EvoLaps version 2: enhanced visual exploration of phylogeographic scenarios

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Summary

EvoLaps is a web-based platform aimed at visualizing the spatio-temporal spread of pathogens. It is based on the annotated maximum clade credibility tree obtained through a BEAST continuous phylogeographic inference.

Changes of locations (transitions), in a "Top-Down" reading of the tree (from the root to its leaves), are represented on a cartographic background using paths between them. The set of paths makes a phylogeographic scenario. A raw reading of these transitions produces complex scenarios. EvoLaps helps to analyze them with brush selection, highlight processes, and animation tools. EvoLaps also offers the possibility to discretize the continuous locations into spatial clusters. The EvoLaps clustering is dynamic and iterative, allowing more or less detailed phylogeographic scenarios according to specific spatio-temporal scales.

EvoLaps also provides tools to corroborate third-party variables associated to the phylogeographic scenario such as the overimposition of intensity maps, or estimate of ancestral character states from discrete variables.

Future directions

- methodological developments such as **(i)** clustering of localities based on the spatial distribution AND the phylogenetic tree topology, **(ii)** introduction of phylodynamic and statistical methods, **(iii)** graph theory approach in the design of transition trees,
- technical developments to optimize EvoLaps analyses.

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Exemple: Rice Yellow Mottle Virus in East Africa

- A phylogeographic scenario is represented on a geographical map through a set of paths between ancestral and sampled locations (transitions), whose thickness, opacity, color and curvature are proportional to time. The grey geographical zones correspond to areas of uncertainty of the ancestral localities. Highlighted transitions (green and purple colors) is done on the fly and in an interconnected way between the graphical components (here the geographical map, the phylogenetic tree and the migration distance curves). The scenario can be animated gradually over time, or at time intervals, over the entire phylogenetic tree or over a particular clade.
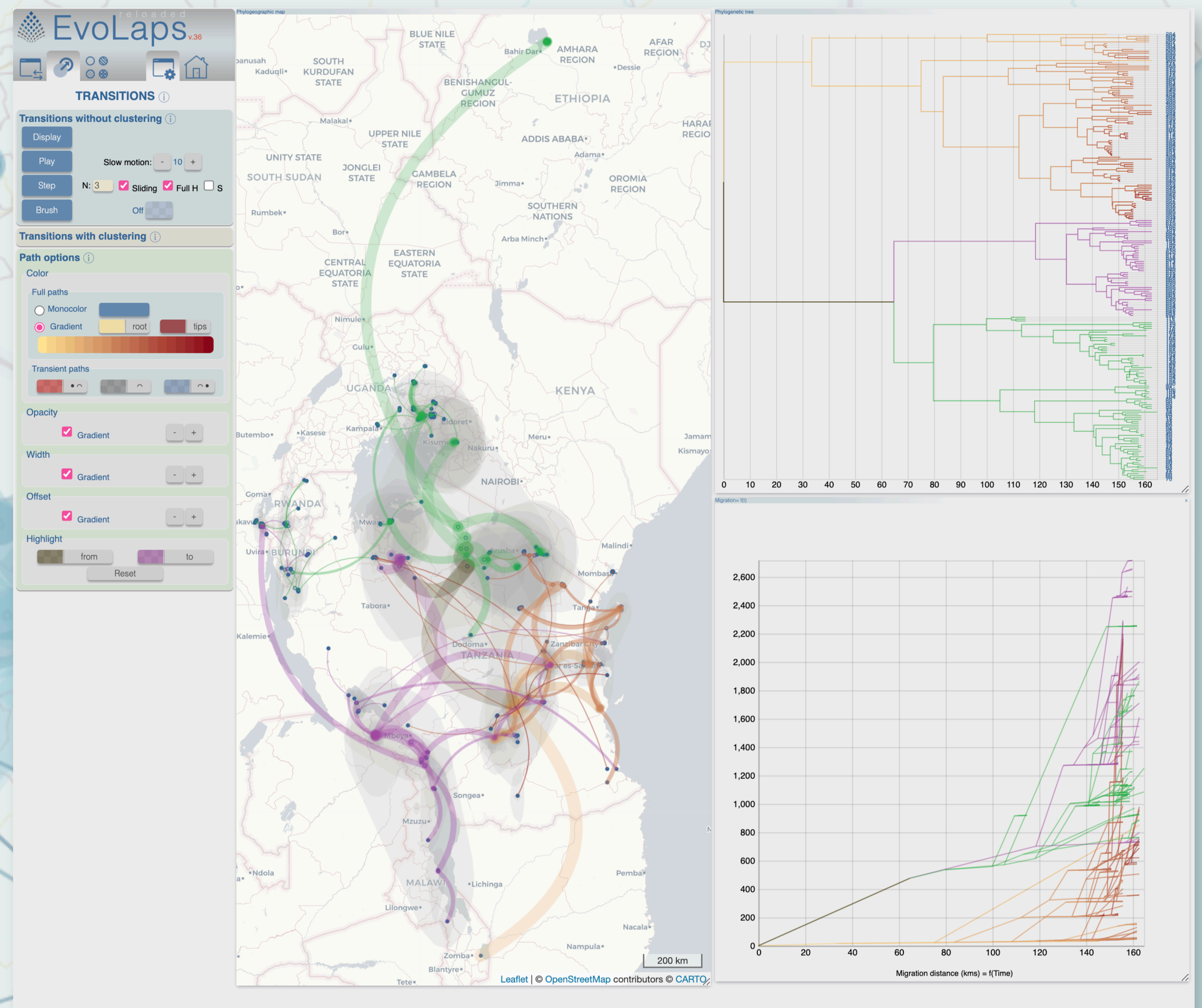
- Clustering sampled and ancestral localities makes it possible to produce synthetic views of the phylogeographic scenario, with the production of a tree of transitions or matrices of inter-regional exchanges. Clustering is dynamic and iterative, using different methods/tools such as lasso, anchor, clade selection, latitude/longitude grid, K-means. An analysis is initialized with a small number of large clusters, and selected clusters can be subdivided afterwards for a higher resolution.