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SylvX: a viewer for phylogenetic tree reconciliations

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Abstract

Motivation: Reconciliation methods aim at recovering the evolutionary processes that shaped the history of a given gene family including events such as duplications, transfers and losses by comparing the discrepancies between the topologies of the associated gene and species trees. These methods are also used in the framework of host/parasite studies to recover co-diversification scenarios including co-speciation events, host-switches and extinctions. These evolutionary processes can be graphically represented as nested trees. These interconnected graphs can be visually messy and hard to interpret, and despite the fact that reconciliations are increasingly used, there is a shortage of tools dedicated to their graphical management. Here we present SylvX, a reconciliation viewer which implements classical phylogenetic graphic operators (swapping, highlighting, etc.) and new methods to ease interpretation and comparison of reconciliations (multiple maps, moving, shrinking sub-reconciliations).

Availability and implementation: SylvX is an open source, cross-platform, standalone editor available for Windows and Unix-like systems including OSX. It is publicly available at www.sylvx.org.

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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, losses, transfers 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 is compared to that of host species infected by these parasites. Here a different set of evolutionary events is considered including co-speciation events, duplications, extinctions and host switches. 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) versus evolutionary distance (Y) versus paralogs (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. a 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 (Scornavacca *et al.,* 2014) and NOTUNG (Vernot *et al.* 2008) output can be imported. SylvX output format is PostScript or SVG (easily editable 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 versatile 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
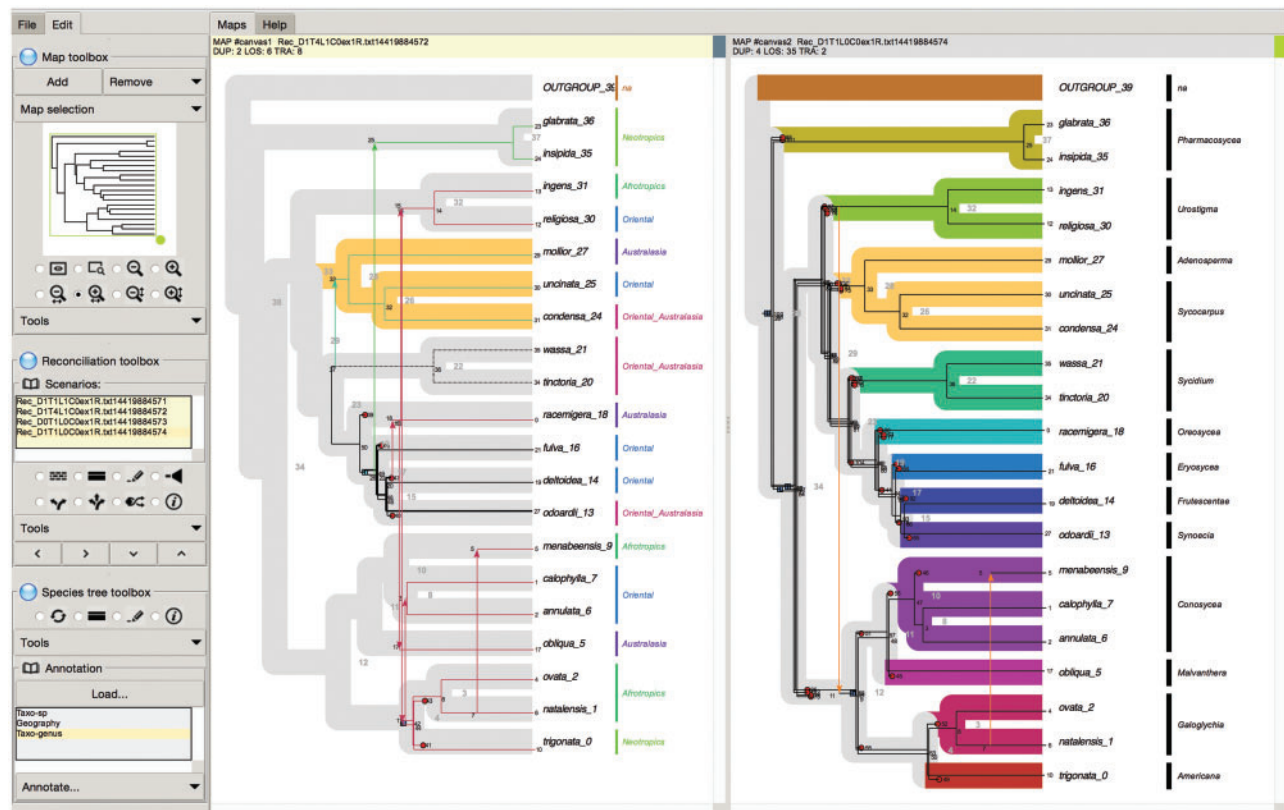
Fig. 1. Screenshot of a SylvX session. The left side of the interface gathers the *Map* toolbox, the *Reconciliation(s)* toolbox and the *Species tree* toolbox. The right side stacks maps. Duplications are represented by blue squares, losses by red crosses and transfers by arrows (variable colors). The '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 different costs for evolutionary events

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).

References

Conow,C. *et al.* (2010) Jane: a new tool for the cophylogeny reconstruction problem. *Algor. Mol. Biol.*, **5**, 1–10.

Cruaud,A. *et al.* (2012) An extreme case of plant-insect codiversification: figs and fig-pollinating wasps. *Syst. Biol.*, **61**, 1029–1047.

Doyon,J.P. *et al.* (2010) An efficient algorithm for gene/species trees parsimonious reconciliation with losses, duplications and transfers. In: *Proceedings of the 2010 International Conference on Comparative Genomics, RECOMB-CG'10*, Springer-Verlag, Berlin, Heidelberg, pp. 93–108.

Merkle,D. and Middendorf,M. (2005) Reconstruction of the cophylogenetic history of related phylogenetic trees with divergence timing information. *Theory Biosci.*, **123**, 277–299.

Munzner,T. *et al.* (2003) TreeJuxtaposer: Scalable Tree Comparison using Focus+Context with Guaranteed Visibility Proc. SIGGRAPH 2003. *ACM Trans. Graph.*, **22**, 453–462.

Kim,N. and Lee,C. (2007) Three-dimensional phylogeny explorer: distinguishing paralogs, lateral transfer, and violation of "molecular clock" assumption with 3D visualization. *BMC Bioinformatics*, **8**, 213.

Page,R.D.M. and Charleston,M.A. (1998) Trees within trees: phylogeny and historical associations. *Tree*, **13**, 356–359.

Scornavacca,C. *et al.* (2014) Joint amalgamation of most parsimonious reconciled gene trees. *Bioinformatics*, **31**, 841–348.

Sennblad,B. *et al.* (2007) PrIMETV: a viewer for reconciled trees. *BMC Bioinformatics*, **8**, 148.

Vernot,B. *et al.* (2008) Reconciliation with non-binary species trees. *Journal of Computational Biology*, **15**, 981–1006.