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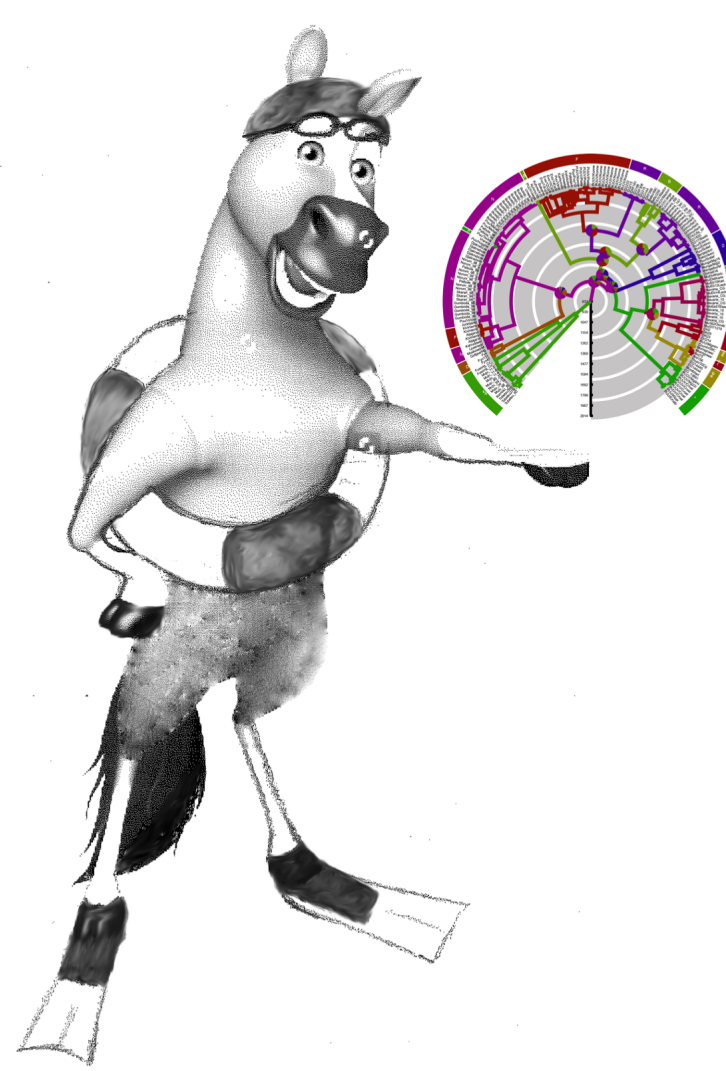
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AquaPony: visualization and interpretation of phylogeographic information on phylogenetic trees



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<http://www.atgc-montpellier.fr/aquapony>

Introduction

- Visualization and interpretation of phylogeographical scenarios is increasingly used in many biological fields.
- Several tools can infer ancestral traits for internal nodes in a phylogeny. Visualizing such information and its uncertainty remains tedious with current tools. Comparing alternative scenarios is even more complicated.
- We present AquaPony (AP, for « Annotation QUICK Analysis on PhyLOgeNY »), a web-based tool that facilitates such operations.

Implementation

- AP can be used on the ATGC web platform.
- AP is implemented in JavaScript language, its code source is freely available under Cecill Licence.
- AP is fast enough for displaying very large trees.
- AP can be easily incorporated in other web-based applications.

Software description and main features

- AP takes as input an evolutionary tree, whose nodes are annotated with some inferred traits.
- The input file is parsed to extract annotations that can be drag & dropped from the *List of Annotations* and the Annotation panel (Fig 1).



Figure 1: AP interface showing the List of annotations and annotations panels.

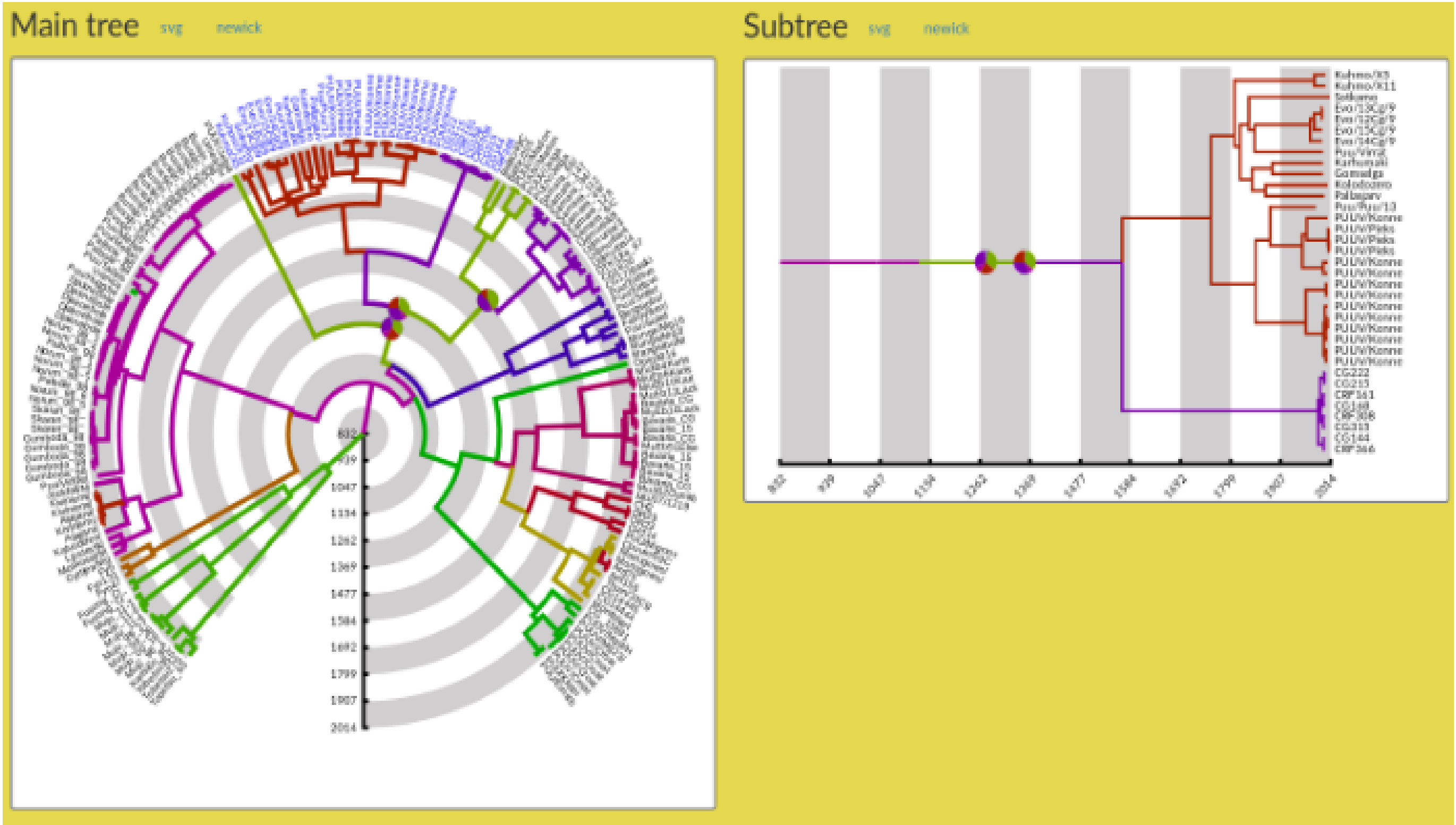


Figure 2: AP interface showing the Main tree and subtree panels.

- AP displays the tree (Main tree panel), and some chosen subtree (subtree panel) (Fig 2).
- Probabilities of trait states for a node are shown as a piechart, materializing the uncertainty of ancestral annotations (Fig 2).
- Branch supports are represented by color points (given a chosen threshold) (Fig 3).

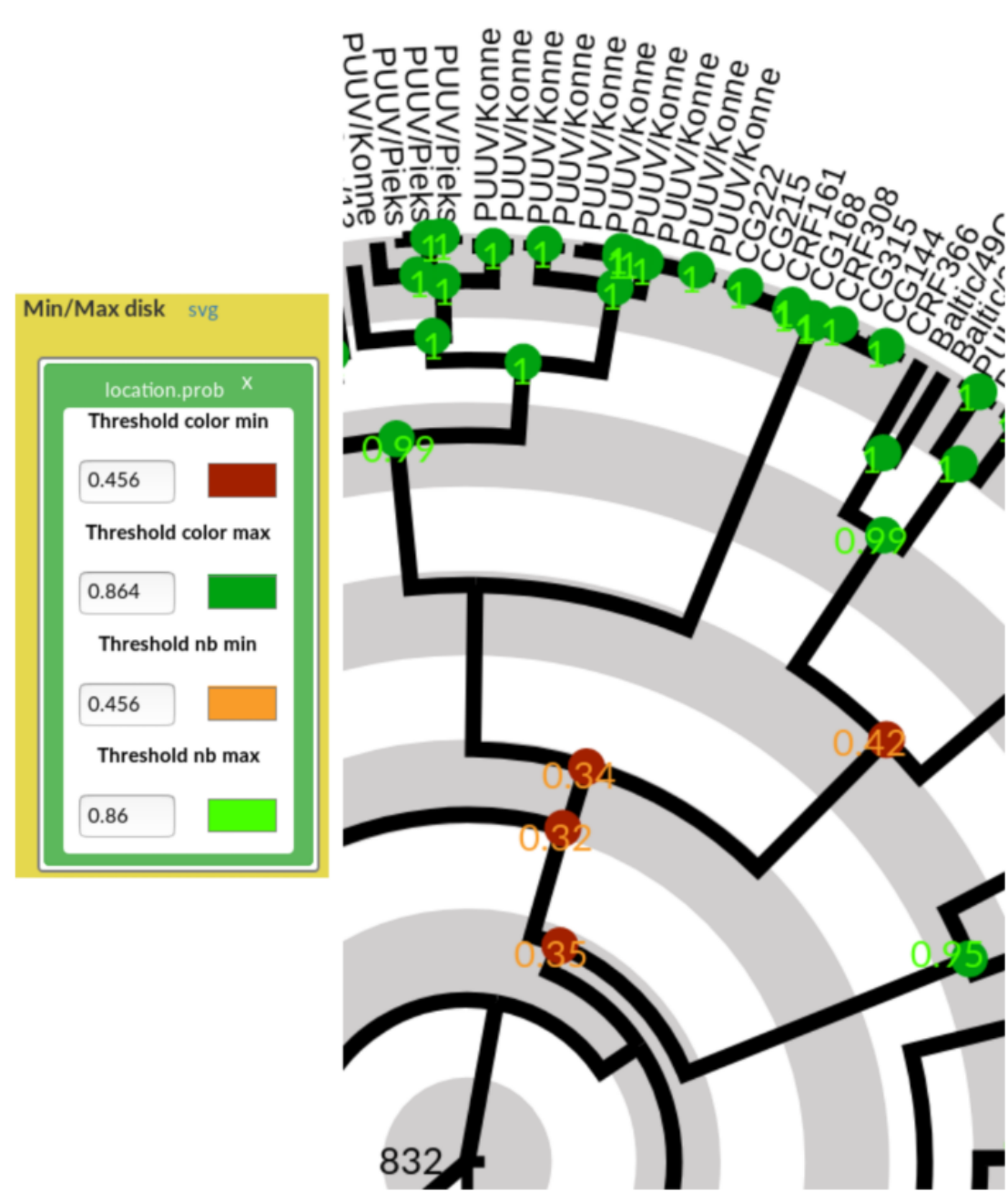


Figure 3: Representation of branch supports according to the chosen threshold (green point if >, red if <)

- The Scenarios panel (Fig 4) displays two alternatives scenarios upon selection of a leaf or node. They are shown as multi-color horizontal bars with the associated time scale.



Figure 4: AP interface showing Scenarios panels.

- To help comparing scenarios, a score that combines the probabilities of their trait states, is computed and displayed right of them.

Conclusions and perspectives

- AP eases some manipulations that remain tedious with other tools as the gestion of the uncertainty and the comparison of alternative phylogeographical scenarios along a branch in the tree.
- AP provides a dynamic interface implemented as a lightweight web-browser, platform independent, application. Its open source code allows for future extensions and new features.
- Extension to visualize evolutionary networks and study of pertinent scenarios' scores belong to future work.