What is DoubleRecViz?

DoubleRecViz is a tool for visualizing and editing double reconciliations between phylogenetic trees at three levels: transcript, gene and species. DoubleRecViz makes use of an extension of the recPhyloXML model (developed for gene-species tree reconciliation) to represent joint transcript-gene and gene-species tree reconciliations. DoubleRecViz is implemented using the Dash library, which is a toolbox that provides dynamic visualization functionalities for web data visualization in Python.

DoubleRecViz takes as input one the following types of object:

- a `<doubleRecPhylo>` object containing 1 species tree (`<spTree>` object) followed by 1 to n sets such that each set is composed of 1 reconciled gene tree (`<recGeneTree>` object) followed by 0 to n reconciled transcript trees (`<recTranscriptTree>` object).
- a `<recPhylo>` object containing 1 species tree (`<spTree>` object) followed by 1 to n reconciled gene trees (`<recGeneTree>` object)
- a `<recPhylo>` object containing 1 gene tree (`<gnTree>` object) followed by 1 to n reconciled transcript trees (`<recTransTree>` object)

DoubleRecViz makes use of the doubleRecPhyloXML and recTransTreeXML grammars which are extensions of the recPhyloXML and recGeneTreeXML grammars inherited from phyloXML and designed to describe reconciled gene-species tree reconciliations (detailed description of the recPhyloXML and recGeneTreeXML grammars).

Example of `<doubleRecPhylo>` objects for transcript-gene-species tree reconciliations, and `<recPhylo>` objects for a transcript-gene and gene-species tree reconciliations can be found in the testData directory of the GitHub repository.

A detailed description of the doubleRecPhyloXML and the recTransTreeXML formats can be found below.

doubleRecPhyloXML and recTransTreeXML

XML for transcript-gene-species tree reconciliation

XML Schema Definition (XSD) files: see here

Introduction

The **doubleRecPhyloXML** format is designed to represent transcript-gene-species tree reconciliations. The **recTransTreeXML** format is designed to represent transcript-gene tree reconciliations. They are extensions of the recPhyloXML and recGeneTreeXML grammars which were designed to describe gene-species tree reconciliations

doubleRecPhyloXML

The recPhyloXML grammar describes a reconciliation as a set comprised of a species tree (`<spTree>` tag) followed by one or more reconciled gene trees (`<recGeneTree>` tag).

The doubleRecPhyloXML grammar enriches the recPhyloXML grammar by allowing reconciled gene trees to be followed by one or more reconciled transcript trees (`<recTransTree>` tag described below).

Below is the skeleton of a `<doubleRecPhylo>` object with a species tree, followed by a first reconciled gene tree with two reconciled transcript trees, a second reconciled gene tree with one reconciled transcript tree, and a third reconciled gene tree with zero reconciled transcript tree.

```
<doubleRecPhylo>
  <spTree>
    species tree as defined in the recPhyloXML grammar
    ...
  </spTree>
  <recGeneTree>
    1st recGeneTreeXML reconciled gene tree as defined in the recPhyloXML grammar
    ...
  </recGeneTree>
  <recTransTree>
    1st recTransTreeXML reconciled transcript tree with 1st gene tree
    ...
  </recTransTree>
  <recTransTree>
    2nd recTransTreeXML reconciled transcript tree with 1st gene tree
    ...
  </recTransTree>
  <recGeneTree>
    2nd recGeneTreeXML reconciled gene tree as defined in the recPhyloXML grammar
    ...
  </recGeneTree>
  <recTransTree>
    1st recTransTreeXML reconciled transcript tree with 2nd gene tree
    ...
  </recTransTree>
  <recGeneTree>
    3rd recGeneTreeXML reconciled gene tree as defined in the recPhyloXML grammar
    ...
  </recGeneTree>
</doubleRecPhylo>
```

recTransTreeXML

The [recGeneTreeXML](#) grammar contains an `<eventsRec>` tag that is included inside a `<clade>` tag to allow the representation of the evolutionary events associated to branches and nodes of a reconciled gene tree.

The recTransTreeXML grammar enriches the recGeneTreeXML grammar by extending the set of evolutionary events that can be included in an `<eventsRec>` object.

The set of possible evolutionary events that can be included inside an `<eventsRec>` object in the recTransTreeXML grammar are then:

- those inherited from the annotation of bifurcation nodes in a reconciled gene tree (`<recGeneTree>` object): `<speciation>`, `<duplication>`, `<branchingOut>`, and `<leaf>`.

- those specific to the recTransTreeXML grammar: `<creation>`, and `<loss>`. A `<creation>` tag describes a transcript lineage undergoing a bifurcation due to the creation of a new lineage of transcript isoforms, and a `<loss>` tag describes the loss of a transcript isoform.

Examples

- doubleRecPhylo example for transcript-gene-species tree reconciliations: Download [here](#)

- recPhylo example for gene-species tree reconciliations: Download [here](#)
- recPhylo example for transcript-gene tree reconciliations: Download [here](#)

See additional examples of `<doubleRecPhylo>>` and `<recPhylo>` objects containing `<recTransTree>` tags in input files examples provided in the [GitHub repository](#).

Webserver

- [DoubleRecViz](#)