Treerecs with Seaview: gene tree inference from alignment to reconciliation, with a graphical interface

Eric Tannier,
INRIA, LBBE, University of Lyon

Phylogenetic software workshop, Montpellier
August 17, 2018

Phylogenetic reconciliation

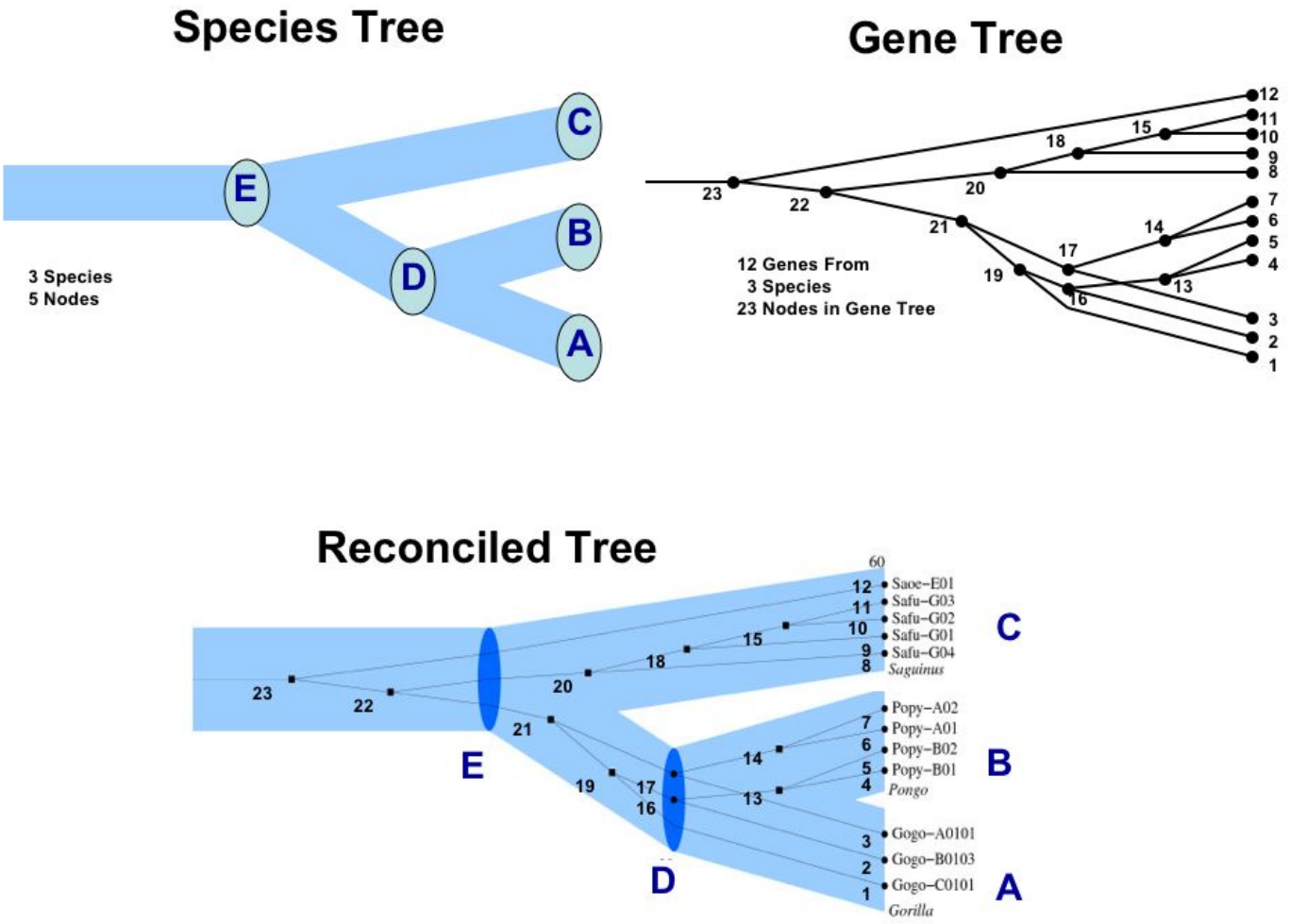
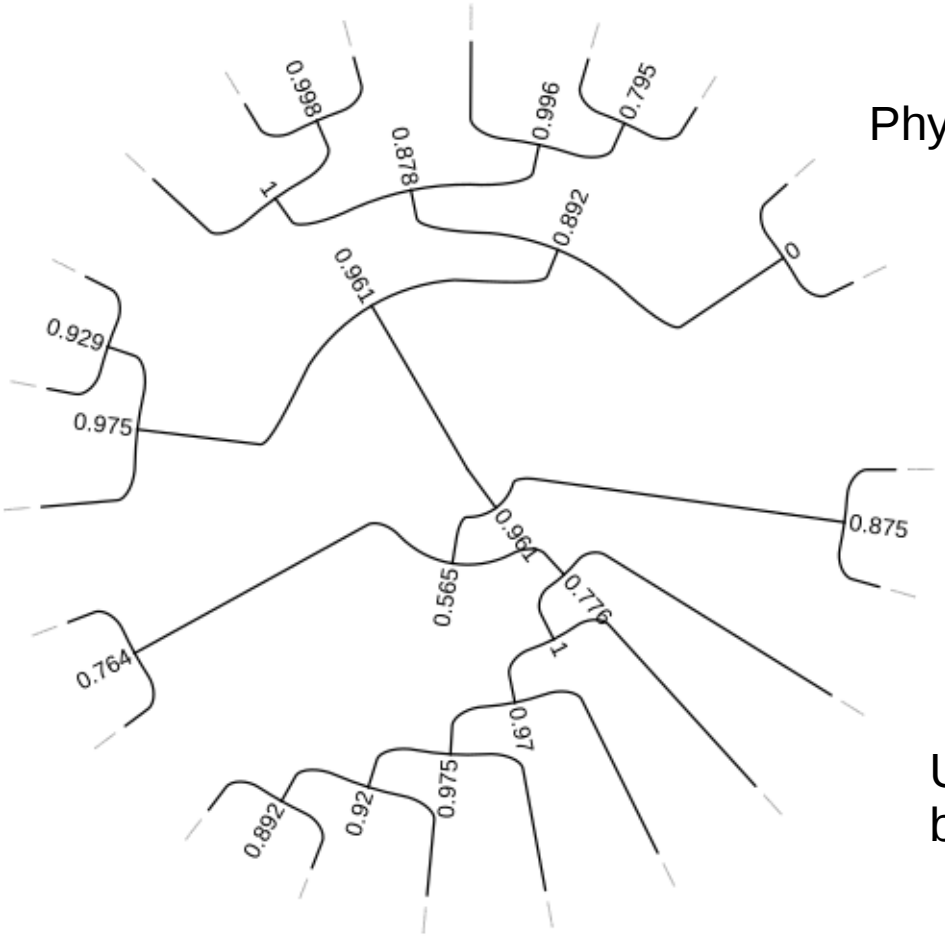


Fig from IpTOL, 2011

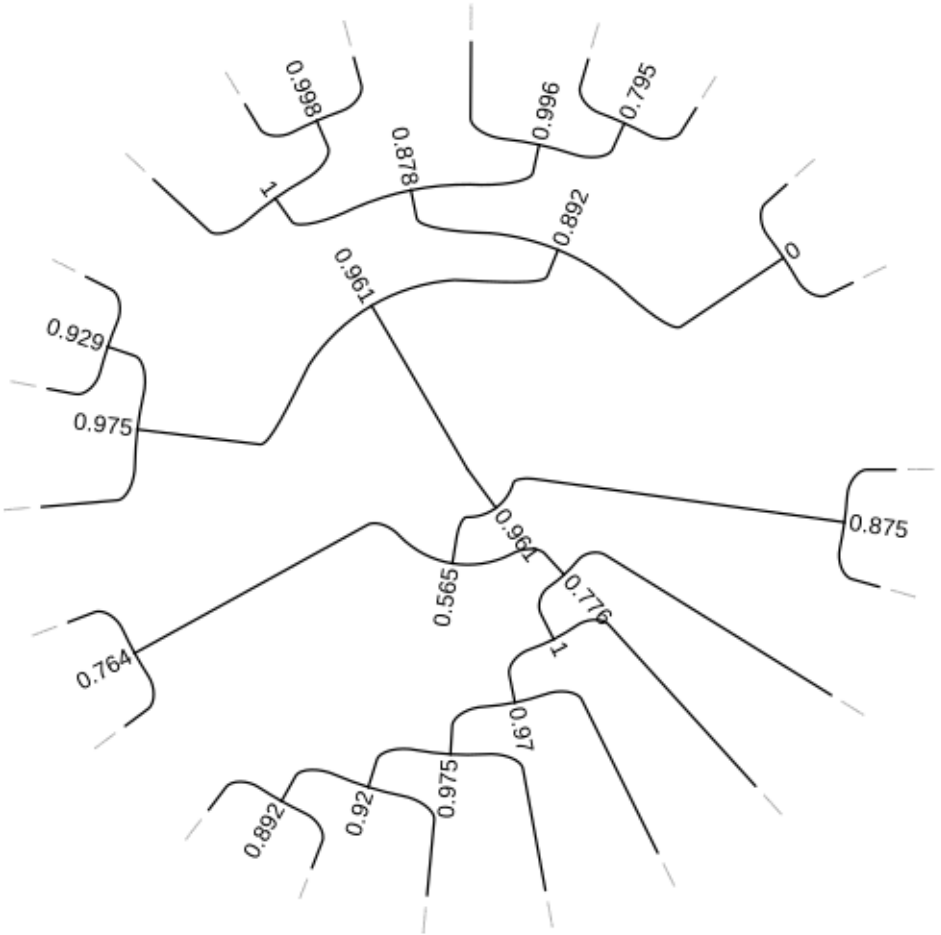
Typical output of a phylogenetic inference method from multiple sequence alignment

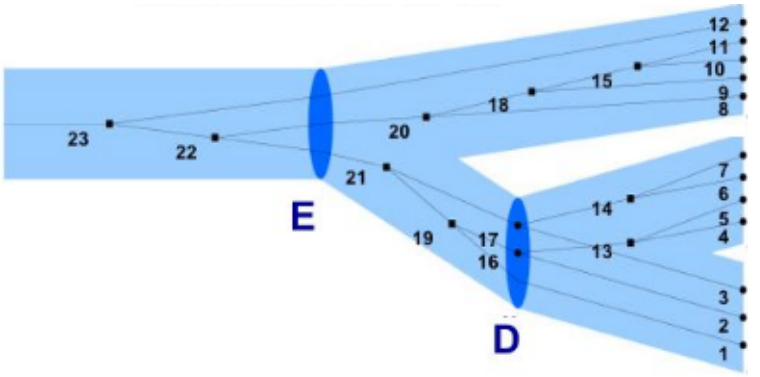


PhyML, RAxML, IQTree, FastTree,…

Unrooted, several uncertain branches

Different equivalent solutions (topology and root) according to the alignment might have a different reconciliation score (different D,T,L scenarios)





A good offer of phylogenetic reconciliation tools

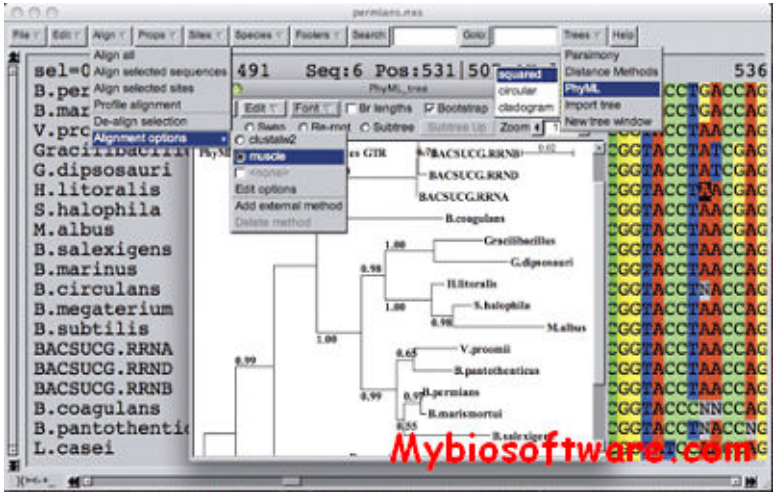
ecceTera, Notung, Ranger-DTL, Prime-GSR, ALE, …

- Usability is not optimal:

Notung has a nice graphical inferface,
but no integrative tool like **Seaview**

ecceTera is very efficient but dependent on
several libraries

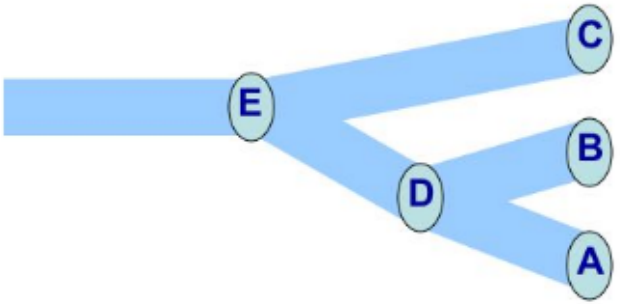
Formats are very strict (gene-species mapping)

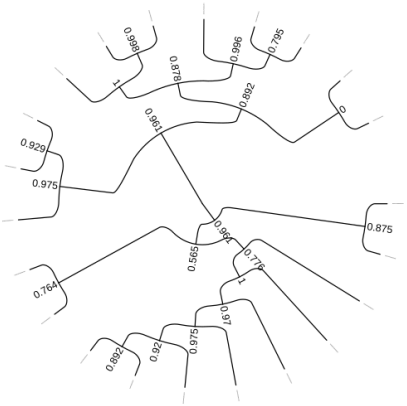


- Basic functions are not always implemented

None of these software can easily and efficiently
correct and root a gene tree

Basic functionning





Input:

unrooted gene tree,
species tree,
threshold for supports
(can be estimated),
duplication and loss scores
(by default 2 and 1, can be estimated)

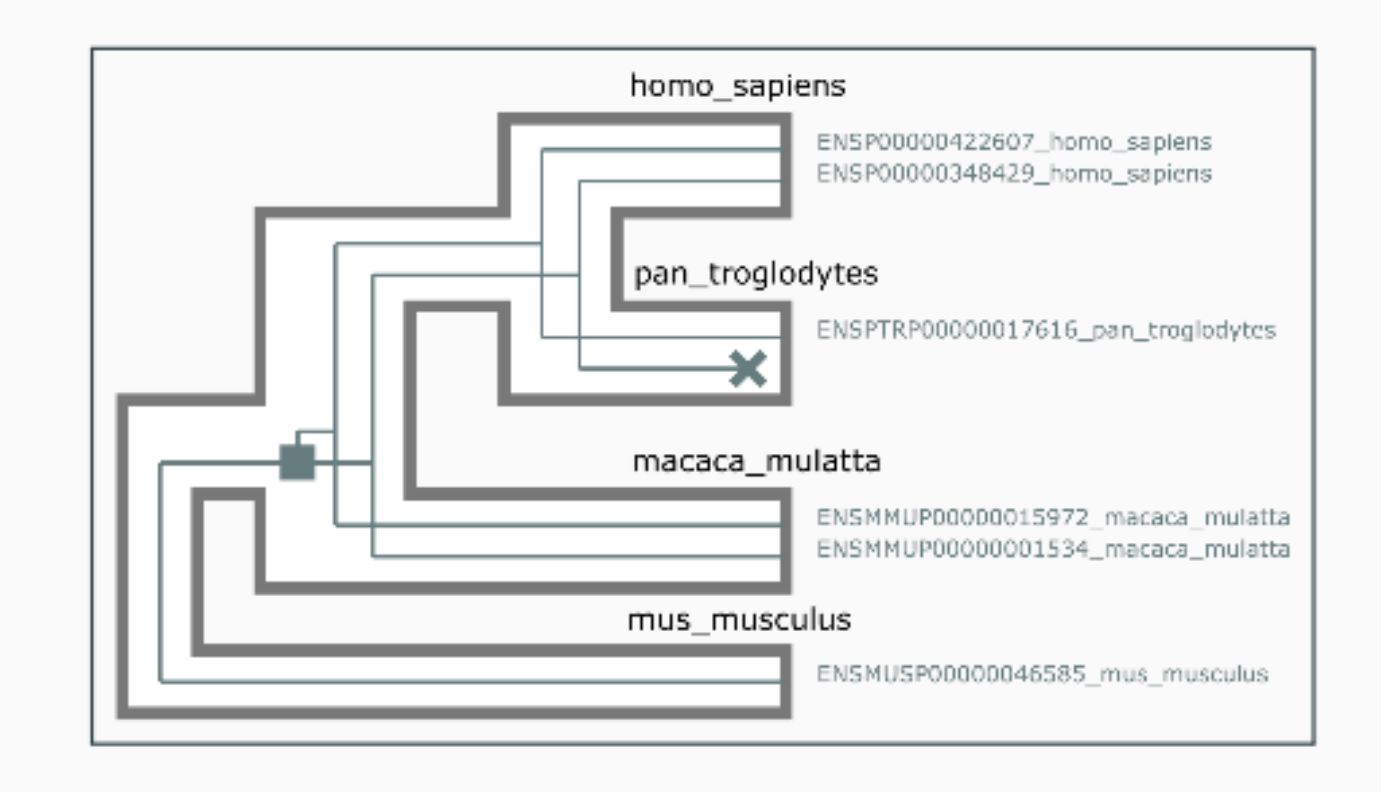
Output:

rooted gene tree and reconciliation,

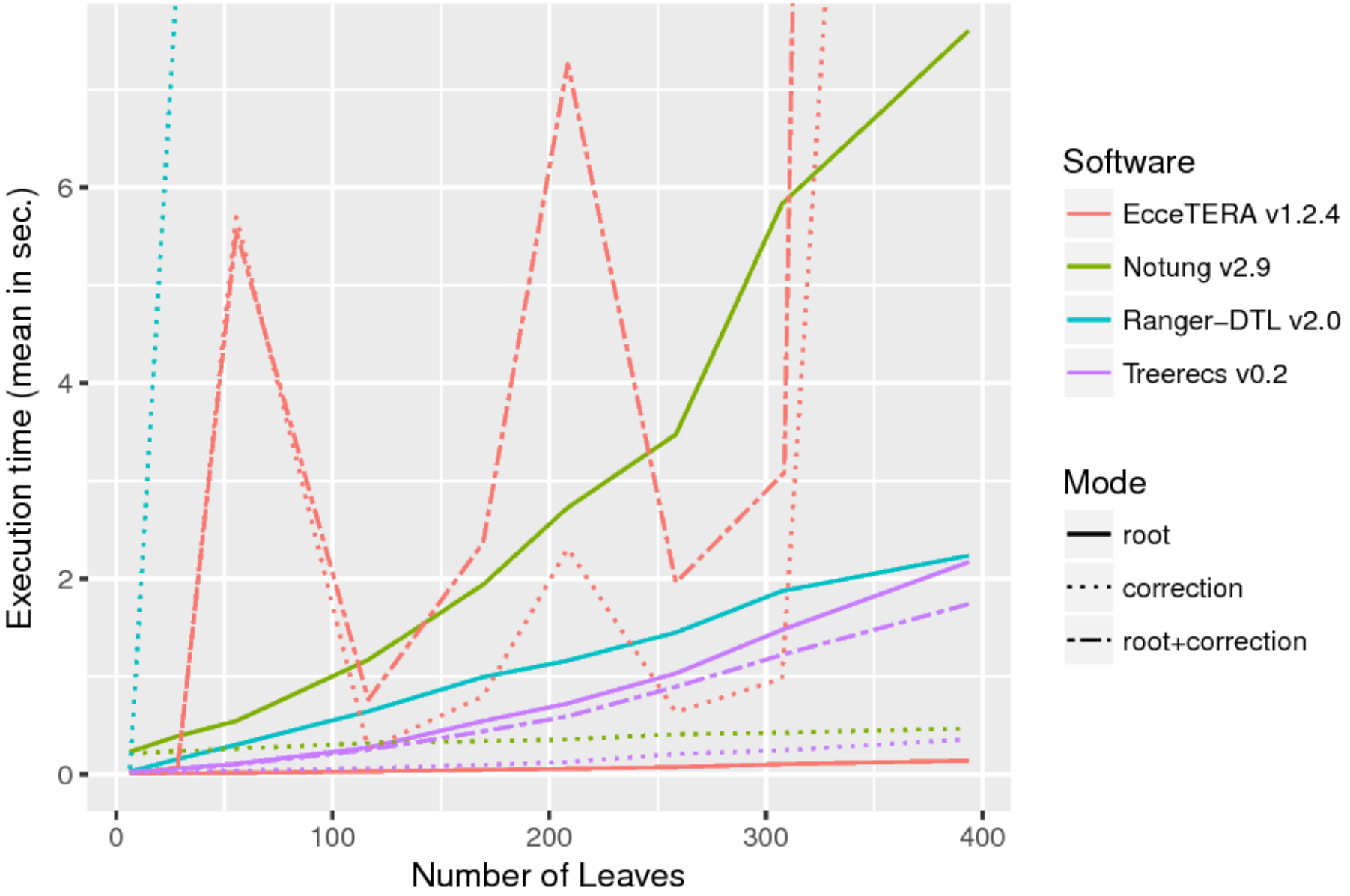
keeping all supported branches (above thresh

minimizing the duplication-loss score
(among all such rooted gene trees)

SVG output of a reconciled tree

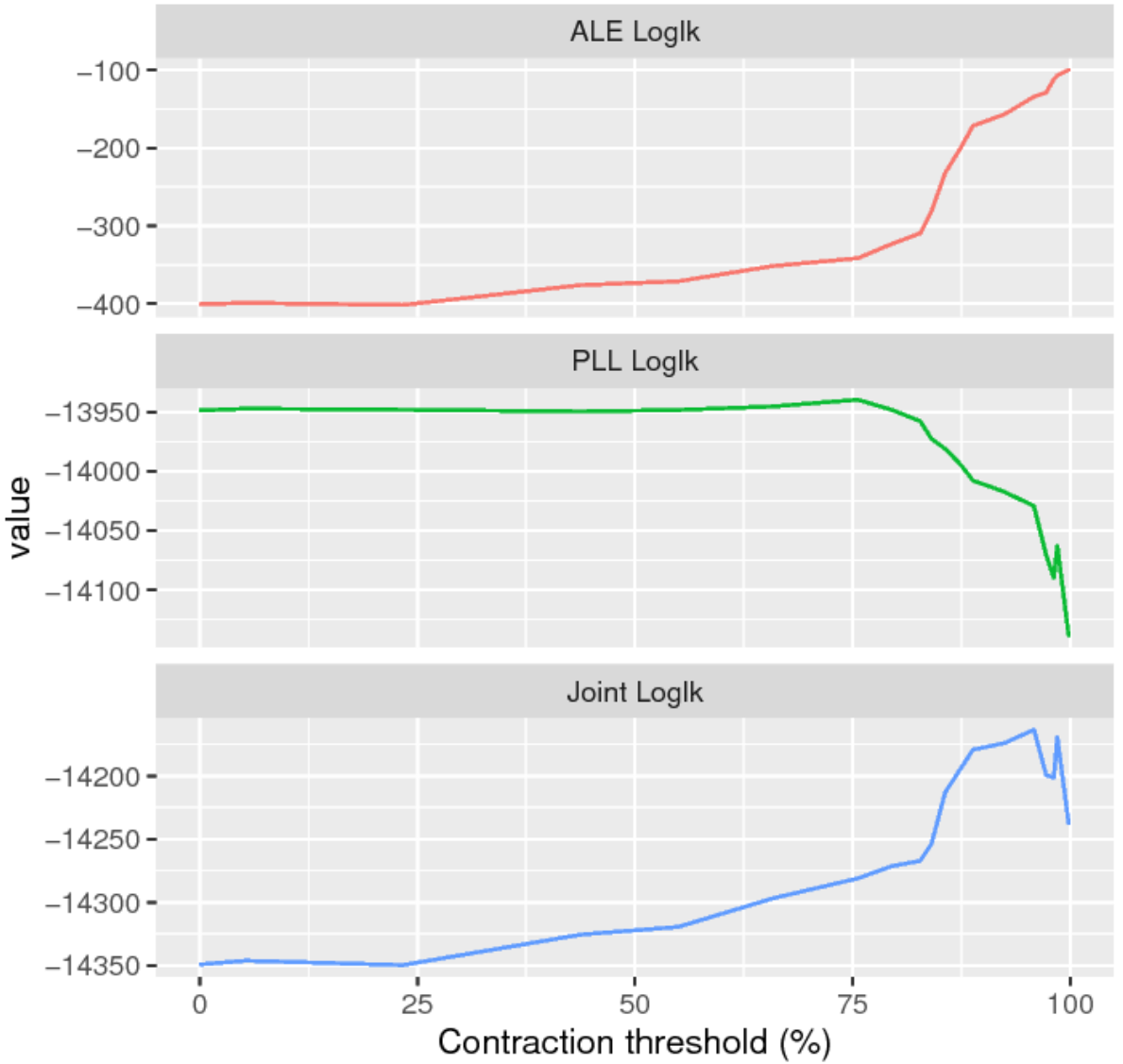


Efficiency


Execution time (mean in sec.)
0
2
4
6
0
100
200
300
400
Number of Leaves
Software
EcceTERA v1.2.4
Notung v2.9
Ranger–DTL v2.0
Treerecs v0.2
Mode
root
correction
root+correction

Integration with phylogeny based on multiple sequence alignment

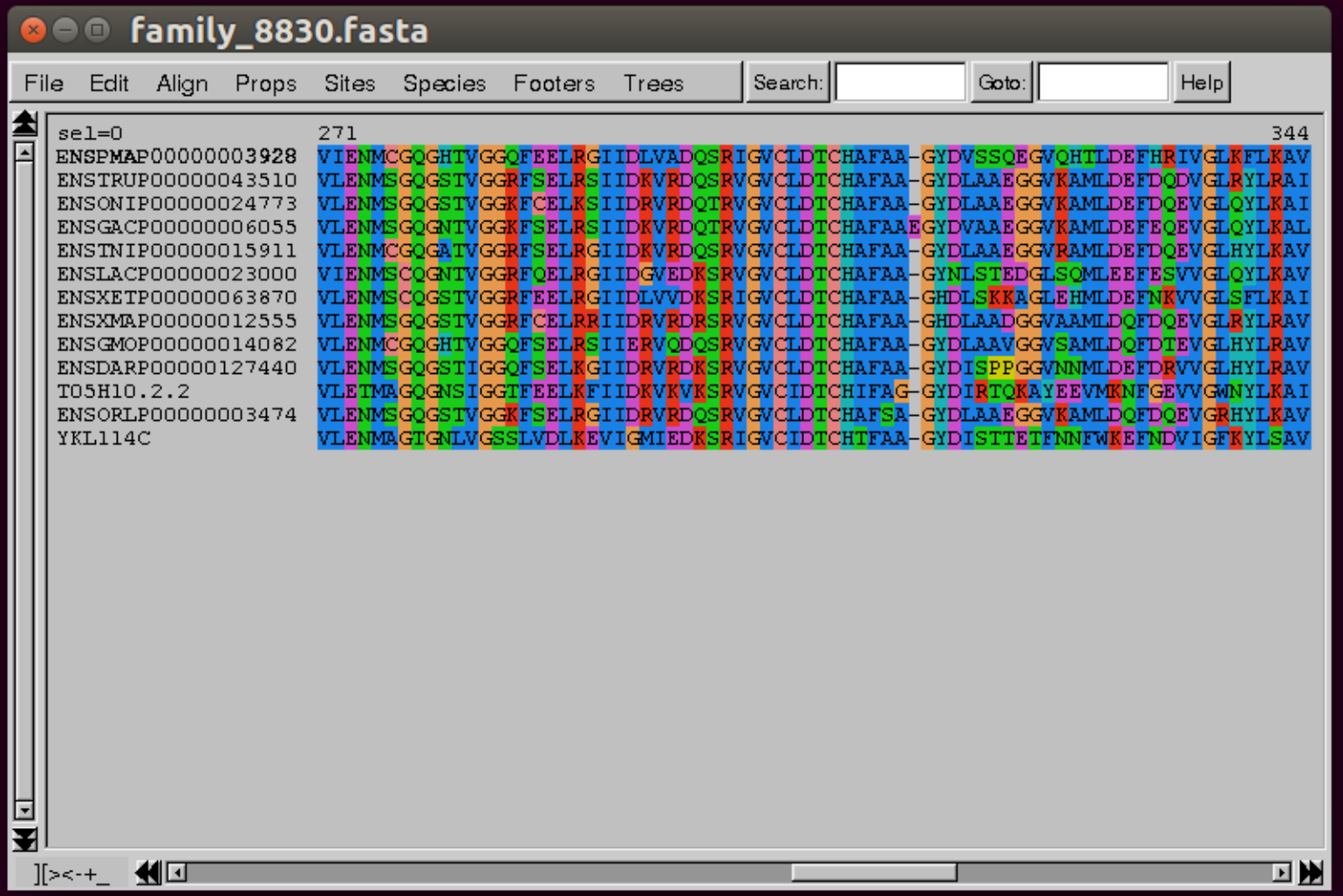
Treerecs can also take a multiple sequence alignment of genes or proteins as input



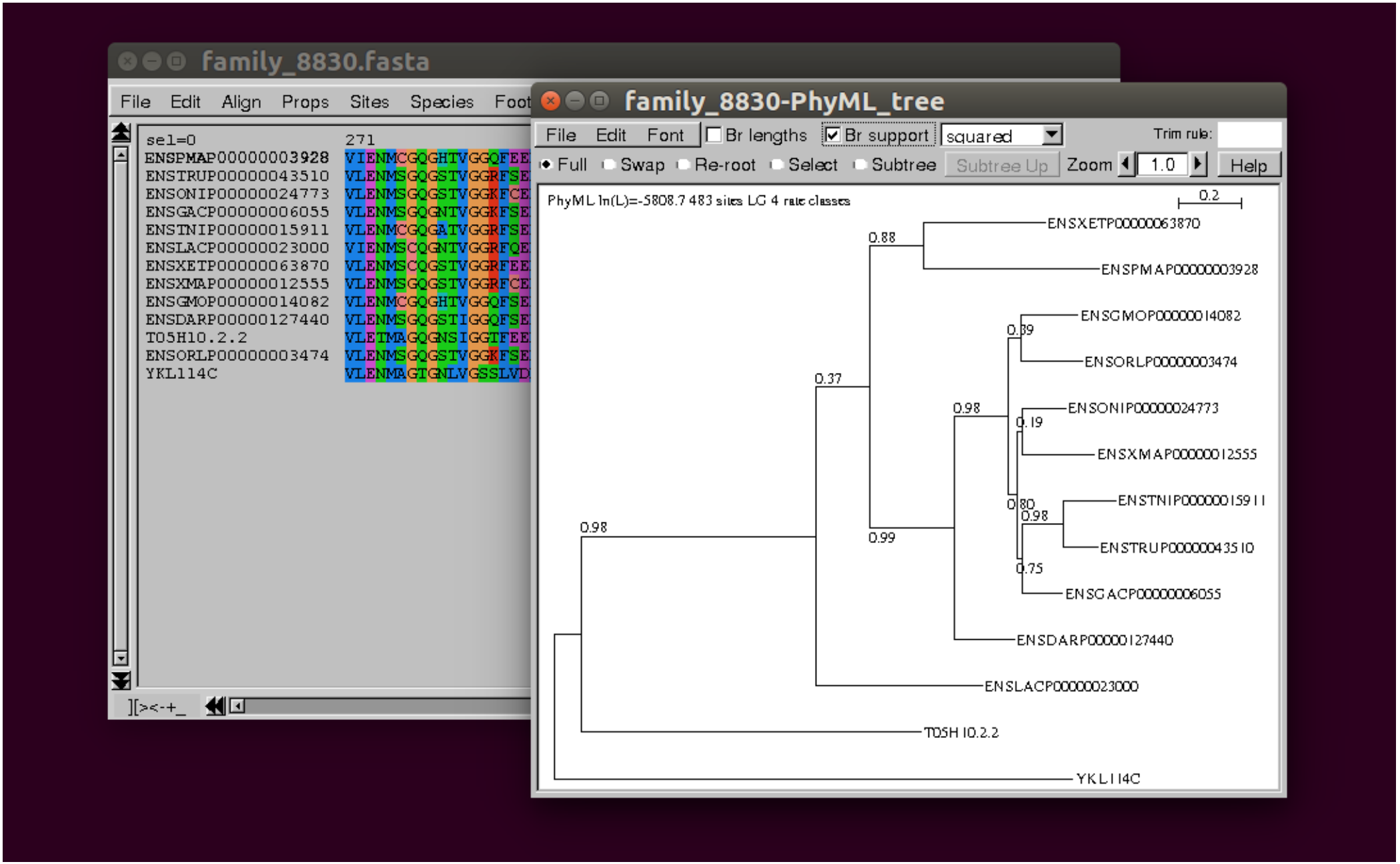
Support threshold estimation with integrated likelihood

Integration with Seaview

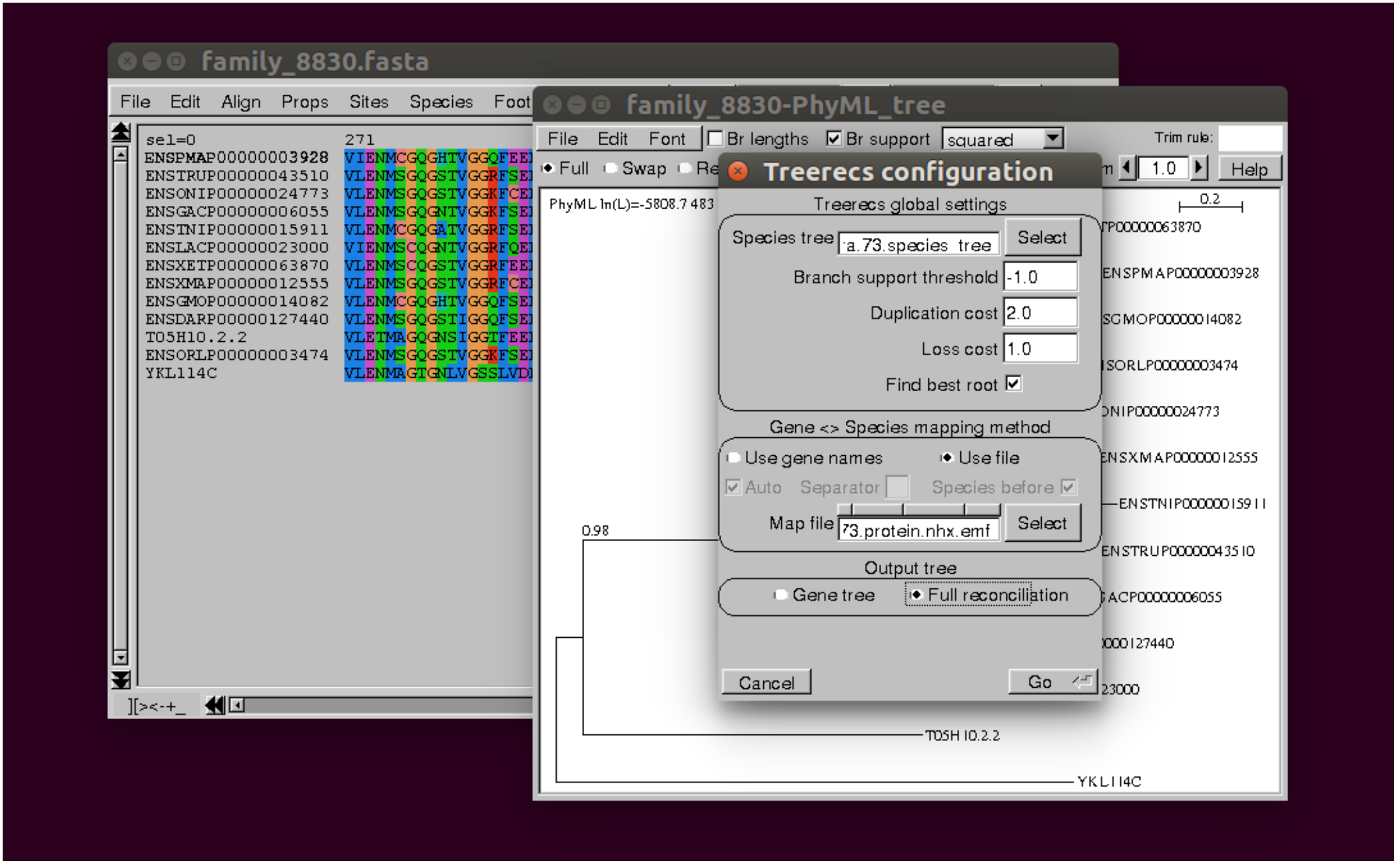
Integration with Seaview



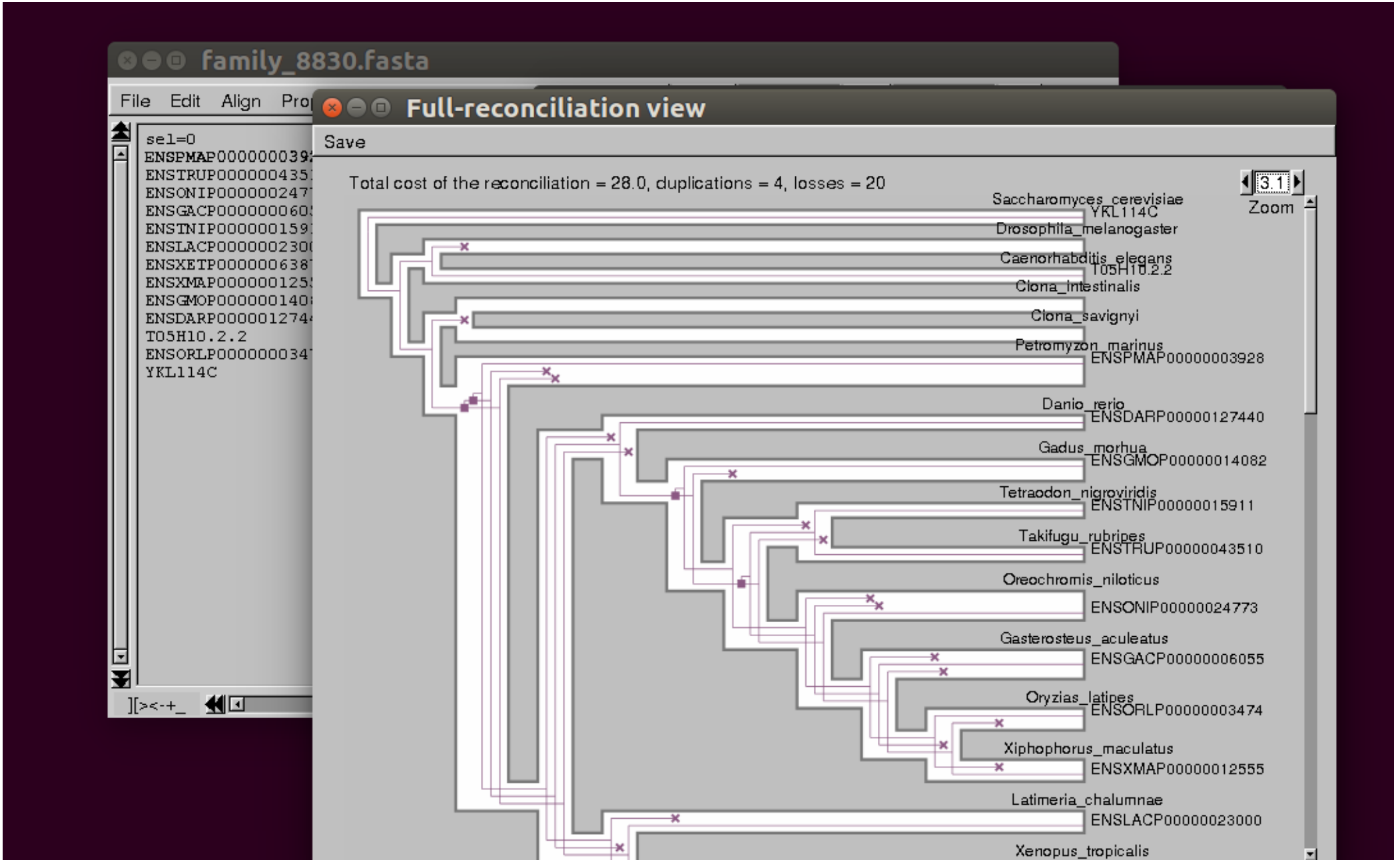
Integration with Seaview



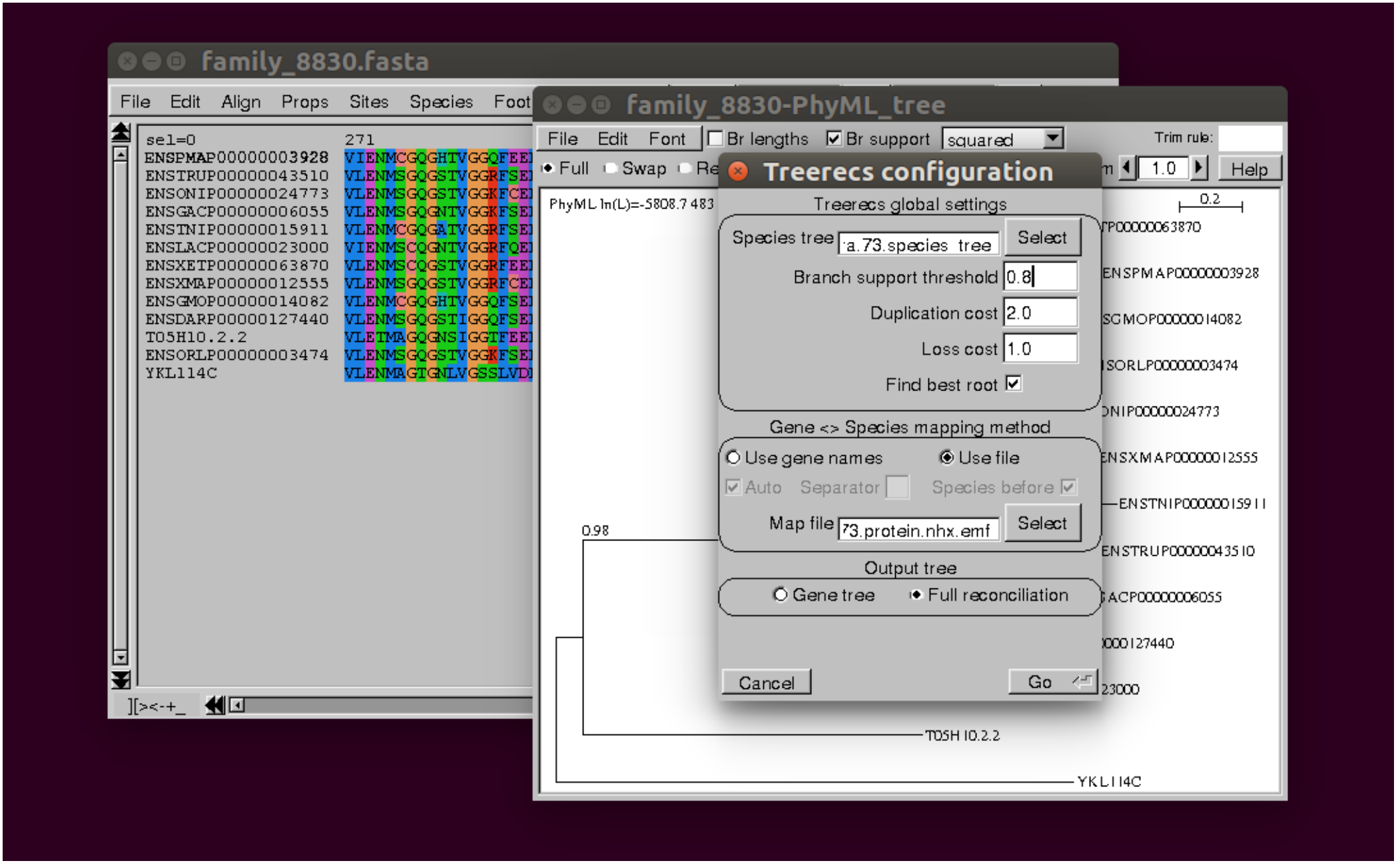
Integration with Seaview



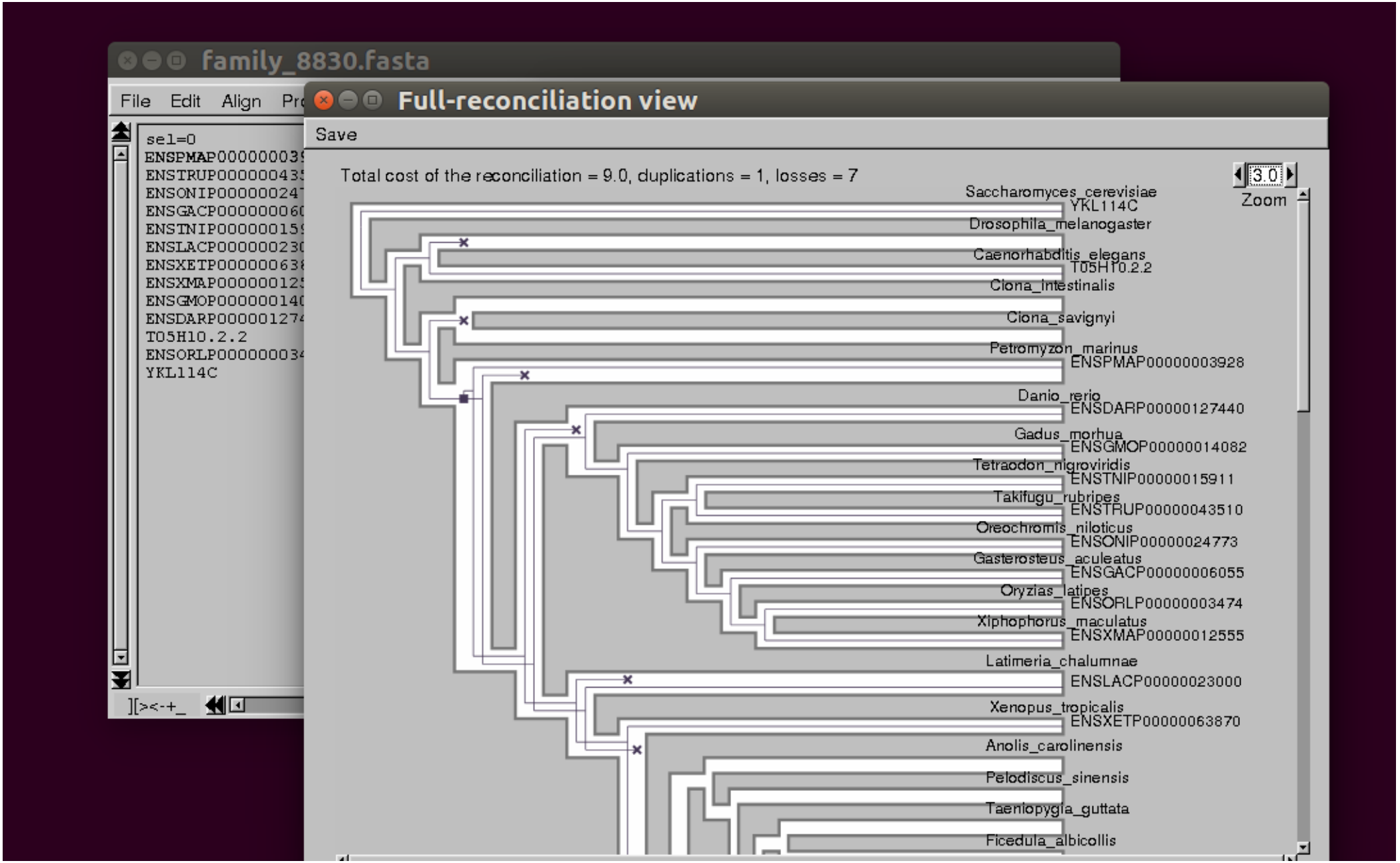
Integration with Seaview



Integration with Seaview



Integration with Seaview



Ongoing developments

- For the moment we have only duplications and losses

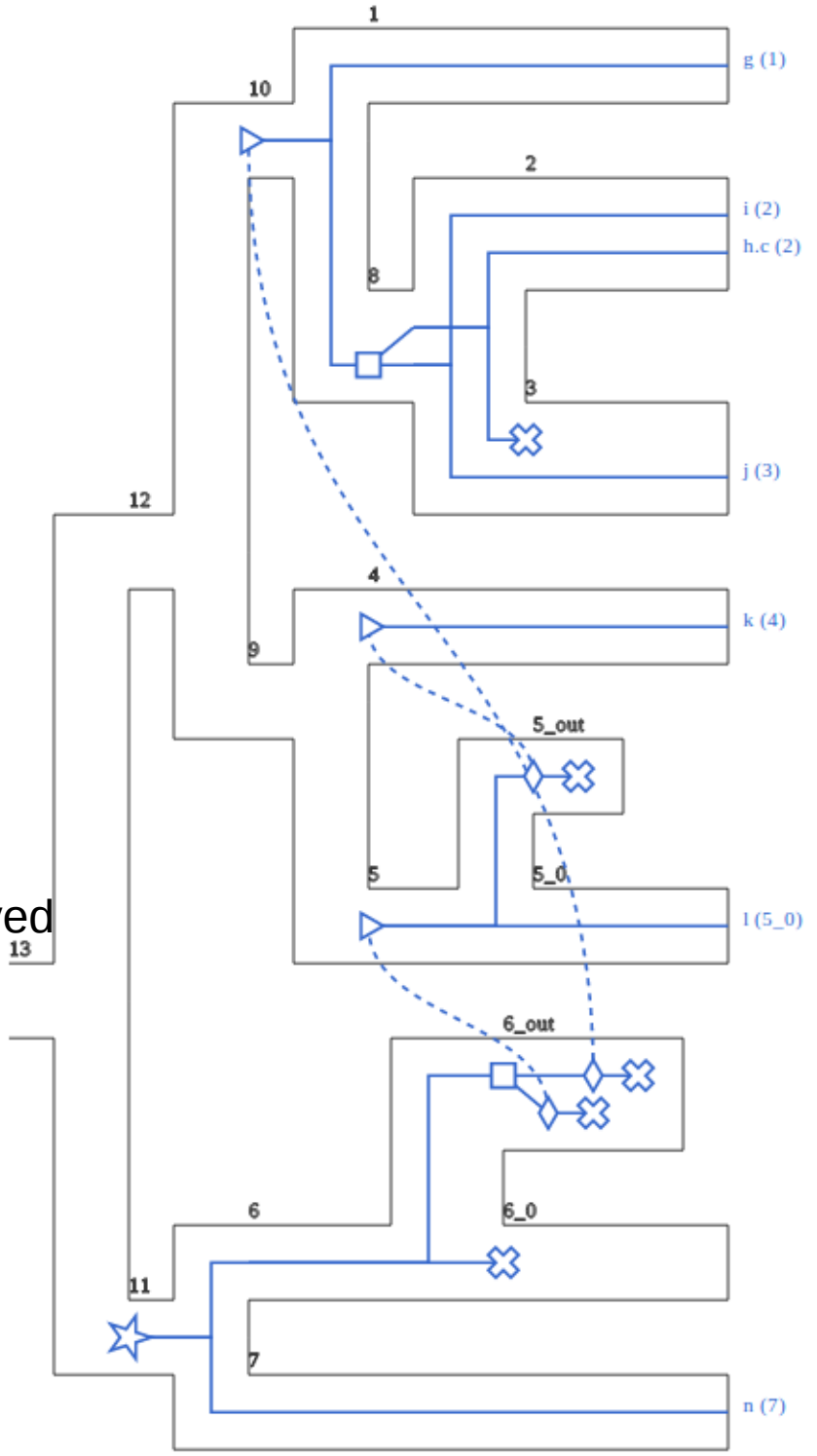
We will soon have transfers, based on ecceTera and ALE (short term)

We would like to have deep coalescence intergrated (long term)

- For the moment the species tree needs to be fully resolved

We will soon allow unresolved species tree (mid term)

We will soon allow no species tree at all, searching it in databases or reconstructing it from gene trees (long term)



With the participation of

Nicolas Comte
David Parsons

Benoît Morel
Alexandros Stamatakis

Vincent Daubin
Bastien Boussau
Celine Scornavacca
Manolo Gouy