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To cite this version:

HAL Id: hal-01942605
https://hal.umontpellier.fr/hal-01942605
Submitted on 27 May 2020

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Phylogenetics

SylvX: a viewer for phylogenetic tree reconciliations
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Associate Editor: Prof. Alfonso Valencia
ABSTRACT

Motivation: Reconciliation methods aim at recovering the evolutionary processes that shaped the history of a given gene family. Such a history is composed of speciation events, duplications, transfers and losses, and other evolutionary events affecting particular genes at specific times in evolution (Page et al., 1998). Reconciliation methods are also used in co-diversification studies where the phylogeny of parasite species compared to that of host species infected by these parasites. Here a different set of evolutionary events is considered including co-speciation events, duplications, and transfers. Few tools are currently available to visualize reconciliations: Tarzan/CoRe-PA (Merkle et al., 2005), Jane (Conow et al., 2010) and PrIMETV (Sennblad et al., 2007) packages use a two-dimensional Euclidean slanted layout for the representation of reconciliations. The 3DPE editor (Kim et al., 2007) uses a 2.5D representation of a slanted layout, crossing species (X) vs. evolutionary time (Y) vs. parasites (Z). In spite of these powerful tools for illustrating how a “guest” tree (e.g., a gene history) evolves inside a host tree (e.g., species tree), these interconnected graphs can be visually hard to interpret when the number of evolutionary events depicted is high. Another issue is that the available viewers lack the ability to compare reconciliations obtained under different settings (e.g., different event costs) or to compare reconciliations for different genes families (or parasite taxa) on the same species tree. The goal of SylvX is the graphical management of such drawings and the generation of publication-ready illustrations.

1. INTRODUCTION

Reconciliation methods compare gene trees and species trees to recover the history of gene families. Such a history is composed of speciation events, duplications, transfers and losses, and other evolutionary events affecting particular genes at specific times in evolution (Page et al., 1998). Reconciliation methods are also used in co-diversification studies where the phylogeny of parasite species compared to that of host species infected by these parasites. Here a different set of evolutionary events is considered including co-speciation events, duplications, and transfers. Few tools are currently available to visualize reconciliations: Tarzan/CoRe-PA (Merkle et al., 2005), Jane (Conow et al., 2010) and PrIMETV (Sennblad et al., 2007) packages use a two-dimensional Euclidean slanted layout for the representation of reconciliations; the 3DPE editor (Kim et al., 2007) uses a 2.5D representation of a slanted layout, crossing species (X) vs. evolutionary time (Y) vs. parasites (Z). In spite of these powerful tools for illustrating how a “guest” tree (e.g., a gene history) evolves inside a host tree (e.g., species tree), these interconnected graphs can be visually hard to interpret when the number of evolutionary events depicted is high. Another issue is that the available viewers lack the ability to compare reconciliations obtained under different settings (e.g., different event costs) or to compare reconciliations for different genes families (or parasite taxa) on the same species tree. The goal of SylvX is the graphical management of such drawings and the generation of publication-ready illustrations.

2. METHODS

SylvX is written in Tcl/Tk. The required input is a species tree (Newick format) and one or several reconciliations in the format outputted by Mowgli (Doyon et al., 2010). Mowgli is included and dynamically linked to SylvX. TERA (Sornavacca et al., 2014) and NOTUNG (Vernot et al., 2007) output can be imported. SylvX output format is PostScript or SVG (easily integrable with many drawing package and keeping a high quality graphics). The reconciliation graphs are based on a species tree (host) using a rectangular layout with a variable thickness line, and a gene history (parasite tree), embedded in the species tree, which is composed of horizontal segments linked by vertical versus connectors. The algorithm displaying reconciliations is based on vertical translation of segments following evolutionary events. For instance, both segments of a duplication are shifted, one upwards and the other downwards. This offset is then inherited by all the subsequent nodes and is cumulative with posterior events.

3. RESULTS

SylvX’s consists of three toolboxes (Fig.1). The first one is related to maps. A map is a resizable and scrollable display space showing a species tree with one superimposed gene reconciliation. The user can add/remove maps and choose which reconciliation to display on a given map from the reconciliation toolbox (see below). Both the species tree and its gene reconciliation are updated by applying a tool (e.g., zoom) from this map toolbox. The second toolbox is specific to reconciliations. In order to display a reconciliation, first, the user needs to target one or several map(s) from the map toolbox, and secondly, select a reconciliation from the list of available ones. The reconciliation toolbox offers graphical operators such as highlighting (line thickness, dash line, foreground color), shrinking, translation or annotation that can be applied to internal nodes of a reconciliation. These operations take into account evolutionary events, including horizontal transfers. For instance, setting a new color to an internal node of a reconciliation also updates the color of all the subsequent horizontal transfers and their descendants. Reconciliations can be synchronized, meaning that a graphical modification on a reconciliation from a given map can be automatically conducted on a selection of maps displaying the same reconciliation. The third toolbox is dedicated to the species tree. A species subtree can be swapped, hidden, highlighted, colored and annotated. Like reconciliations, species trees from several maps can be synchronized.

4. DISCUSSION

The main feature of SylvX is the ability to manage multiple interactive maps of reconciliations. Synchronous highlighting operations between juxtaposed maps ease their comparison. Zooming, annotating (color, text), shrinking sub-parts of the trees help in the interpretation of chains of events. The SylvX method for displaying reconciliations is based on upward and downward translations of segments linked by versatile connectors. Displaying reconciliations having a high number of evolutive events, such as a set of successive duplications, within one (short) species tree segment is still a challenge (superimpositions of a high number of graphical items in a small drawing area). More elaborated methods available in the field of information visualization will be useful, such as the production of symbolic views (e.g., replacing a set of duplications by one « hot spot » in the tree) or tree navigation tools based on Focus/Context distortion such as the accordion zoom (Munzer et al., 2003). Another challenge is a global view of multiple genes histories on a single map/species tree. In this context, flattening or smoothing reconciliation graphs and its evolutionary events will be required to avoid messy visualizations and graphical operators acting locally, manually or automatically must be developed. In the short term, one priority is the ability to import reconciliations from other packages such as PrIMETV (Sennblad et al., 2007).
ACKNOWLEDGEMENTS

We thank Astrid Cruaud & coll. for sharing the fig/fig-wasp dataset. 

Funding: ANR Phylospace.

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Figure 1. Screenshot of a SylvX session. The left side of the interface gathers the Map toolbox, the Reconciliation(s) toolbox and the Species tree toolbox. The right side stacks maps. Duplications are represented by blue squares, losses by red crosses and transfers by arrows (variable colors). The "host-parasite" dataset used in the figure consists of the Ficus/fig wasp dataset by Cruaud et al. (2012). Two maps are in use: the one on the left displays a species tree with a superimposed reconciliation having a color coding based on transfers. The second map displays a reconciliation for the same gene but with a different costs for evolutionary events.