applet's own thread group