

TreeDomViewer: A tool for the visualization of phylogeny and protein domain structure

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Introduction

Phylogenetic analyses and examination of protein domains are critical to comparative genomic studies. TreeDomViewer is a versatile visualization tool available as a PERL web-based interface that analyzes a phylogenetic tree description, multiple sequence alignment, and InterProScan results of the sequences, and generates an interactive phylogenetic tree with the corresponding protein domain information projected onto it.

Innovation

- ▶ Interactive domain structure and phylogeny visualization in one picture.
- ▶ Domain structures are aligned.

System and Methods

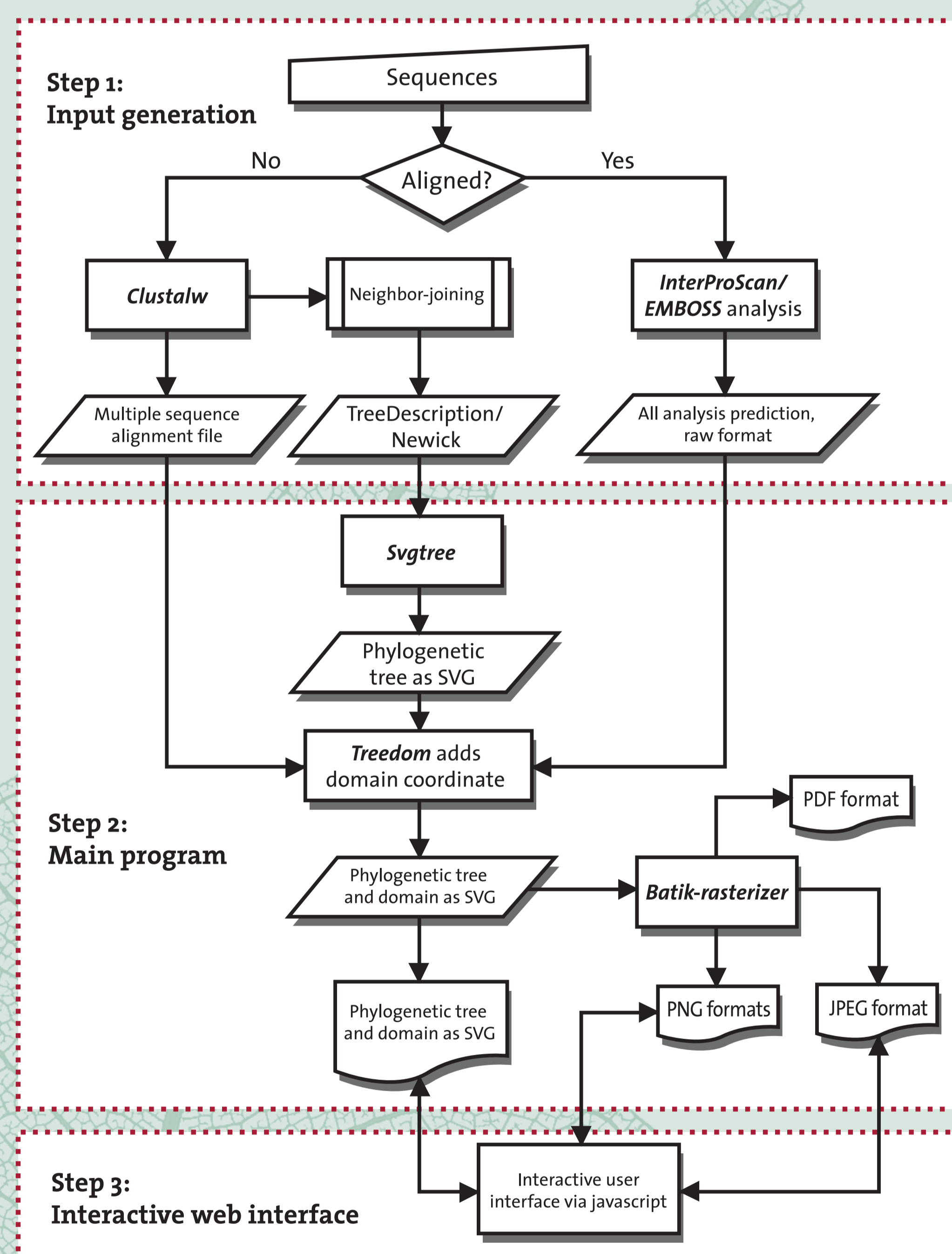
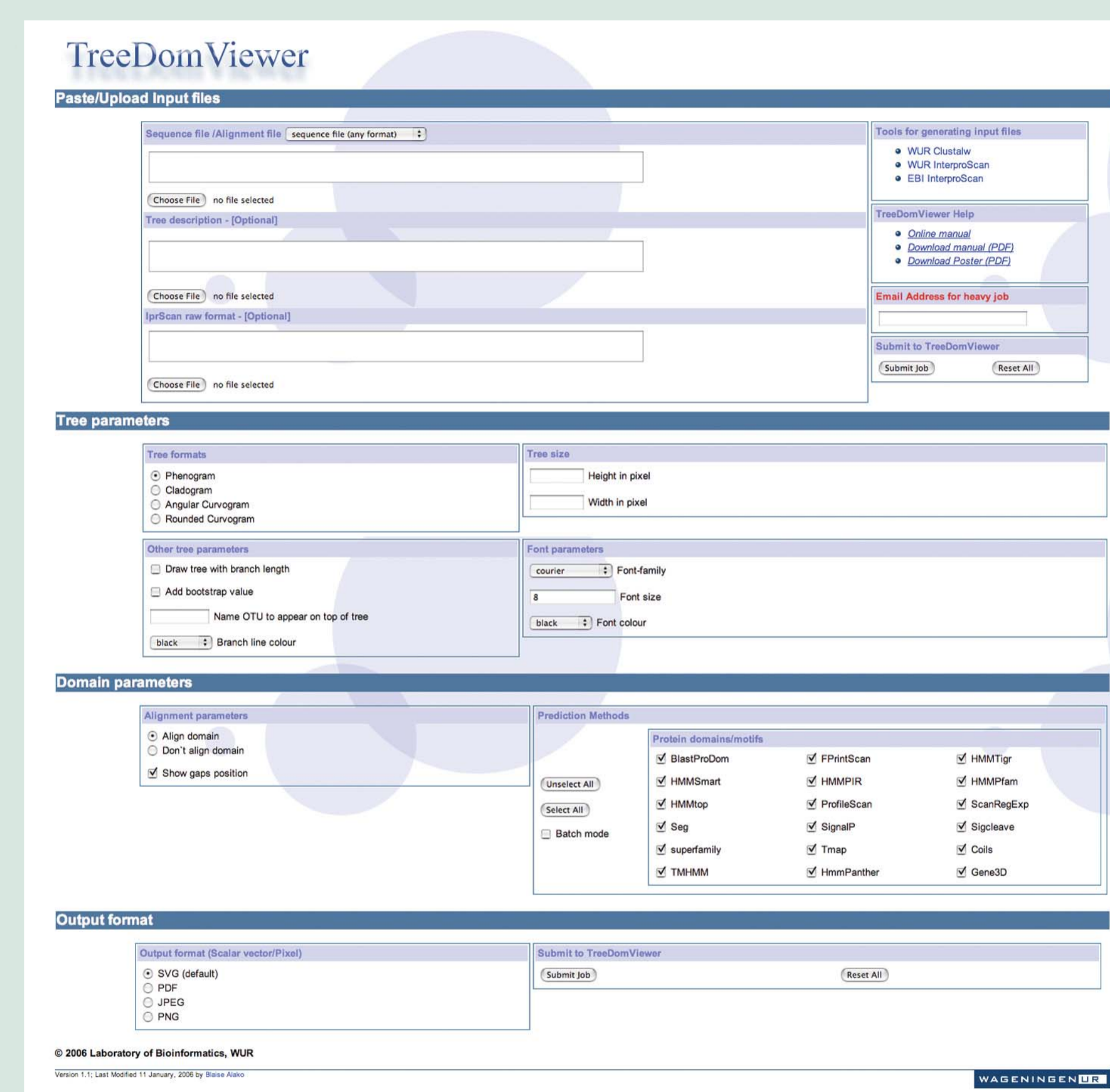


Figure 1 Flow chart of TreeDomViewer illustrating sequence of application implemented. Software tools used are in bold. Three types of data input are processed and domain information is coordinated with the alignment and phylogenetic tree information to produce an interactive SVG output.

Framework

The core application consists of three main programs: *Svtree*, *Treedom*, *batik-rasterizer* developed in C, PERL and JAVA respectively.

Interface



TreeDomViewer programs are full command line tools that can be used as plug-ins for other applications.

Figure 2 A web interface for interacting with TreeDomViewer programs.

TreeDomViewer Output

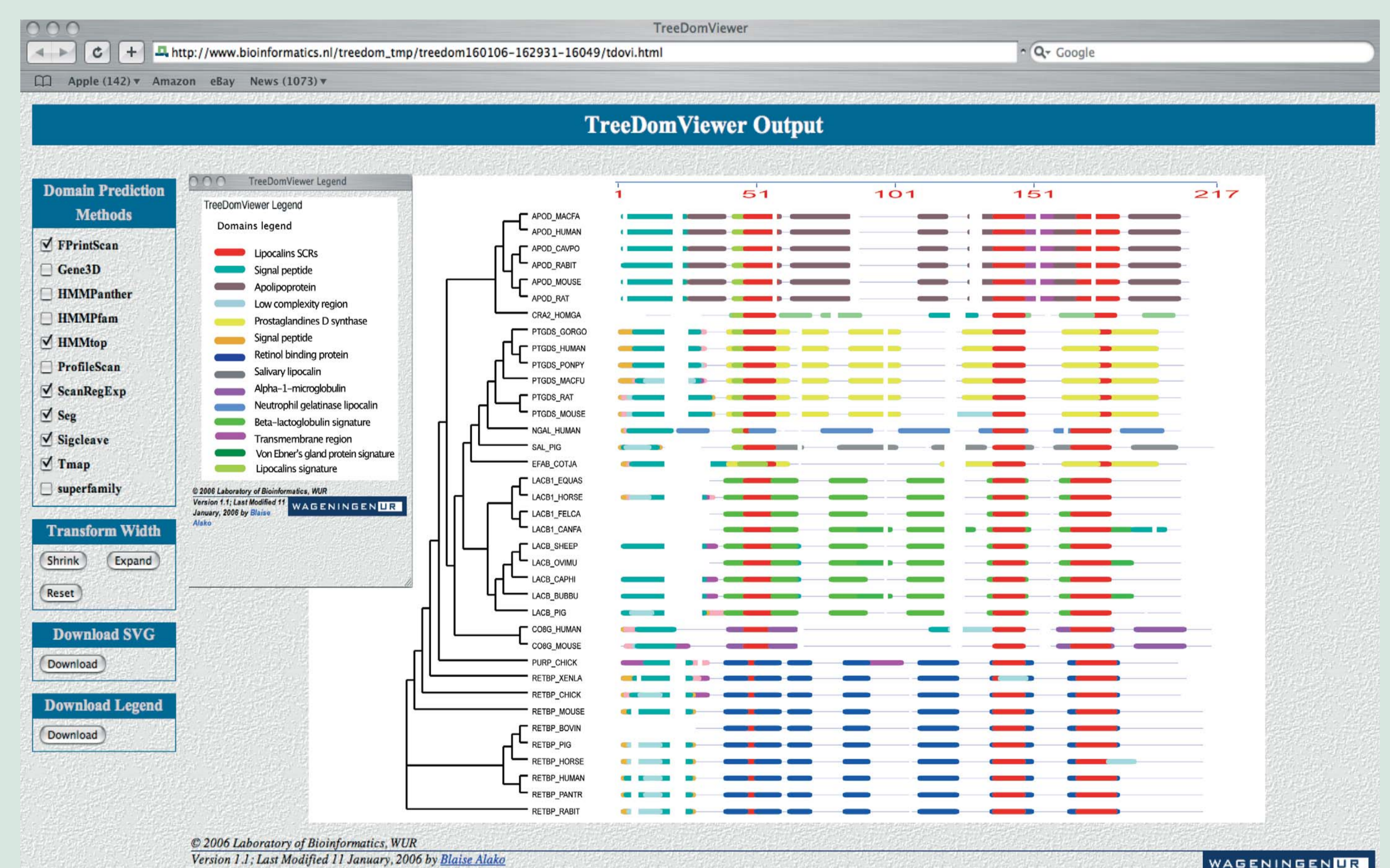


Figure 3 This figure illustrates the default SVG output of 37 lipocalins family members from different species. Shown in red are the main structurally conserved residues (SCRs) that characterize the lipocalins

Conclusion

TreeDomViewer is the first web-based tool in its kind that essentially combines proteins information with phylogeny.

Availability

TreeDomViewer is freely available for academic use at <http://www.bioinformatics.nl/tools/treedom/> Source code can be obtained upon request to the authors.

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