

Data set from (Salemi *et al*, 2008)

To highlight inconsistencies

To highlight nodes with indecisive ancestral annotations

► **To extract an evolutionary scenario**

PhyloType analysis

Study on majority of ML marginal,
Sz>5 Df < 1 Pt >= -0.65

Primary annotations by cluster 100%

Computing time < 5s

Example 1, HIV-1A analysis

Data set = folder DATA-HIV1A, files:

- HIV-1A-tree.txt (tree)
- HIV-1A-annotation.txt (primary annotations)

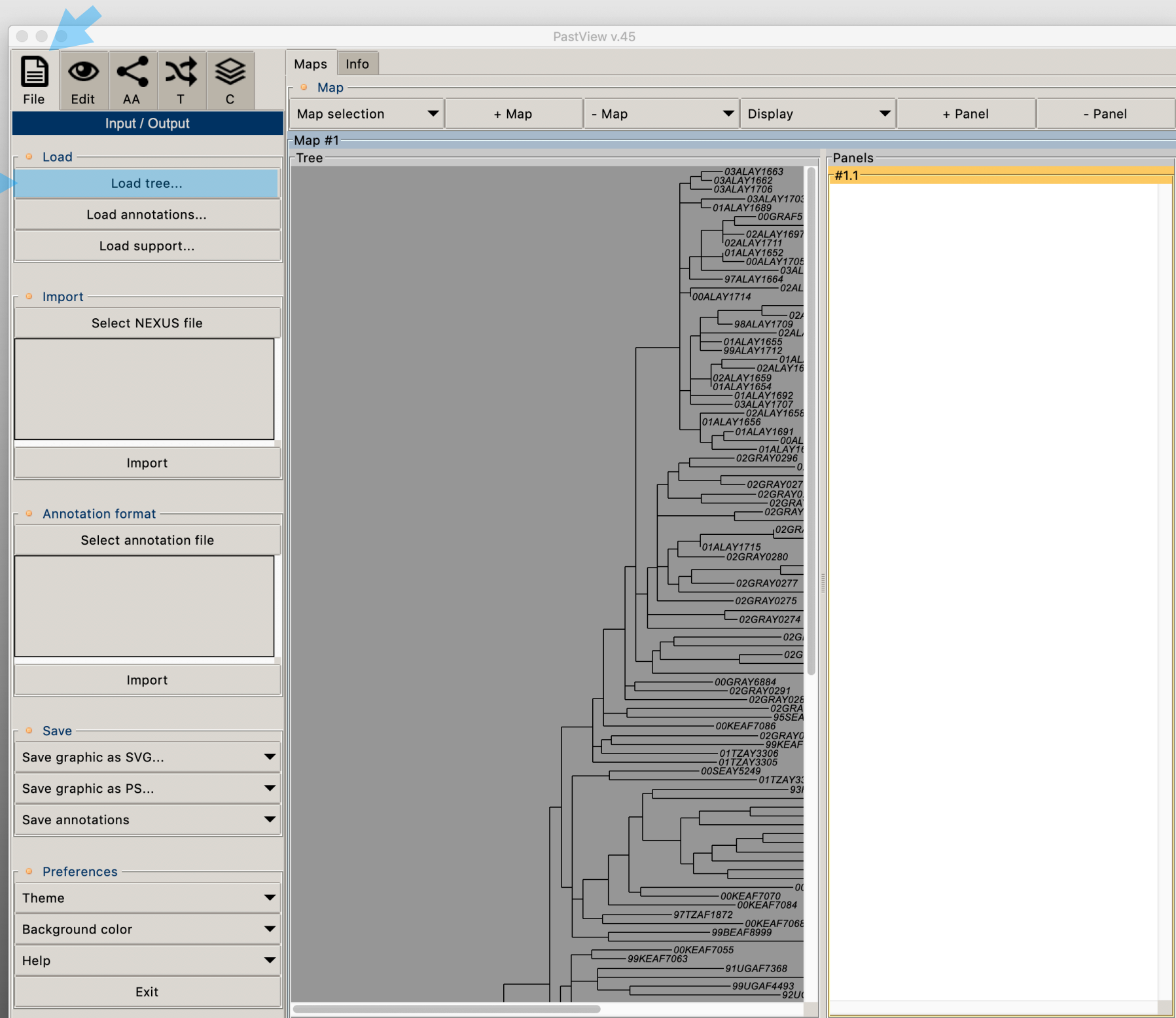
```
HIV-1A-tree.txt
(83FRK03455:0.16809,
(( (97CDAF6238:0.08034,94CYAF6237:0.10559)0.70:0.00530
,(97CDAF6240:0.04761,
(03ESAY2109:0.04105,03ESAY2098:0.02771)0.87:0.02046)0
.68:0.01021)0.97:0.09501,(00CZAY4286:0.07746,
((85UGM62320:0.09015,((00GAAJ3391:0.08297,
(98CMAJ6934:0.05510,
(00GAAJ3398:0.03617,03ESAY2099:0.03707)0.66:0.00303)0
.68:0.00348)0.96:0.02373,
((( (03ESAY2111:0.04048,00GRAF5753:0.01741)0.00:0.000
00,
(98FRAJ0552:0.00429,97FRAJ0558:0.03683)0.75:0.00824)0
.45:0.01188,
(02GRAY0270:0.01527,97YUAF9960:0.05290)0.87:0.01822)1
.00:0.05533,(00SEAY5240:0.07261,(98CMAJ6932:0.07492,
(98CMAJ6933:0.04360,96CMAJ6134:0.04942)0.72:0.00725)0
.91:0.02994)0.77:0.01185)0.06:0.00416,
(00CZAY4248:0.01387,((00CZAY4362:0.03677,
(00CZAY4336:0.00436,00CZAY4296:0.02224)0.00:0.00000)0
.88:0.00888,(00UAAF3968:0.02177,(97BYAF3275:0.01362,
(02SIAJ1139:0.00740,
(03RUAY0393:0.01051,02GRAY0302:0.02615)0.45:0.00462)0
.
94:0.01955)0.00:0.00000)0.71:0.00449)0.83:0.00817)1.0
0:0.05679)0.00:0.00000)0.63:0.00322)0.80:0.00980,
((99SEAY5206:0.03711,(99SDAY2494:0.04645,
(90UGAF7846:0.01791,(99UGAF4478:0.03204,
(00KEAF7083:0.04136,(00KEAF7079:0.04577,
(95SEAF9673:0.06880,
(98UGAF4508:0.07972,98UGAF4509:0.06631)0.76:0.01299)0
```

```
HIV-1A-annotation.txt
Name , Country , CountryCode , Region
'98CMAJ6932','Cameroon','CM','Africa'
'98CMAJ6933','Cameroon','CM','Africa'
'96CMAJ6134','Cameroon','CM','Africa'
'00SEAY5240','Sweden','SE','WestEurope'
'97CDAF6240','Dem.Rep.ofCongo','CD','Africa'
'97CDAF6238','Dem.Rep.ofCongo','CD','Africa'
'97CMAJ6930','Cameroon','CM','Africa'
'97CMAJ6931','Cameroon','CM','Africa'
'98CMAJ6934','Cameroon','CM','Africa'
'00GAAJ3398','Gabon','GA','Africa'
'00GAAJ3391','Gabon','GA','Africa'
'99KEAF7075','Kenya','KE','Africa'
'99KEAF7063','Kenya','KE','Africa'
'99KEAF7065','Kenya','KE','Africa'
'00KEAF7077','Kenya','KE','Africa'
'00KEAF7079','Kenya','KE','Africa'
'00KEAF7089','Kenya','KE','Africa'
'00KEAF7070','Kenya','KE','Africa'
'00KEAF7069','Kenya','KE','Africa'
'00KEAF7068','Kenya','KE','Africa'
'00KEAF7066','Kenya','KE','Africa'
'00KEAF7067','Kenya','KE','Africa'
'00KEAF7080','Kenya','KE','Africa'
'00KEAF7083','Kenya','KE','Africa'
'00KEAF7052','Kenya','KE','Africa'
'00KEAF7055','Kenya','KE','Africa'
'00KEAF7084','Kenya','KE','Africa'
'00KEAF7081','Kenya','KE','Africa'
'00KEAF7086','Kenya','KE','Africa'
```

Example 1, HIV-1A analysis

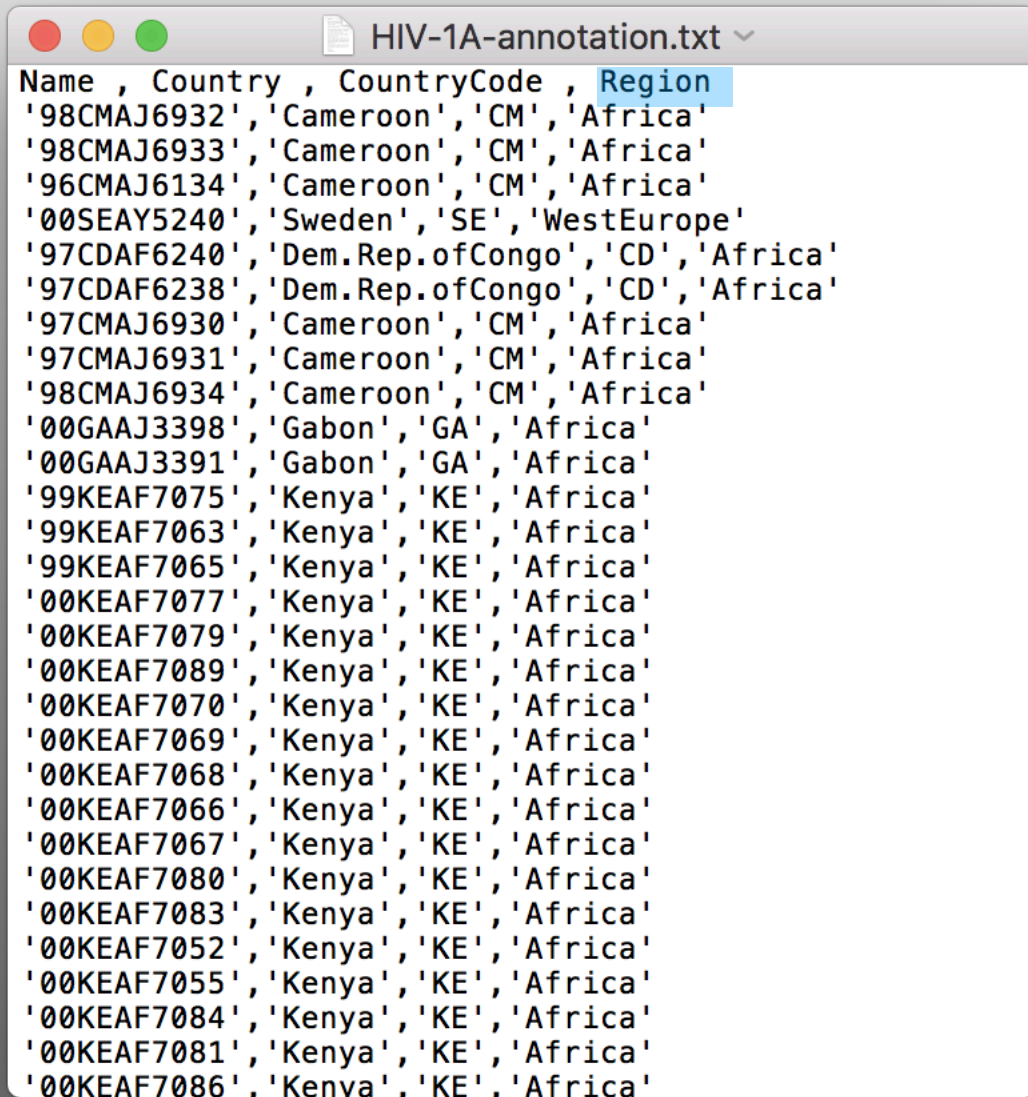
Load the tree

The tree is displayed in the « tree » canvas of the current map



Example 1, HIV-1A analysis

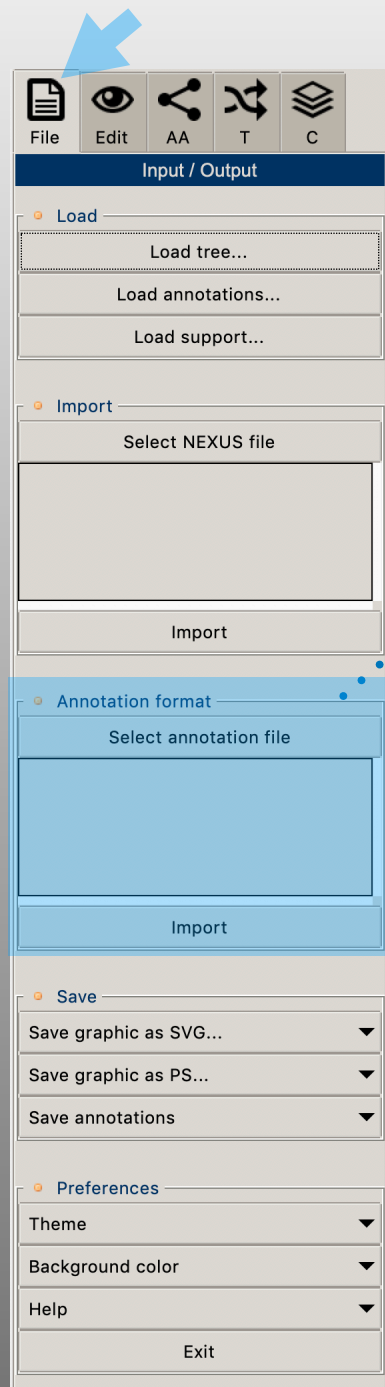
Load the primary annotations



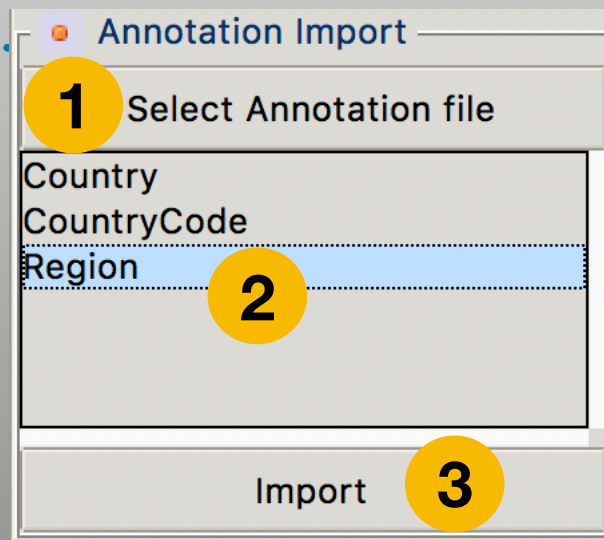
```
HIV-1A-annotation.txt
Name , Country , CountryCode , Region
'98CMAJ6932', 'Cameroon', 'CM', 'Africa'
'98CMAJ6933', 'Cameroon', 'CM', 'Africa'
'96CMAJ6134', 'Cameroon', 'CM', 'Africa'
'00SEAY5240', 'Sweden', 'SE', 'WestEurope'
'97CDAF6240', 'Dem.Rep.ofCongo', 'CD', 'Africa'
'97CDAF6238', 'Dem.Rep.ofCongo', 'CD', 'Africa'
'97CMAJ6930', 'Cameroon', 'CM', 'Africa'
'97CMAJ6931', 'Cameroon', 'CM', 'Africa'
'98CMAJ6934', 'Cameroon', 'CM', 'Africa'
'00GAAJ3398', 'Gabon', 'GA', 'Africa'
'00GAAJ3391', 'Gabon', 'GA', 'Africa'
'99KEAF7075', 'Kenya', 'KE', 'Africa'
'99KEAF7063', 'Kenya', 'KE', 'Africa'
'99KEAF7065', 'Kenya', 'KE', 'Africa'
'00KEAF7077', 'Kenya', 'KE', 'Africa'
'00KEAF7079', 'Kenya', 'KE', 'Africa'
'00KEAF7089', 'Kenya', 'KE', 'Africa'
'00KEAF7070', 'Kenya', 'KE', 'Africa'
'00KEAF7069', 'Kenya', 'KE', 'Africa'
'00KEAF7068', 'Kenya', 'KE', 'Africa'
'00KEAF7066', 'Kenya', 'KE', 'Africa'
'00KEAF7067', 'Kenya', 'KE', 'Africa'
'00KEAF7080', 'Kenya', 'KE', 'Africa'
'00KEAF7083', 'Kenya', 'KE', 'Africa'
'00KEAF7052', 'Kenya', 'KE', 'Africa'
'00KEAF7055', 'Kenya', 'KE', 'Africa'
'00KEAF7084', 'Kenya', 'KE', 'Africa'
'00KEAF7081', 'Kenya', 'KE', 'Africa'
'00KEAF7086', 'Kenya', 'KE', 'Africa'
```

This is a matrixXvariables of annotations, we want to do an analysis based on the « Region » variable, we have to extract and translate it to the PastView format

Example 1, HIV-1A analysis



Select the Strains x Variables file (1) then select the « Region » variable (2), and Clic the Import button (3)



```
HIV-1A-annotation.txt
Name , Country , CountryCode , Region
'98CMAJ6932', 'Cameroon', 'CM', 'Africa'
'98CMAJ6933', 'Cameroon', 'CM', 'Africa'
'96CMAJ6134', 'Cameroon', 'CM', 'Africa'
'00SEAY5240', 'Sweden', 'SE', 'WestEurope'
'97CDAF6240', 'Dem.Rep.ofCongo', 'CD', 'Africa'
'97CDAF6238', 'Dem.Rep.ofCongo', 'CD', 'Africa'
'97CMAJ6930', 'Cameroon', 'CM', 'Africa'
'97CMAJ6931', 'Cameroon', 'CM', 'Africa'
'98CMAJ6934', 'Cameroon', 'CM', 'Africa'
'00GAAJ3398', 'Gabon', 'GA', 'Africa'
'00GAAJ3391', 'Gabon', 'GA', 'Africa'
'99KEAF7075', 'Kenya', 'KE', 'Africa'
'99KEAF7063', 'Kenya', 'KE', 'Africa'
'99KEAF7065', 'Kenya', 'KE', 'Africa'
'00KEAF7077', 'Kenya', 'KE', 'Africa'
'00KEAF7079', 'Kenya', 'KE', 'Africa'
'00KEAF7089', 'Kenya', 'KE', 'Africa'
```

```
PAELAexport-HIV-1A-annotation-Region-ANNOTATI...
ID,Africa,Albania,EastEurope,Greece,WestEurope

00ALAY1705,0,1,0,0,0
00ALAY1705,0,1,0,0,0
00ALAY1705,0,1,0,0,0
00ALAY1713,0,1,0,0,0
00ALAY1713,0,1,0,0,0
00ALAY1713,0,1,0,0,0
00ALAY1713,0,1,0,0,0
00ALAY1714,0,1,0,0,0
00ALAY1714,0,1,0,0,0
```

The file « HIV-1A-annotationREGION.txt » is created (same file's path as HIV-1A-annotation.txt)

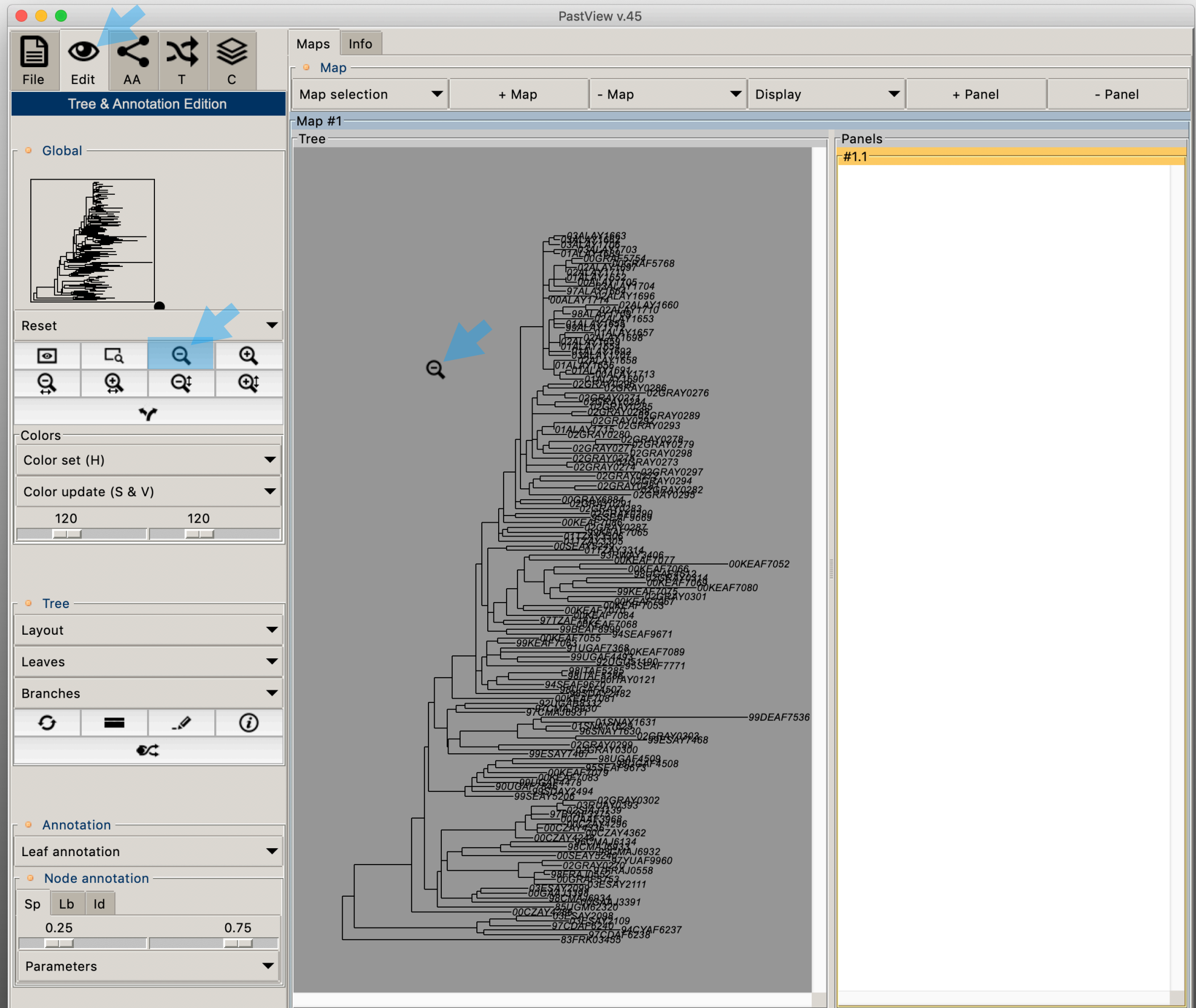
Load the annotations,
select the file HIV-1A-
annotationREGION.txt:



Example 1, HIV-1A analysis

Edit the tree

Select the « zoom out » tool and left click the canvas to see the whole tree

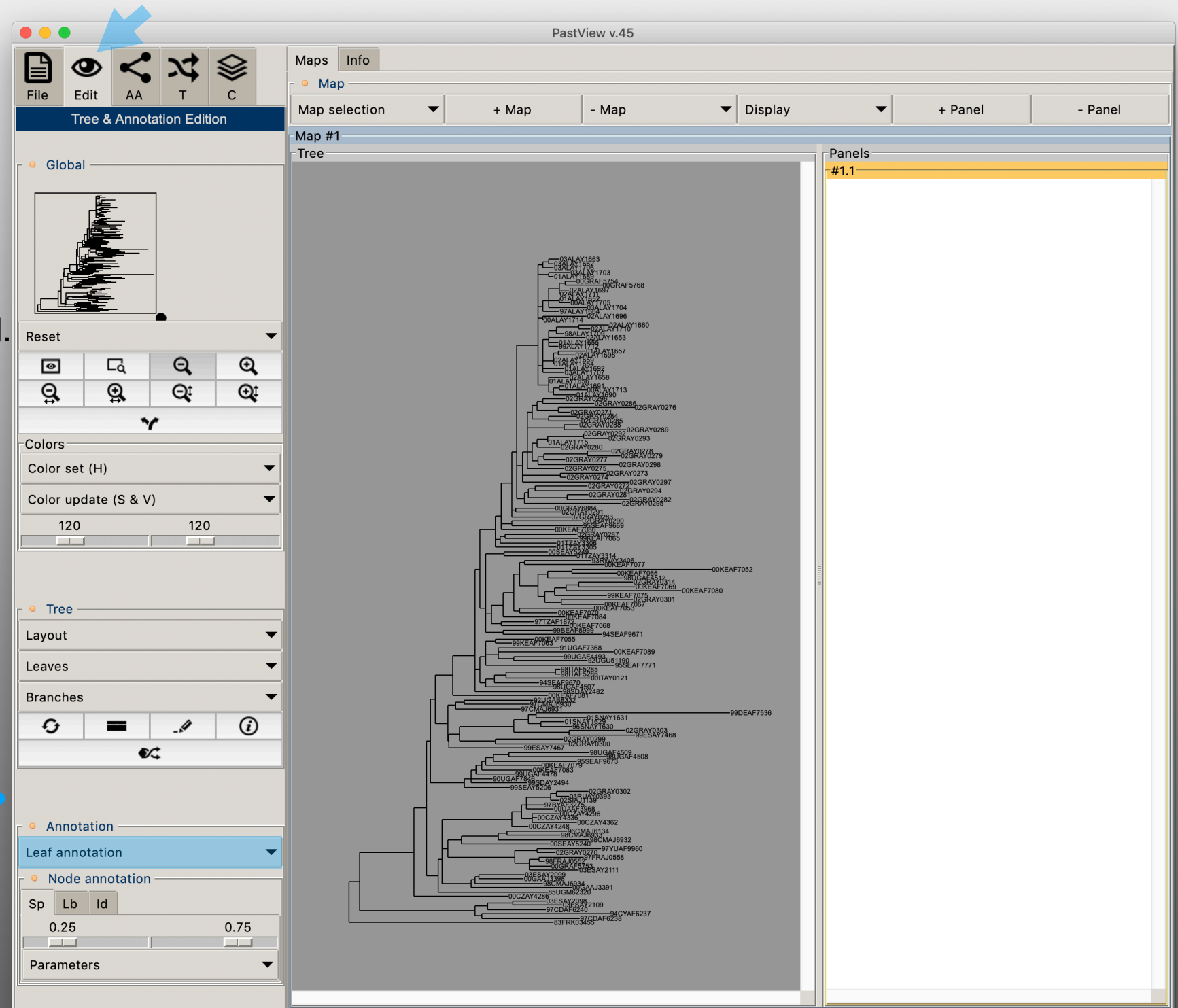
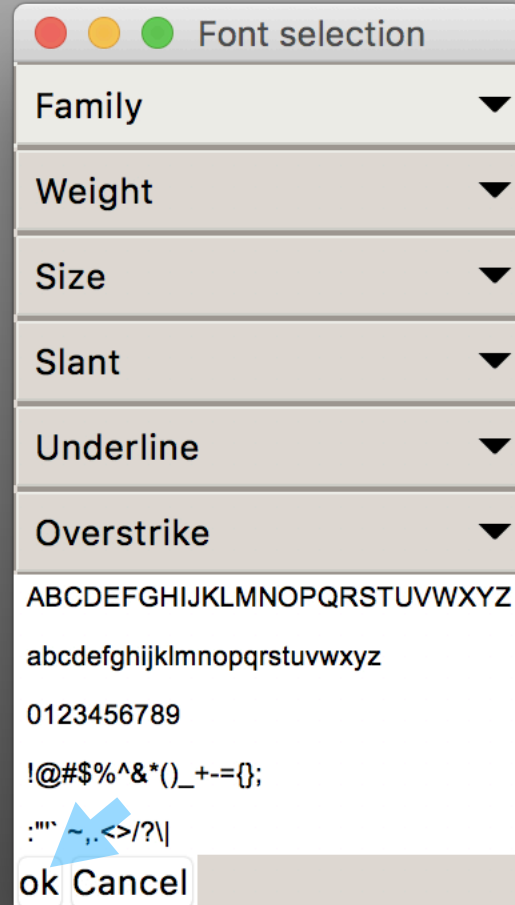


Example 1, HIV-1A analysis

Edit the tree

Switch the leaves label font to
« Arial 7 normal » (example)

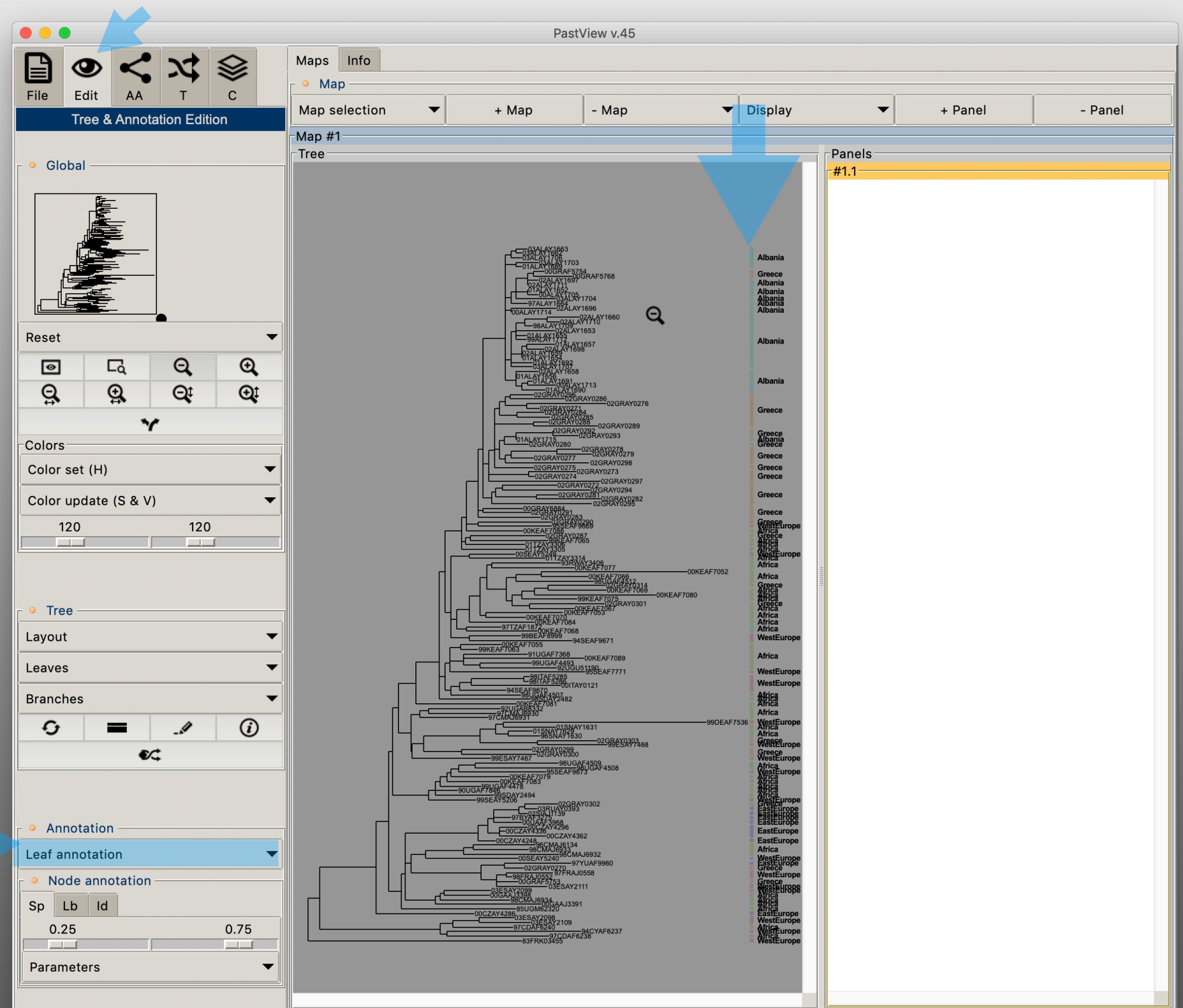
« Edit » toolbox, « Tree » sub-toolbox,
« Leaves » menu then « Font » command.
Select the new font, then clic the « ok »
button



Example 1, HIV-1A analysis

Display primary annotations in regard of Leaves

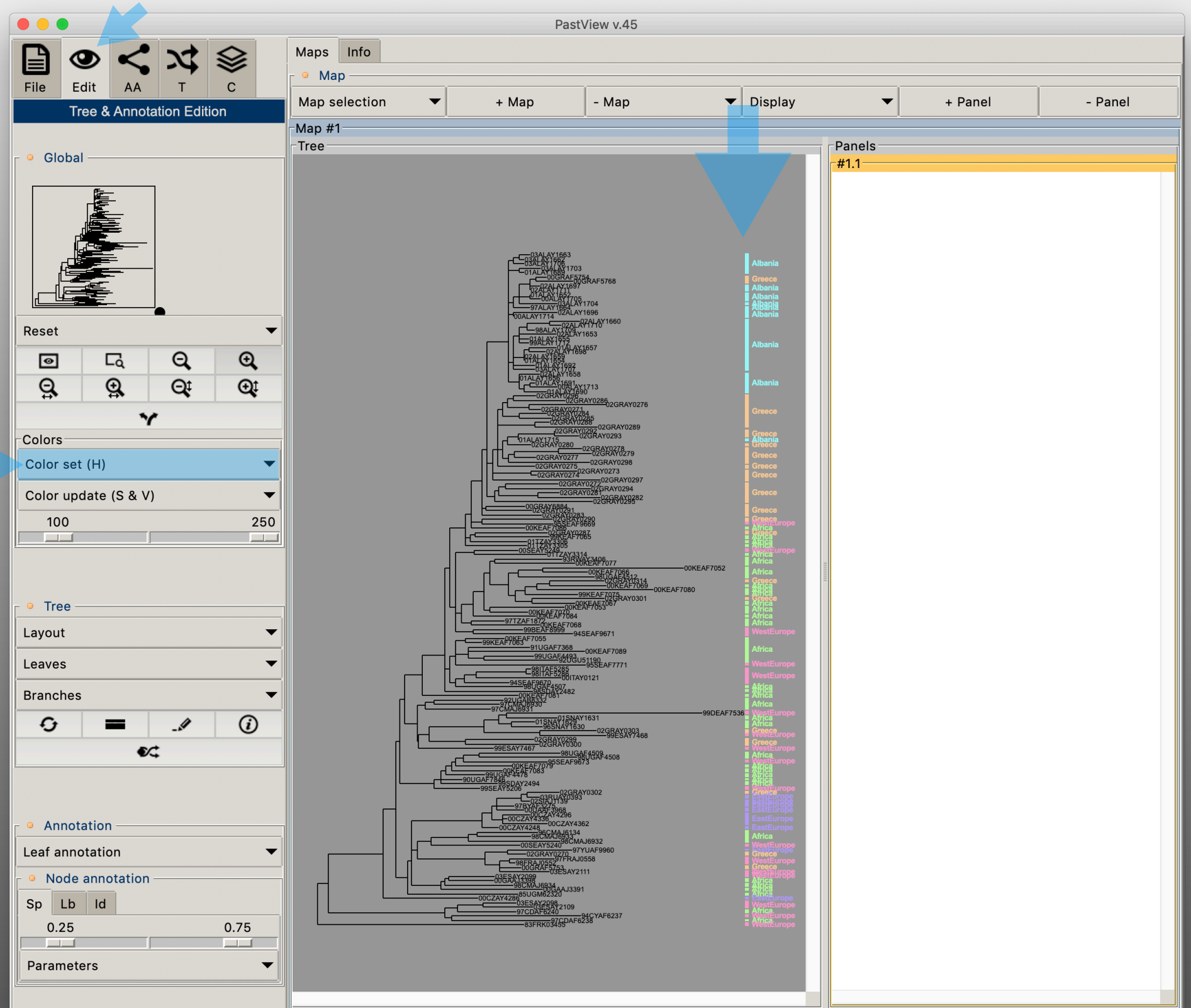
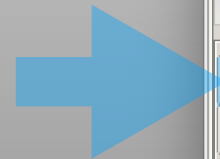
From the « edit » toolbox and the « Annotation » sub-toolbox, clic the « Leaf annotation » menu and select the command « Color brackets with text »



Example 1, HIV-1A analysis

Display primary annotations in regard of Leaves

Update the color palette with the command « Equalize » from the « Color set (H) » menu

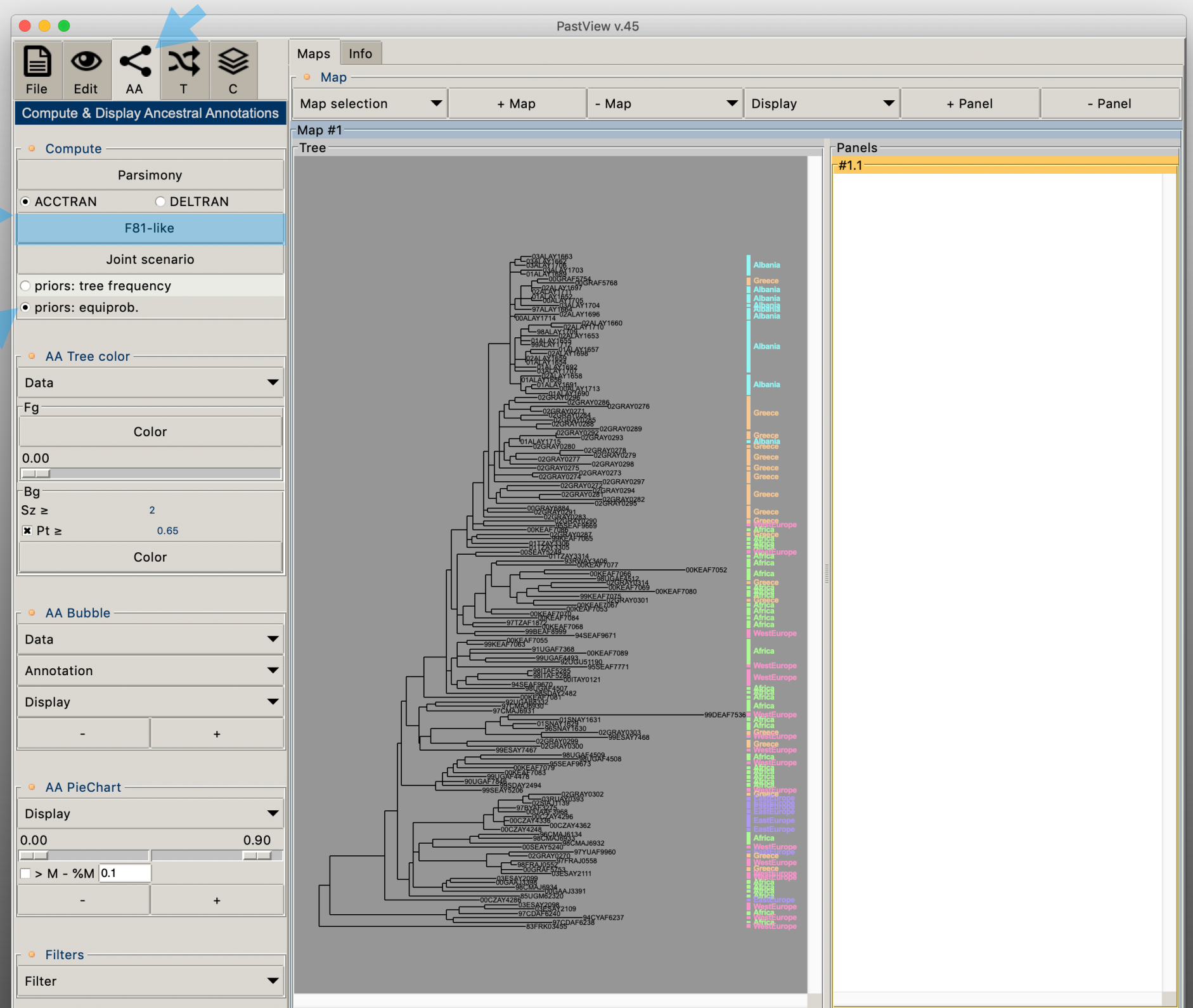


Example 1, HIV-1A analysis

Compute ancestral annotations by marginal maximum likelihood

Select the « AA » tab and clic the « F81-like » button

In this example we use the option of equiprobability for the annotations



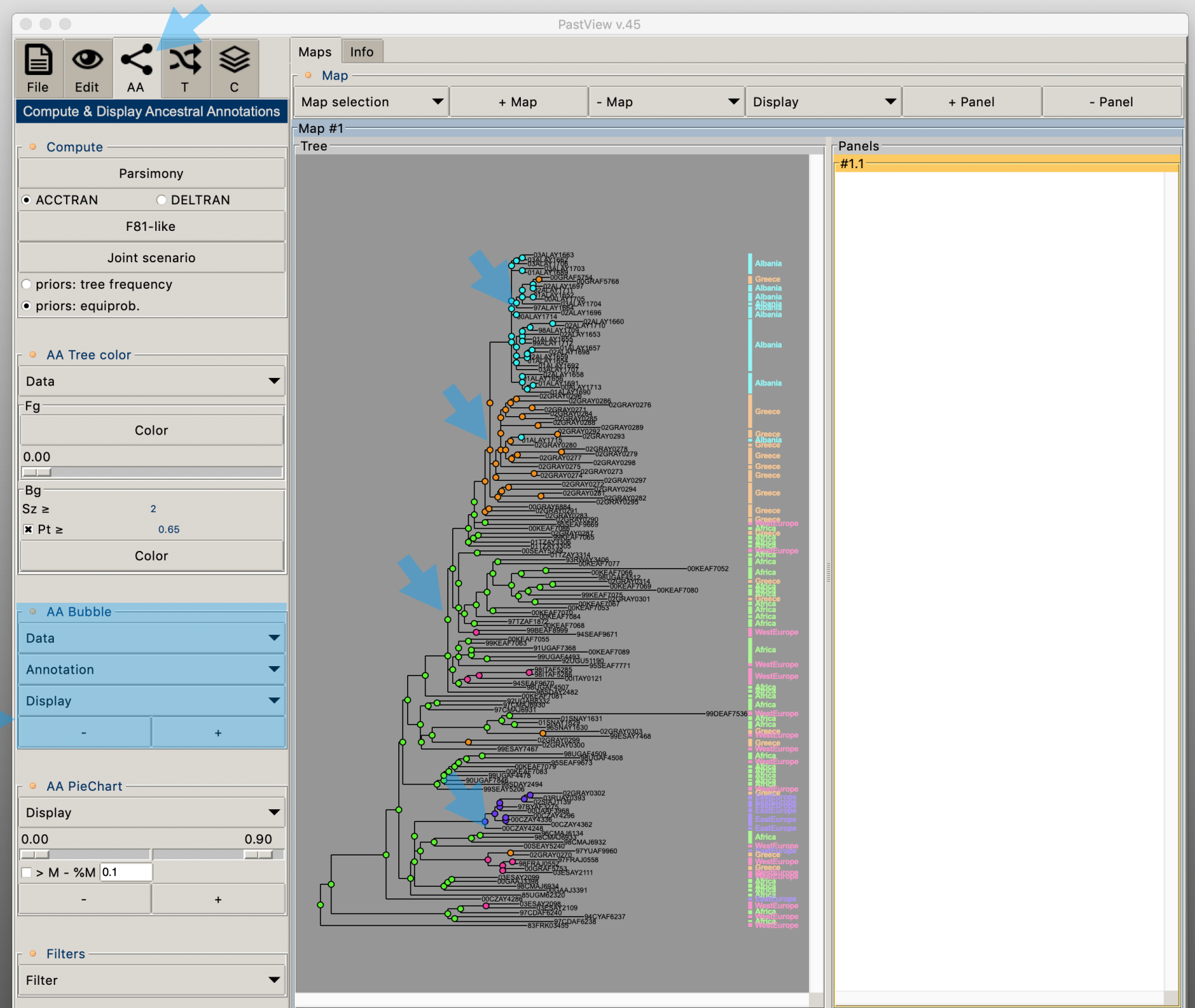
Example 1, HIV-1A analysis

Display the majority annotation from the ancestral annotations computed by marginal maximum likelihood

From the « AA » tab and the « AA Bubble » select the « Majority » option from the « Display » menu, and select the « Select all » command from the « Selection » menu

Use the - and + button to change the size of the bubbles.

To restrict the view to one or several specific annotation select/unselect them from the « selection menu »

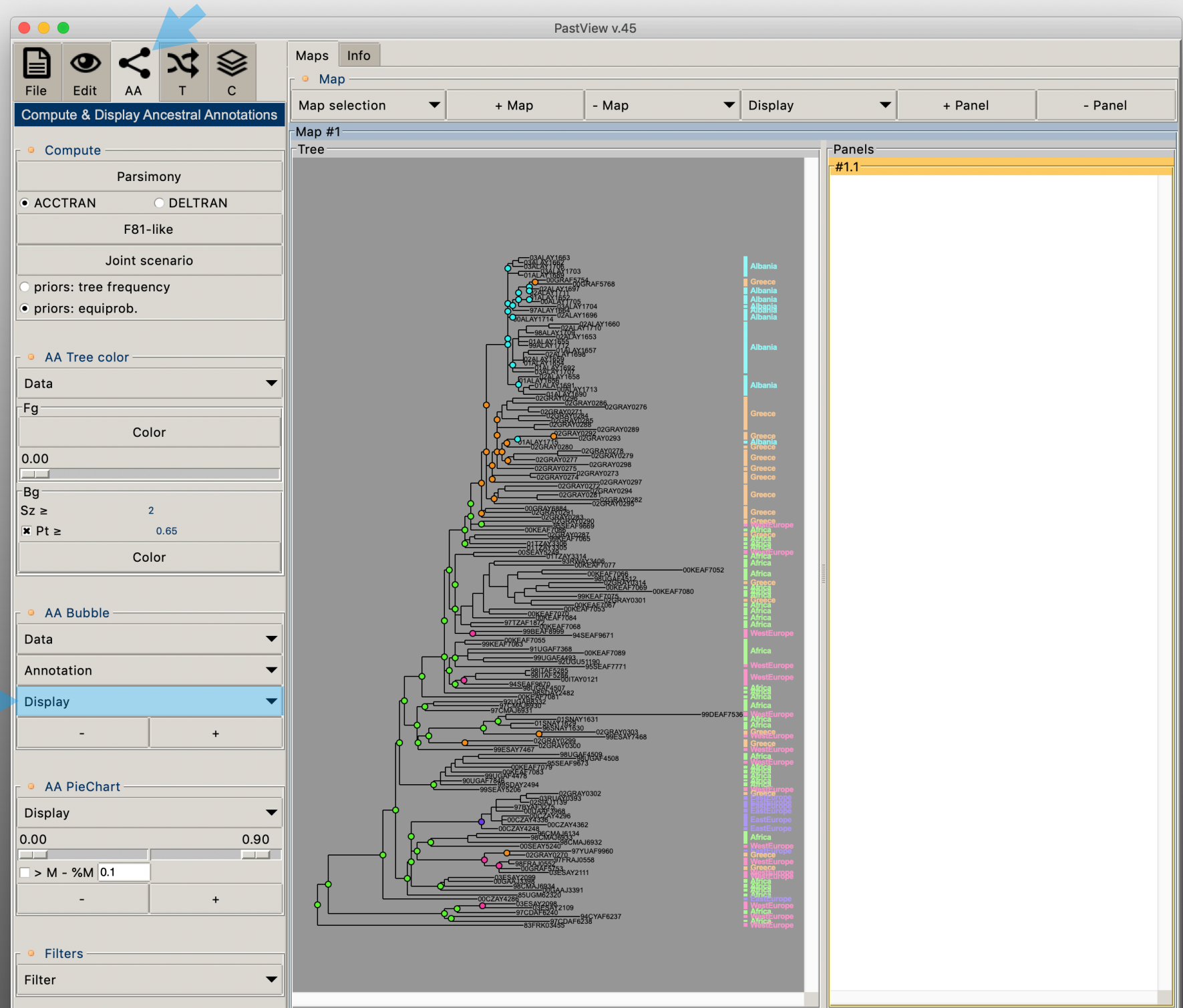


Example 1, HIV-1A analysis

Display a simplified view of the bubbles showing the majority annotation from the ancestral annotations computed by F81-like method

Select the « Simplify view » from the « Display » command

With this simplified view, bubbles are displayed only if there is a transition underlying somewhere in the tree



Display piecharts for nodes having several annotations with high but close probabilities

In this view piecharts are displayed only if the node has annotations with a probability higher or equal to the value of the maximum of the marginal posterior probabilities minus 40% of its value

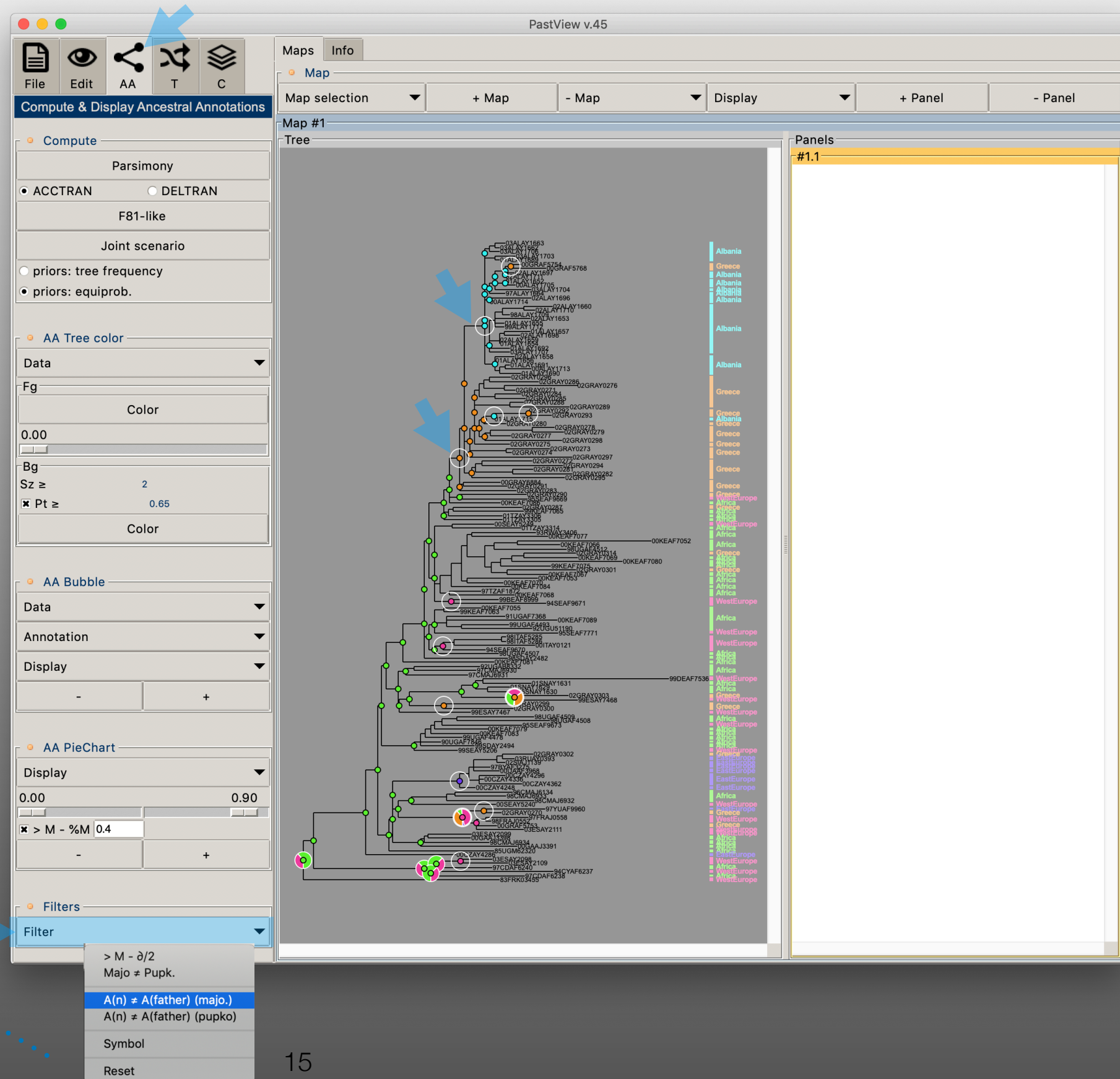
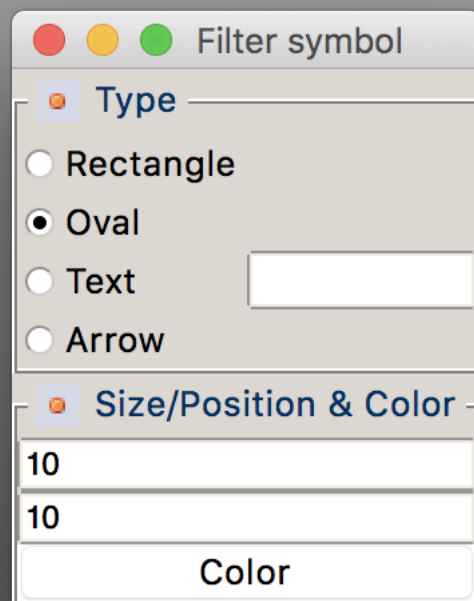


Example 1, HIV-1A analysis

Highlight the nodes coming out of a transition

From the « AA Piechart » and the filter menu, select the command: « $A(n) \neq A(\text{father})$ (majo.) ». This command will highlight nodes having a majority annotation different from the one of the father node.

The symbol used to highlight the nodes can be tuned (shape, size, color...) with the « Filter symbol » panel (« Filter » menu, « Symbol » command)



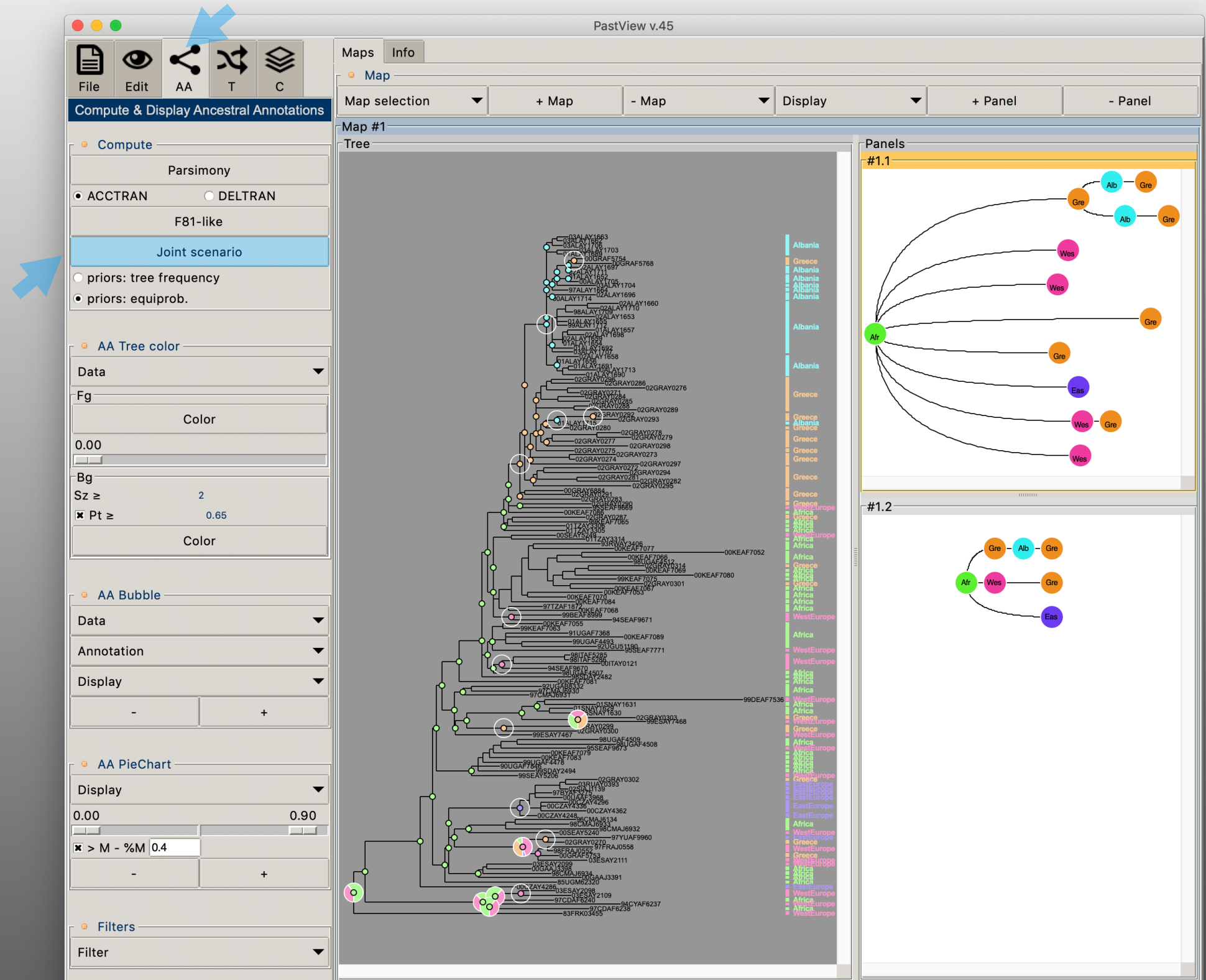


Example 1, HIV-1A analysis

Compute ancestral annotations by joint maximum likelihood

Select the « AA » tab and clic « Max. Like. Joint (Pupko) » button

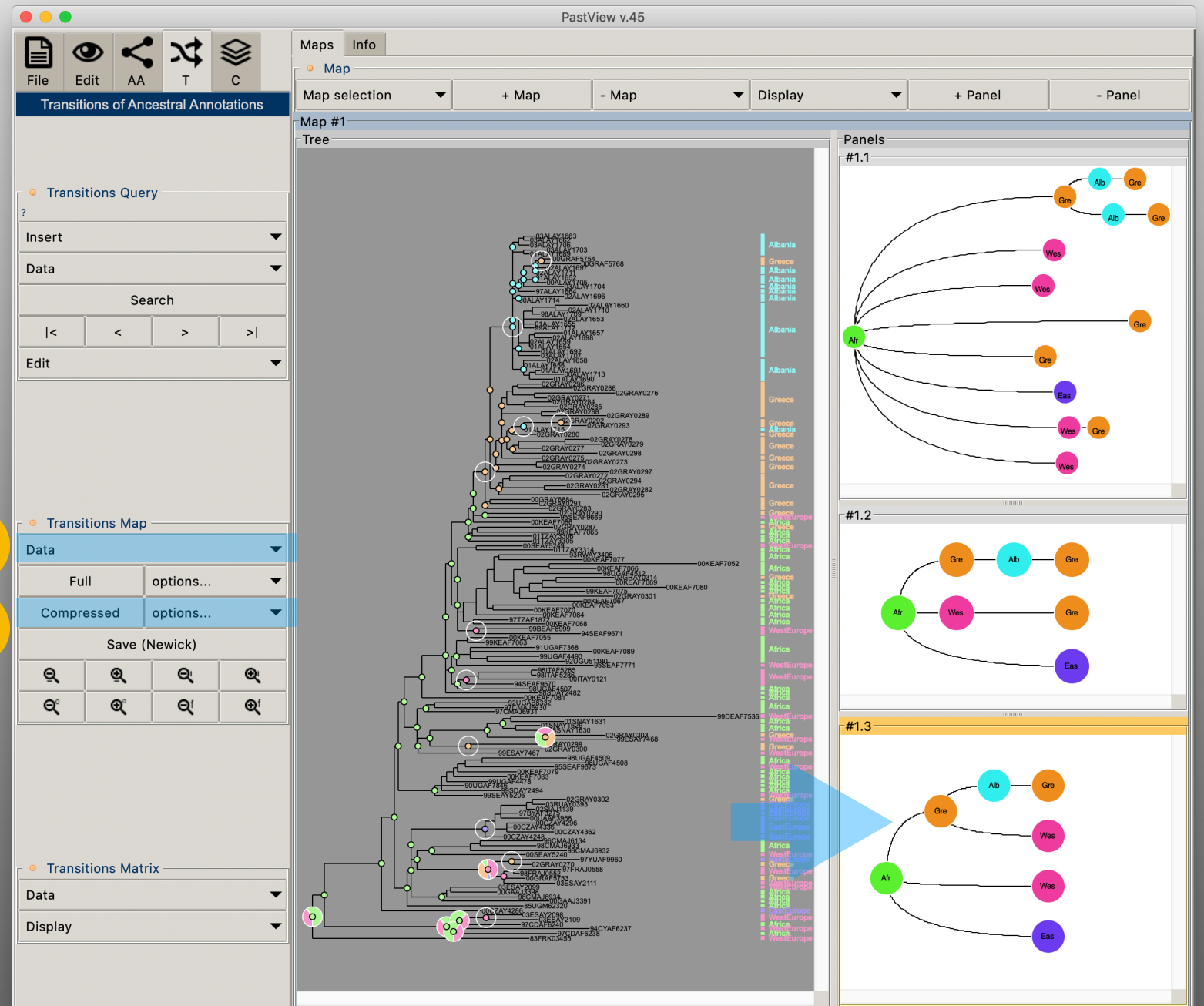
In this example we use the option of equiprobability for the annotations



Example 1, HIV-1 A analysis

Compute a transition map with the ancestral annotations computed by joint maximum likelihood

- 1 Add a panel with the « +Panel » button
- 2 Select the « joint scenario » from the « data » menu
- 3 Display a « Slanted » layout and click the « compressed » button



1 Add a panel

2 From the « AA Tree color » toolbox select the ancestral annotation data set « Majority » (« data » menu)

3 From the « Bg » toolbox set values as following : Sz ≥ 2 & Pt ≥ 0.65 and clic the « Color » button

The screenshot displays the PastView v.45 software interface. The main window shows a phylogenetic tree with nodes colored by ancestral state reconstruction. The left sidebar contains various settings for the analysis, including the method (ACCTRAN), tree color (Data), and bubble size (2). The right sidebar shows four panels of ancestral state reconstructions, labeled #1.1, #1.2, #1.3, and #1.4. Panel #1.1 shows a simple tree with nodes colored by state. Panel #1.2 shows a tree with nodes colored by state and a legend. Panel #1.3 shows a tree with nodes colored by state and a legend. Panel #1.4 shows a tree with nodes colored by state and a legend. The top of the interface has a menu bar with File, Edit, AA, T, and C. The bottom of the interface has a status bar.

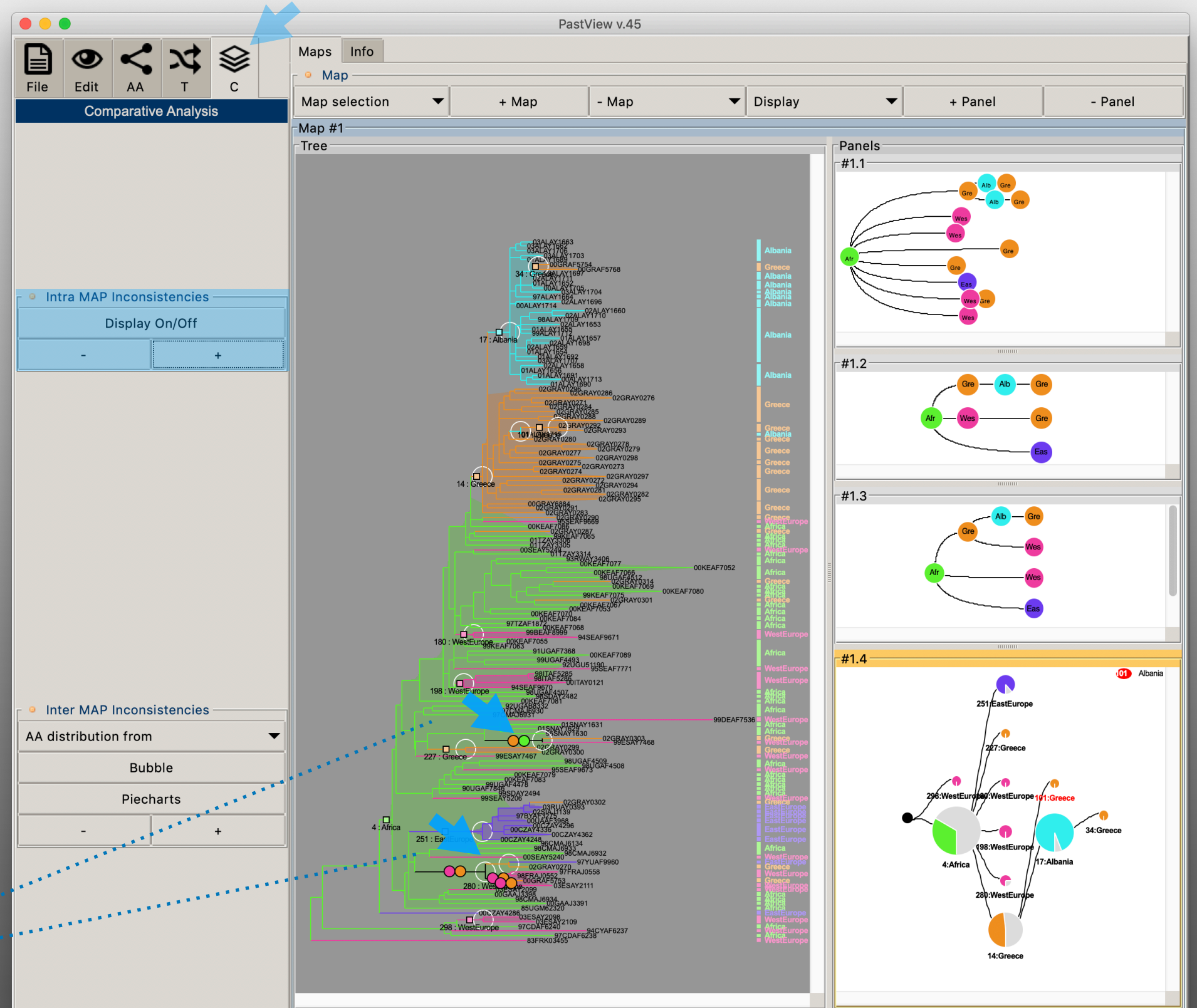
Example 1, HIV-1A analysis

Highlight the inconsistencies of ancestral annotations between marginal (majority) and joint maximum likelihood

Select the « C » tab

Clic the « Display On/Off » button from the « Intra MAP inconsistencies » toolbox. Use the - and + button to adapt the view

The tree is foreground color coded according to the ancestral annotation if it is the same between the different data sets (here joint and marginal). If the ancestral annotation is different bubble are drawn. The first one is the majority of marginal maximum likelihood and the second one is joint maximum likelihood



Example 1, HIV-1A analysis

Export graphic output

From the « File » tab and the « Save » toolbox, save the PastView graphic output to the PostScript format. PostScript is a high quality vectorial format, easily editable

