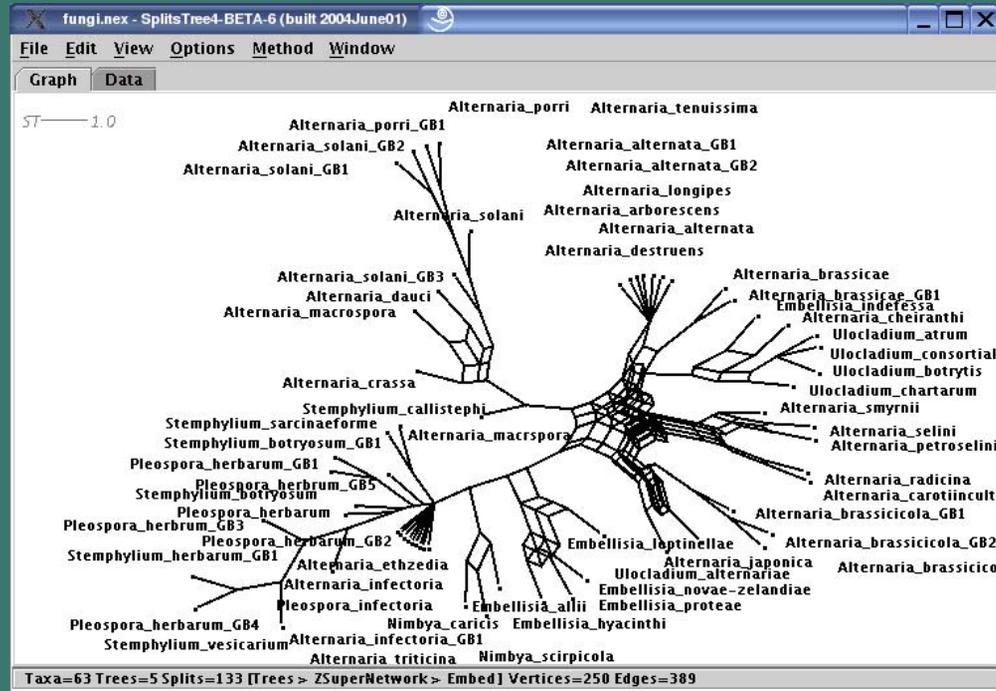


Phylogenetic Networks

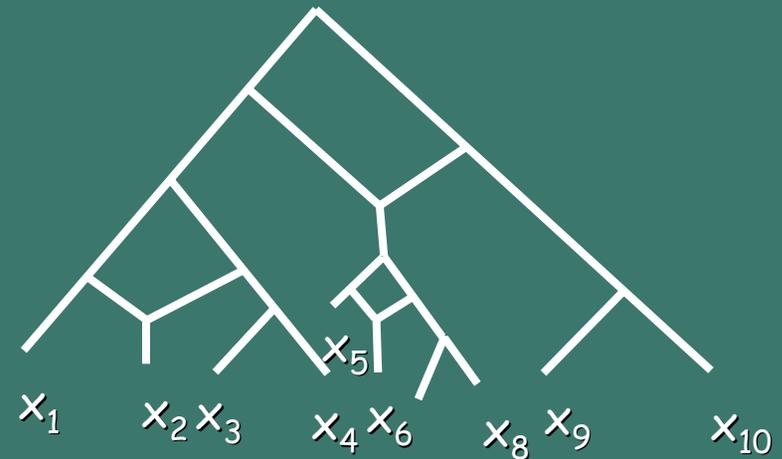
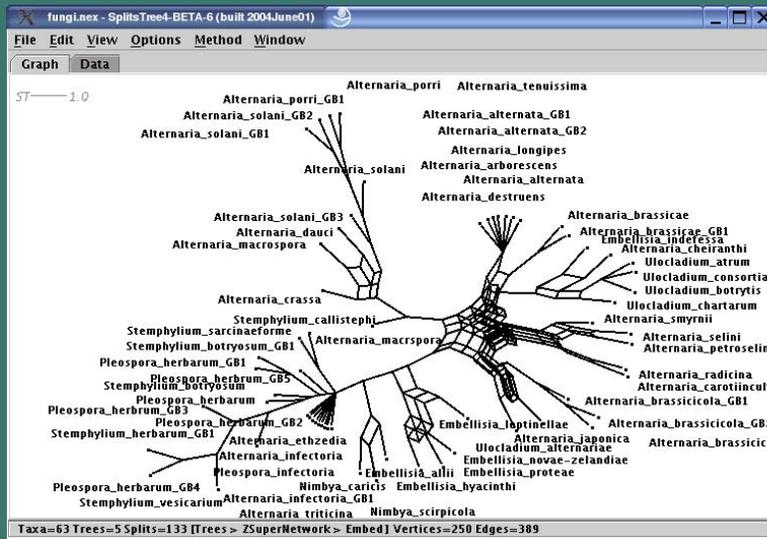


Daniel H. Huson



Phylogenetic Networks

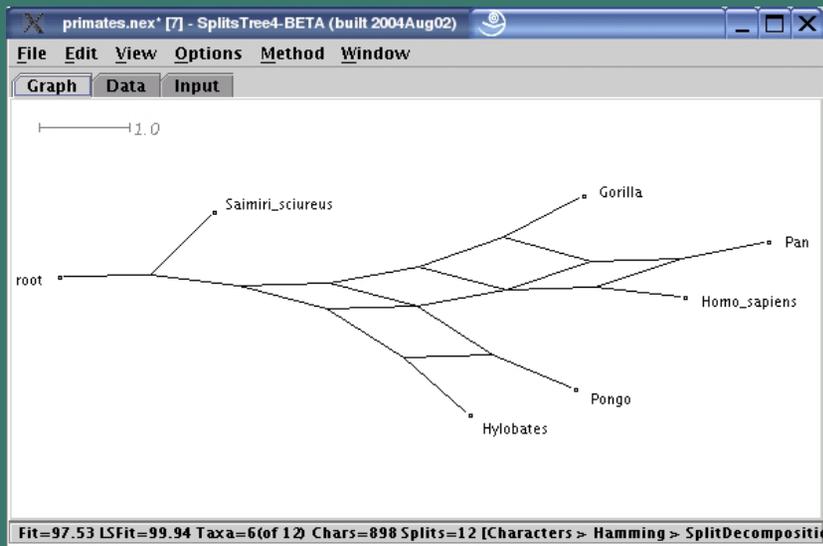
- As a data representation technique
- As a more complex model of evolution



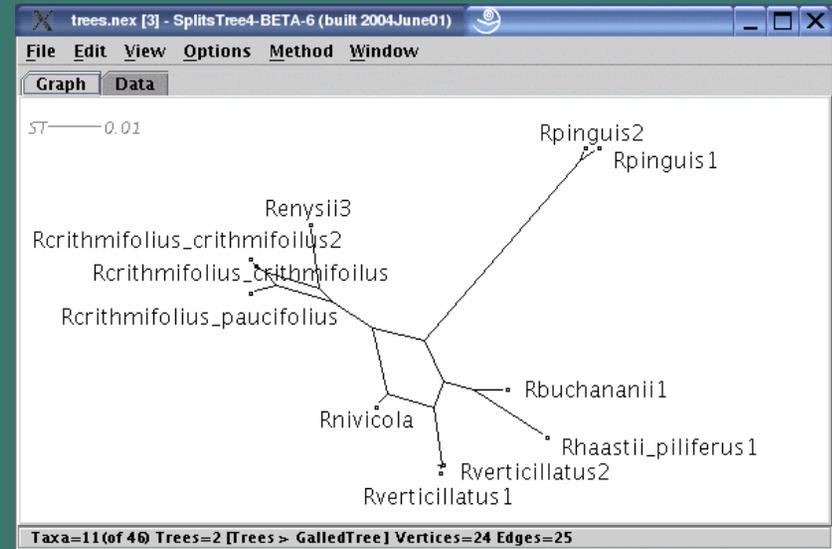
- Splits graphs and others
- Reticulation graphs: such as hybridization graphs or ancestor recombination graphs

Phylogenetic Networks

Either type of graph can be unrooted or rooted



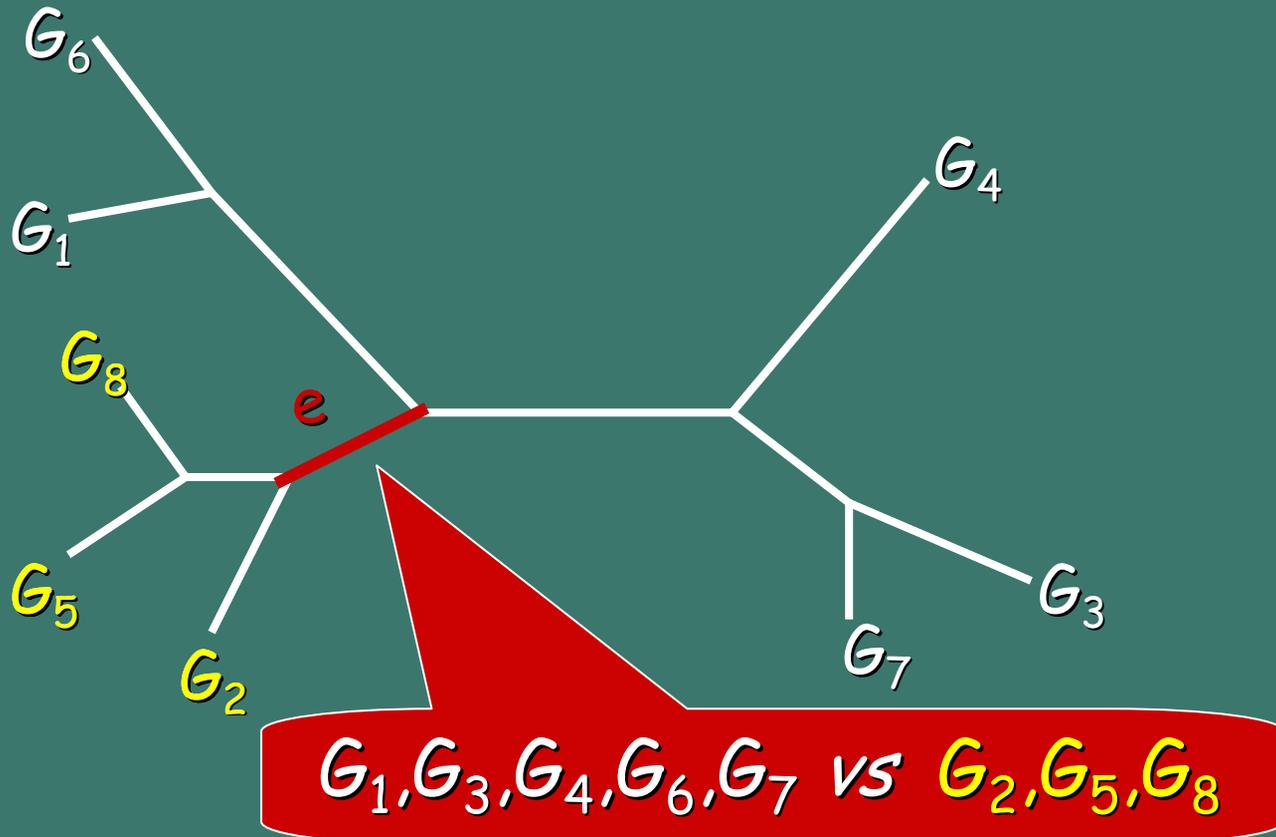
- Rooted splits graph



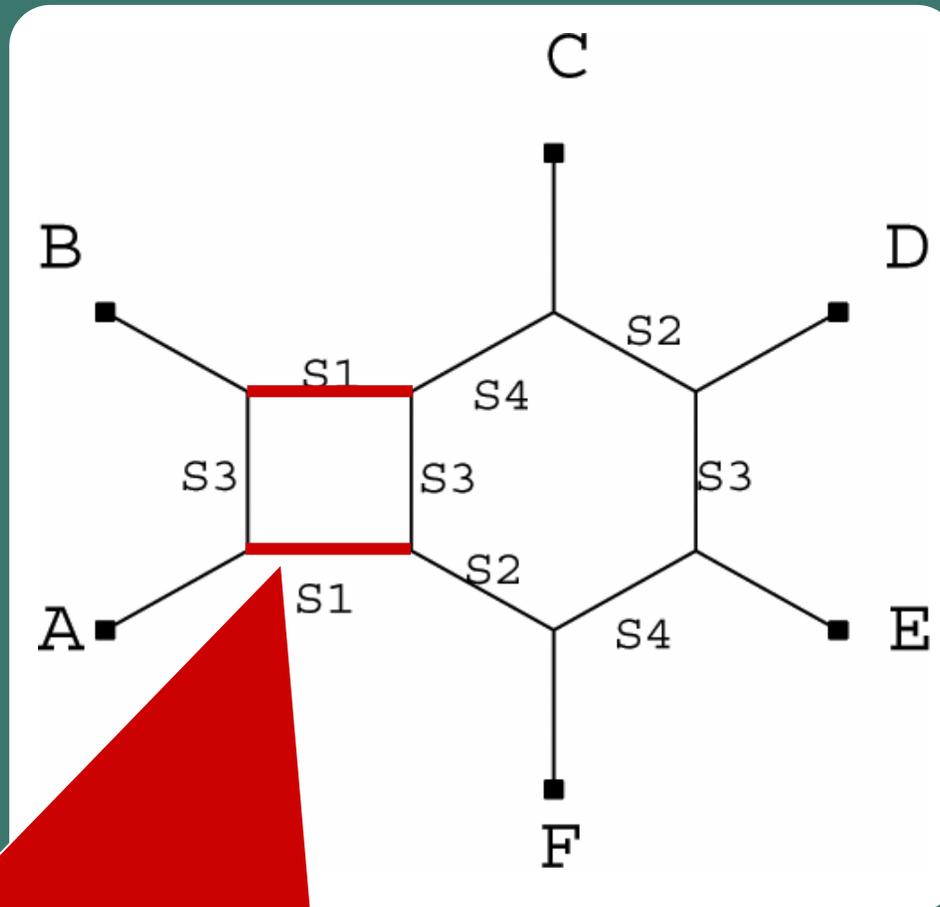
- Unrooted reticulation graph

What is a Splits Graph?

- The split encoding $\Sigma(T)$ of a tree T :



What is a Splits Graph?



Cut-set of parallel edges defines split $\{A, B\}$ vs rest

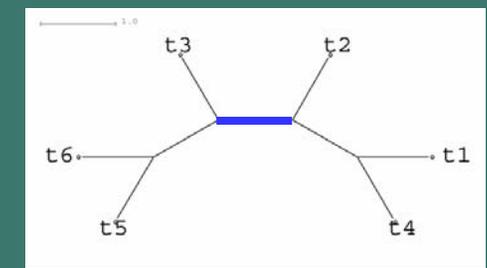
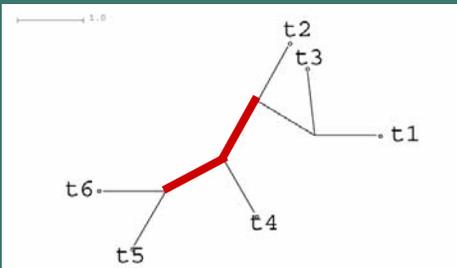
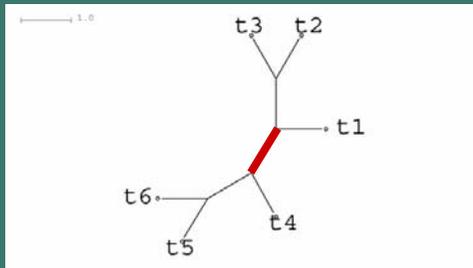
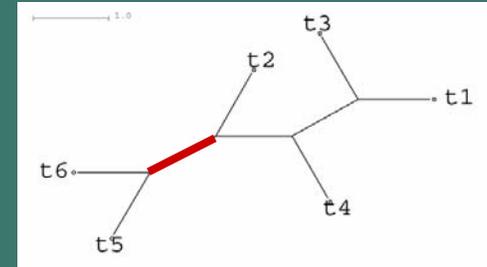
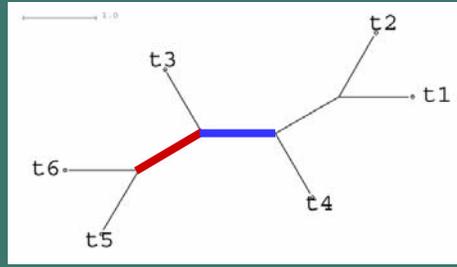
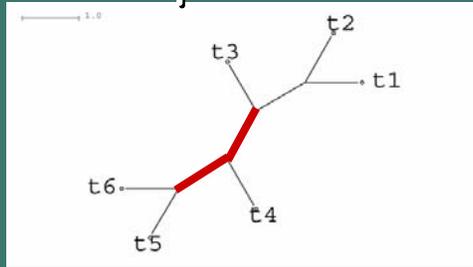
Glossary

- **Splits system Σ** : a set of splits (bipartitionings) of a given taxon set X
- **Splits graph G** : graph representing Σ (includes trees, not necessarily planar!)
- **SplitsTree**: a program providing various algorithms for computing splits graphs
- **Split decomposition**: an algorithm for computing splits from distances
(other: Neighbor-Net, consensus networks, or Z-super networks)

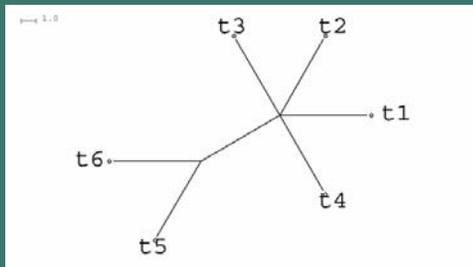


Example: Consensus Networks

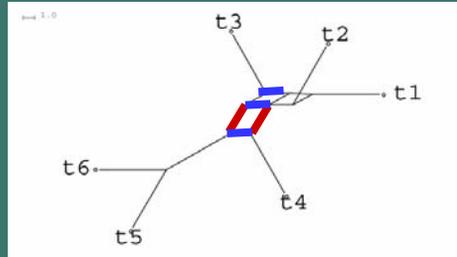
Six input trees:



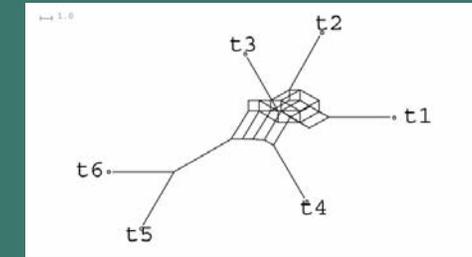
$\Sigma(1/2)$:



$\Sigma(1/6)$:



$\Sigma(0)$:



The image shows a screenshot of the SplitsTree 4 Beta 6 software interface. The main window displays a phylogenetic tree with various taxa listed, including *Alternaria_porri*, *Alternaria_solani*, *Stemphylium_sarcinae*, and *Pleospora_herbarum*. A red callout box highlights the text: "Provides many algorithms for phylogenetic analysis using trees and networks".

SplitsTree 4 Beta 6
Written by: Daniel H. Huson and David Bryant (2004)
with contributions from:
Markus Franz, Miguel Jette, Tobias

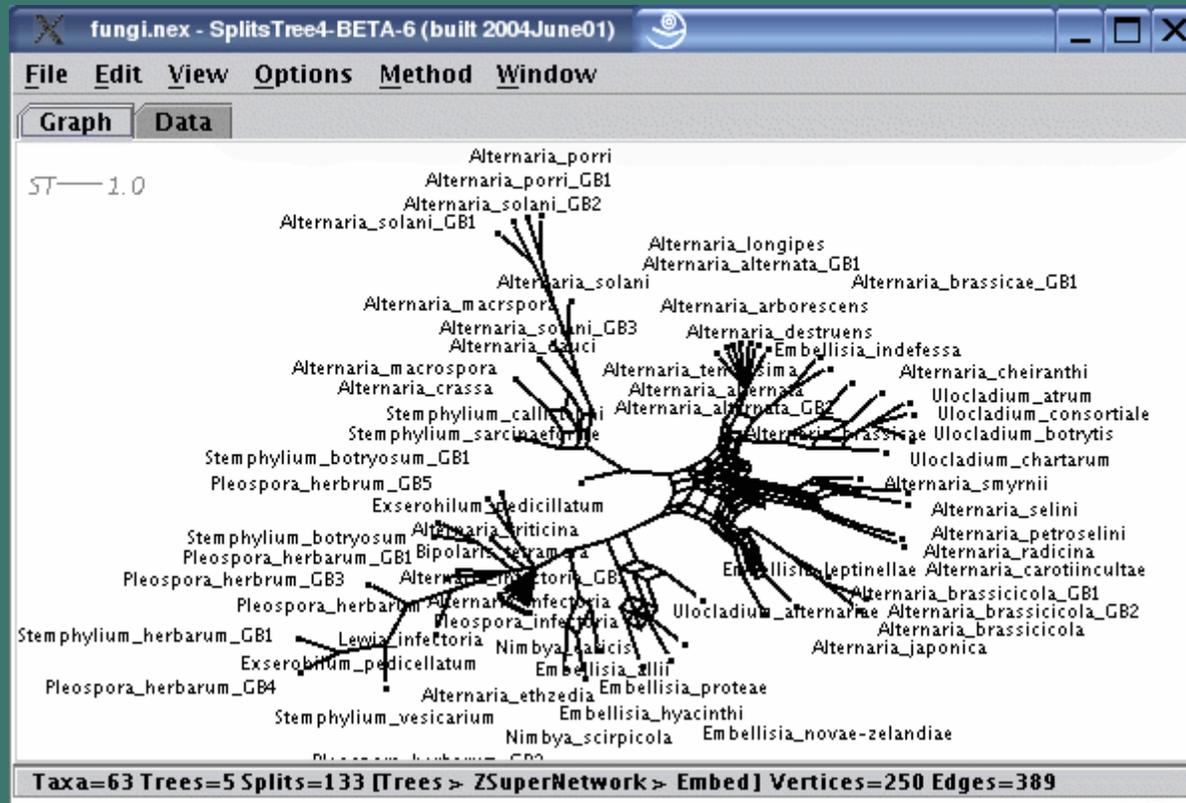
www-ab.informatik.uni-tuebingen.de/~huson/st4/

Provides many algorithms for phylogenetic analysis using trees and networks

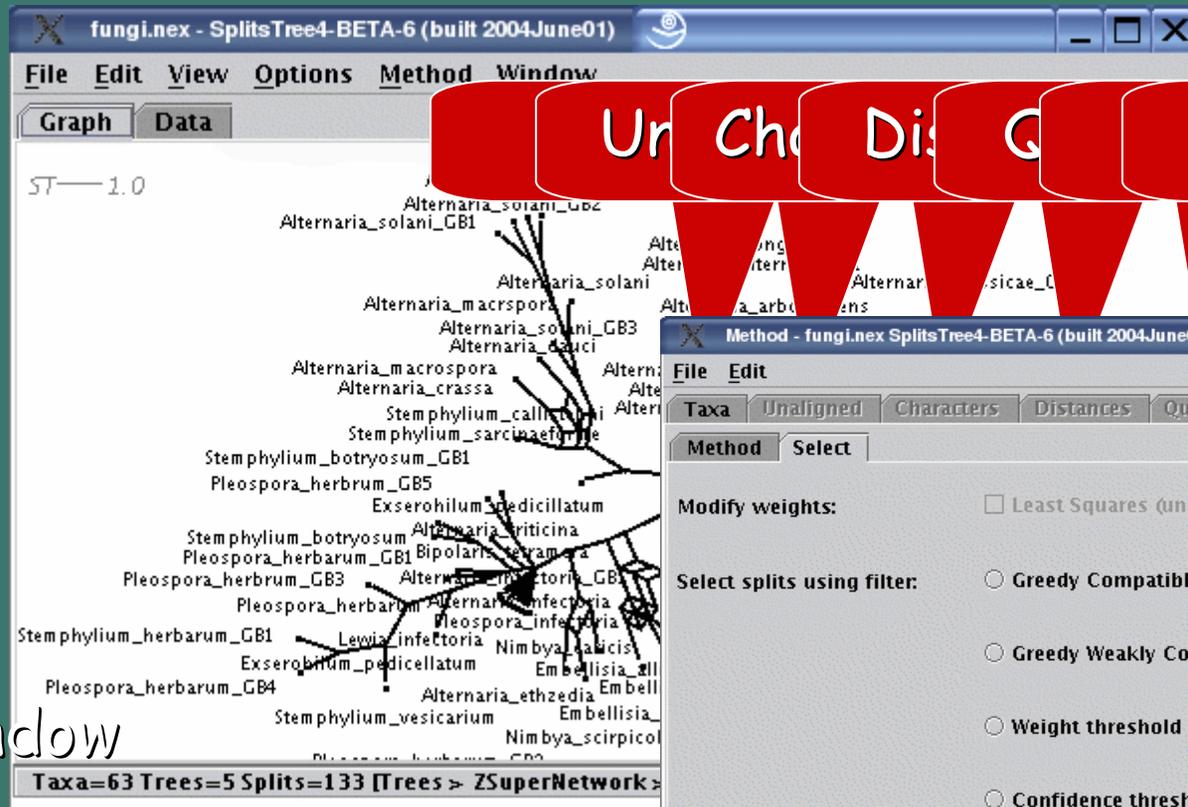
nTaxa= 63 (0 of 63 hidden)



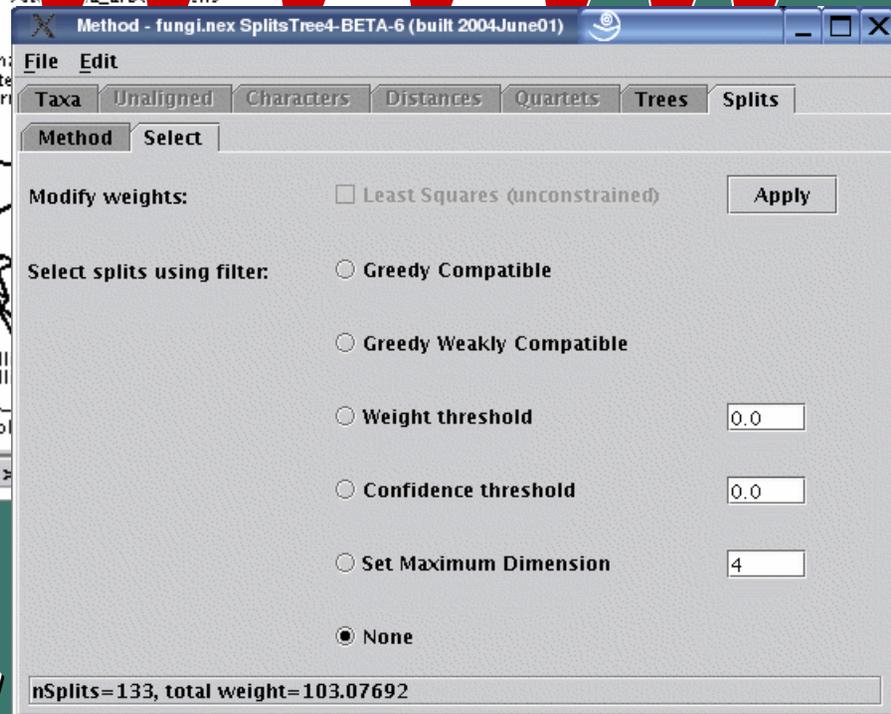
The SplitsTree Program



The SplitsTree Program



Main Window



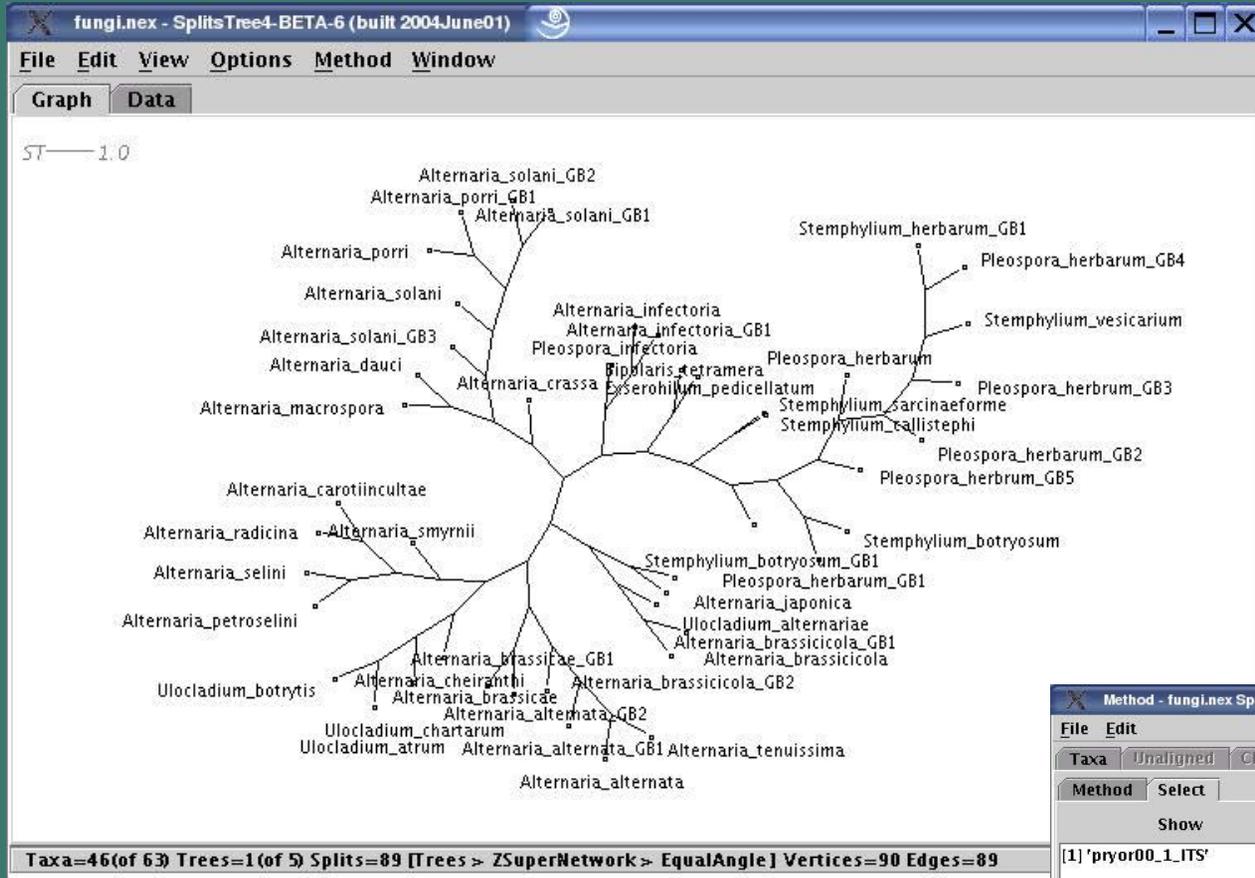
Method Window

Example: Z-Super Network

- Five trees fungal trees from (Pryor 2000) and (Pryor 2003)
- Trees:
 - ITS (two trees)
 - SSU (two trees)
 - Gpd (one tree)
- Numbers of taxa differ: "partial trees"
- Trees from TreeBase
 - Unfortunately, no edge lengths



Individual Gene Trees



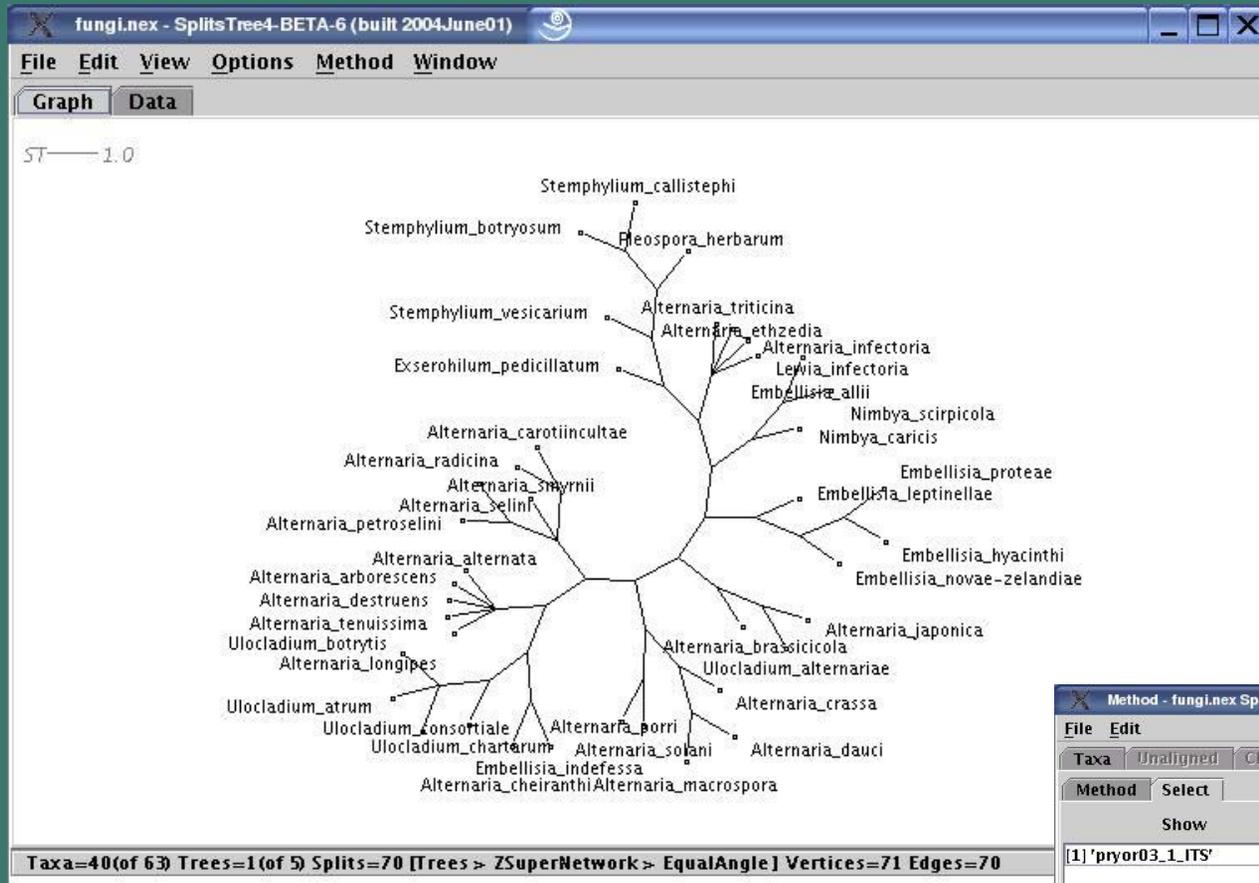
ITS00

46 taxa





Individual Gene Trees



ITS03

40 taxa

Method - fungi.nex SplitsTree4-BETA-6 (built 2004June01)

File Edit

Taxa Unaligned Characters Distances Quartets Trees Splits

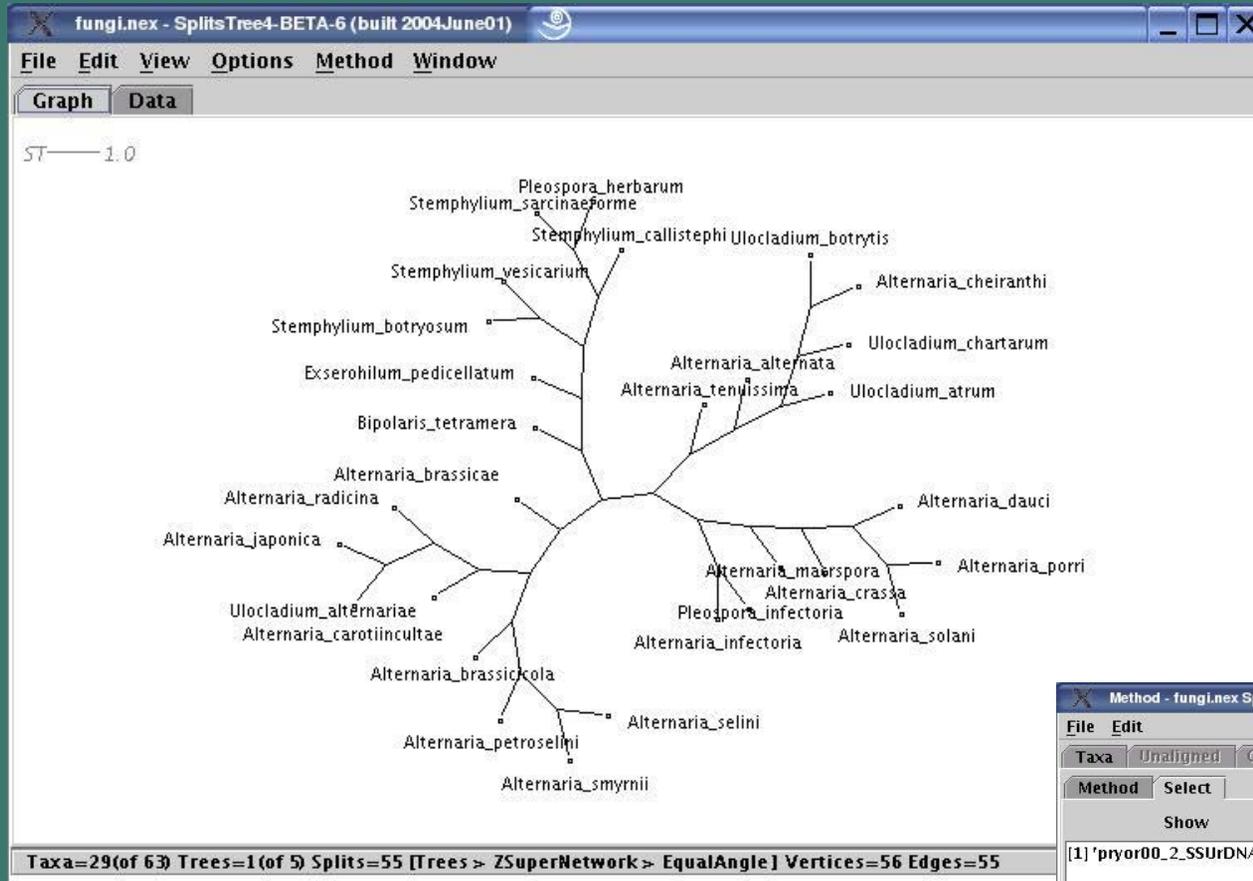
Method Select

Show	Hide	Apply
1) 'pryor03_1_ITS'	'pryor03_2_Ssu'	
	'pryor03_3_gpd'	
	'pryor00_1_ITS'	
	'pryor00_2_SsuDNA'	

nTrees= 1 (4 of 5 hidden)



Individual Gene Trees



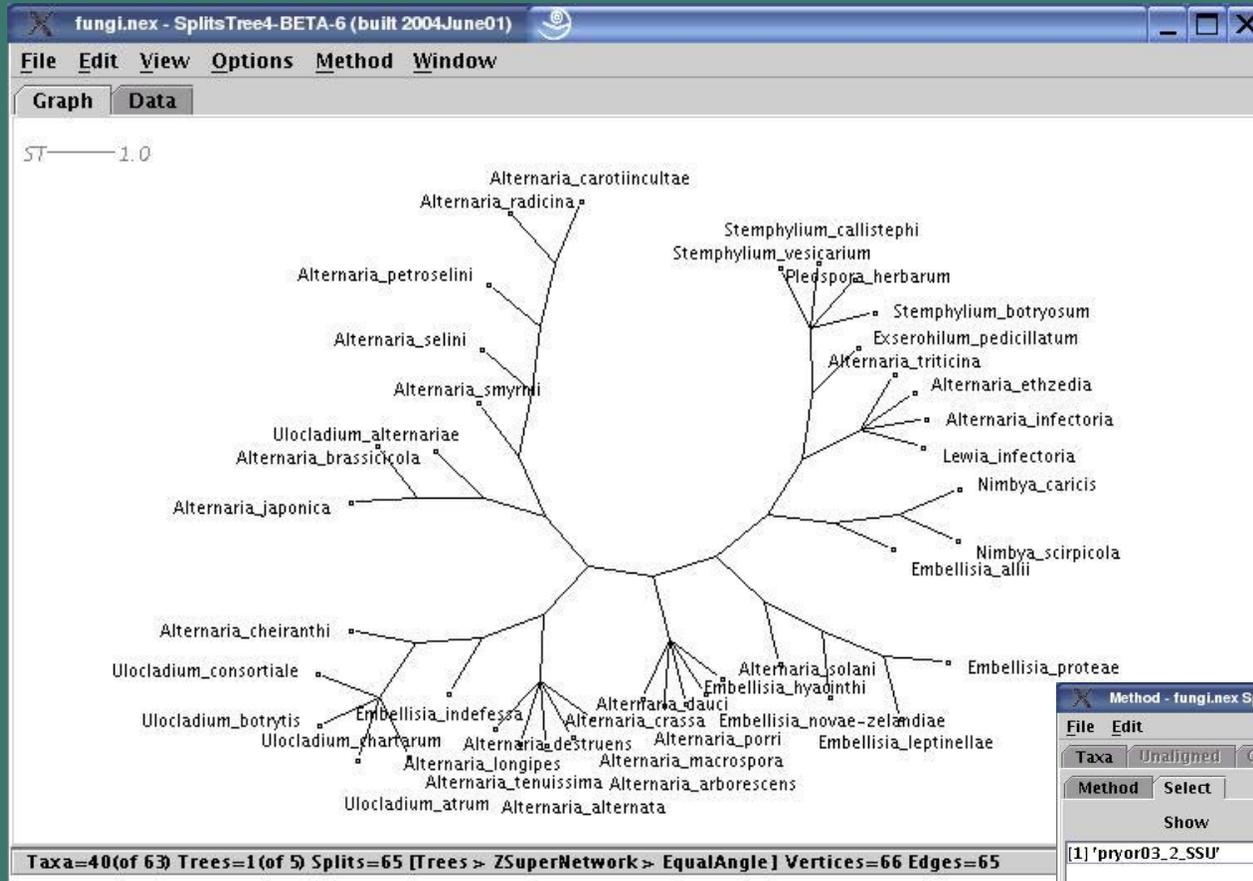
SSU00

29 taxa



Individual Gene Trees

SSU03



40 taxa

Method - fungi.nex SplitsTree4-BETA-6 (built 2004.June01)

File Edit

Taxa Unaligned Characters Distances Quartets Trees Splits

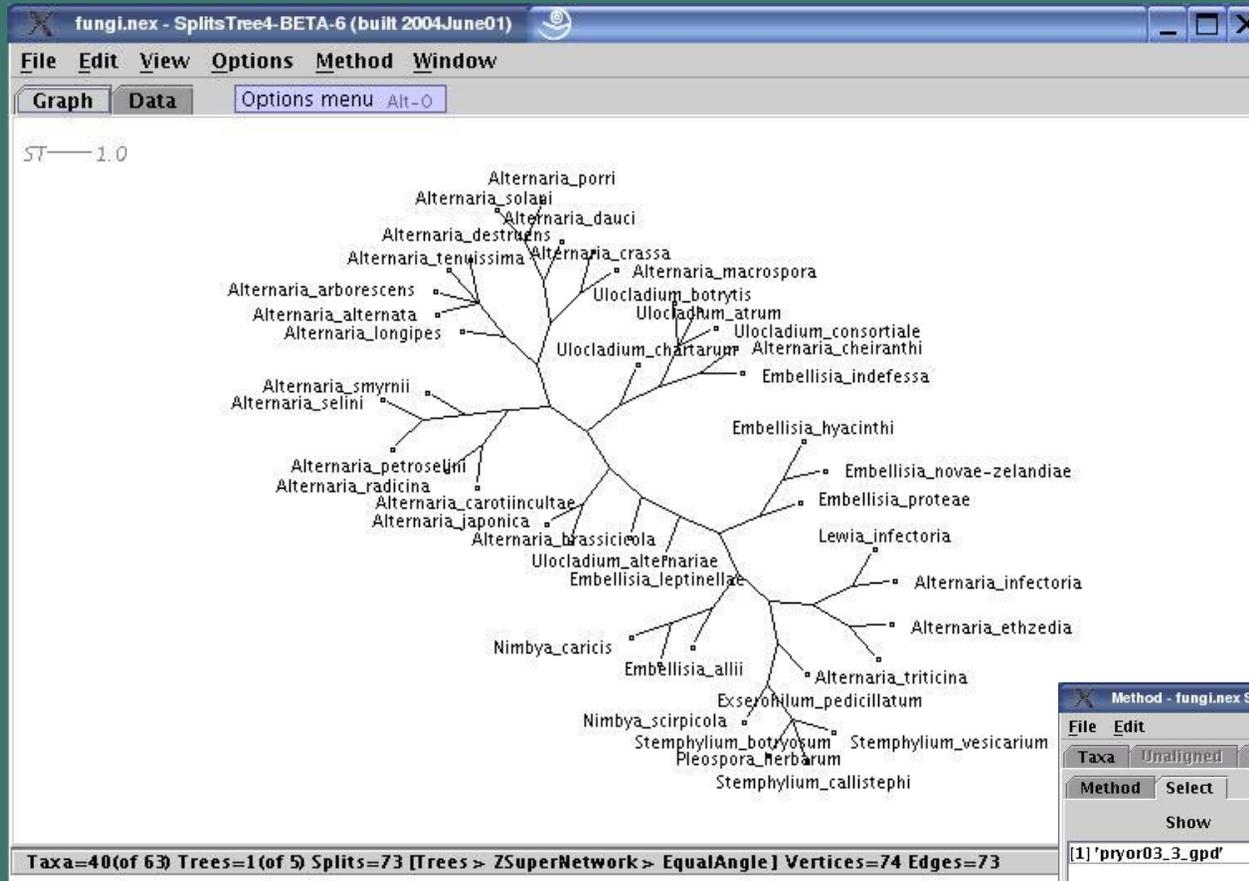
Method Select

Show	Hide	Apply
[1] 'pryor03_2_S5U'	'pryor03_1_ITS'	
	'pryor03_3_gpd'	
	'pryor00_1_ITS'	
	'pryor00_2_S5UrdNA'	

< Show Hide > Show all Hide all

nTrees= 1 (4 of 5 hidden)

Individual Gene Trees



Gpd03

40 taxa

Method - fungi.nex SplitsTree4-BETA-6 (built 2004June01)

File Edit

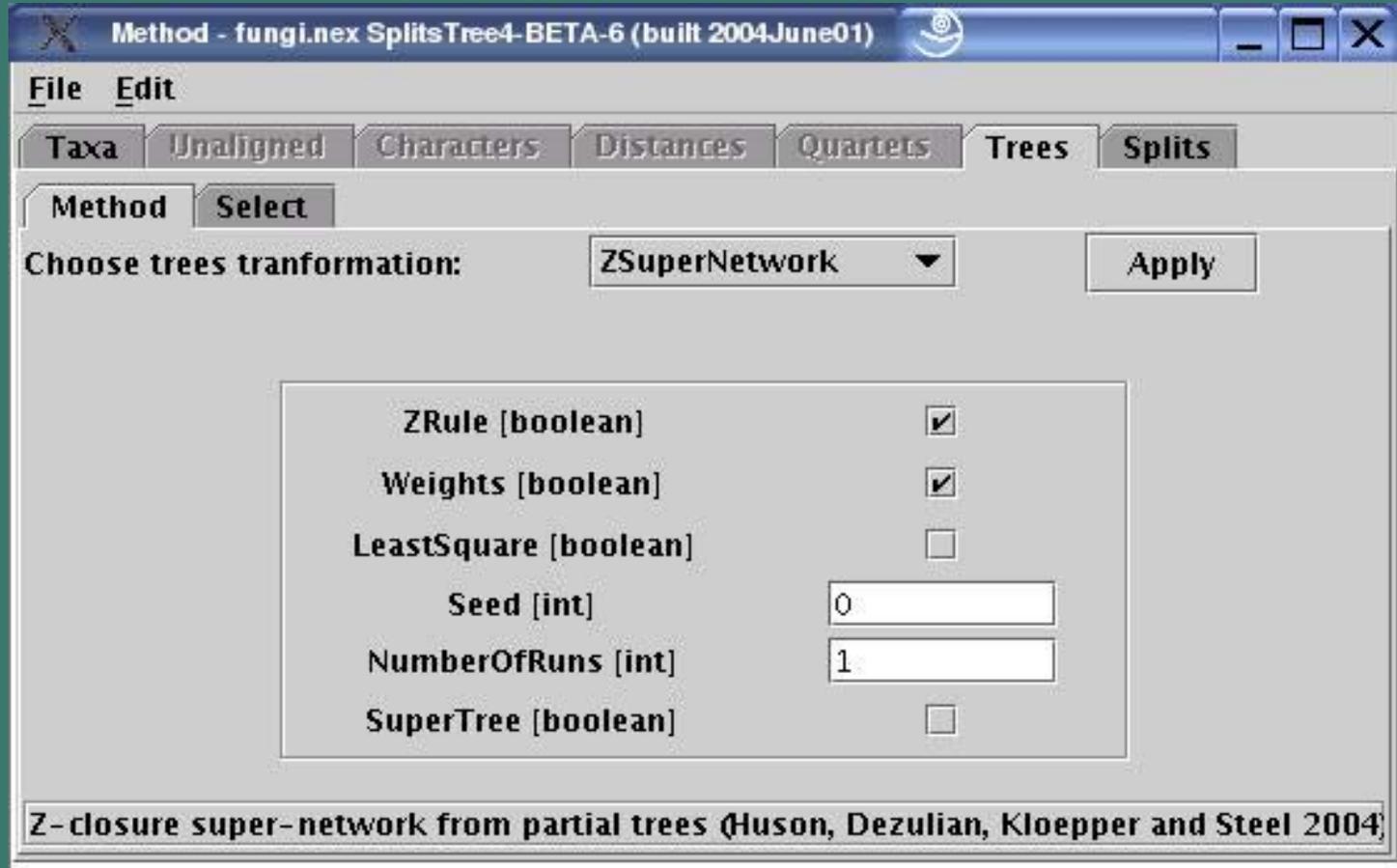
Taxa Unaligned Characters Distances Quartets Trees Splits

Method Select

Show	Hide	Apply
[1] 'pryor03_3_gpd'	'pryor03_1_ITS'	
	'pryor03_2_SSIU'	
	'pryor00_1_ITS'	
	'pryor00_2_SSIUrDNA'	

nTrees= 1 (4 of 5 hidden)

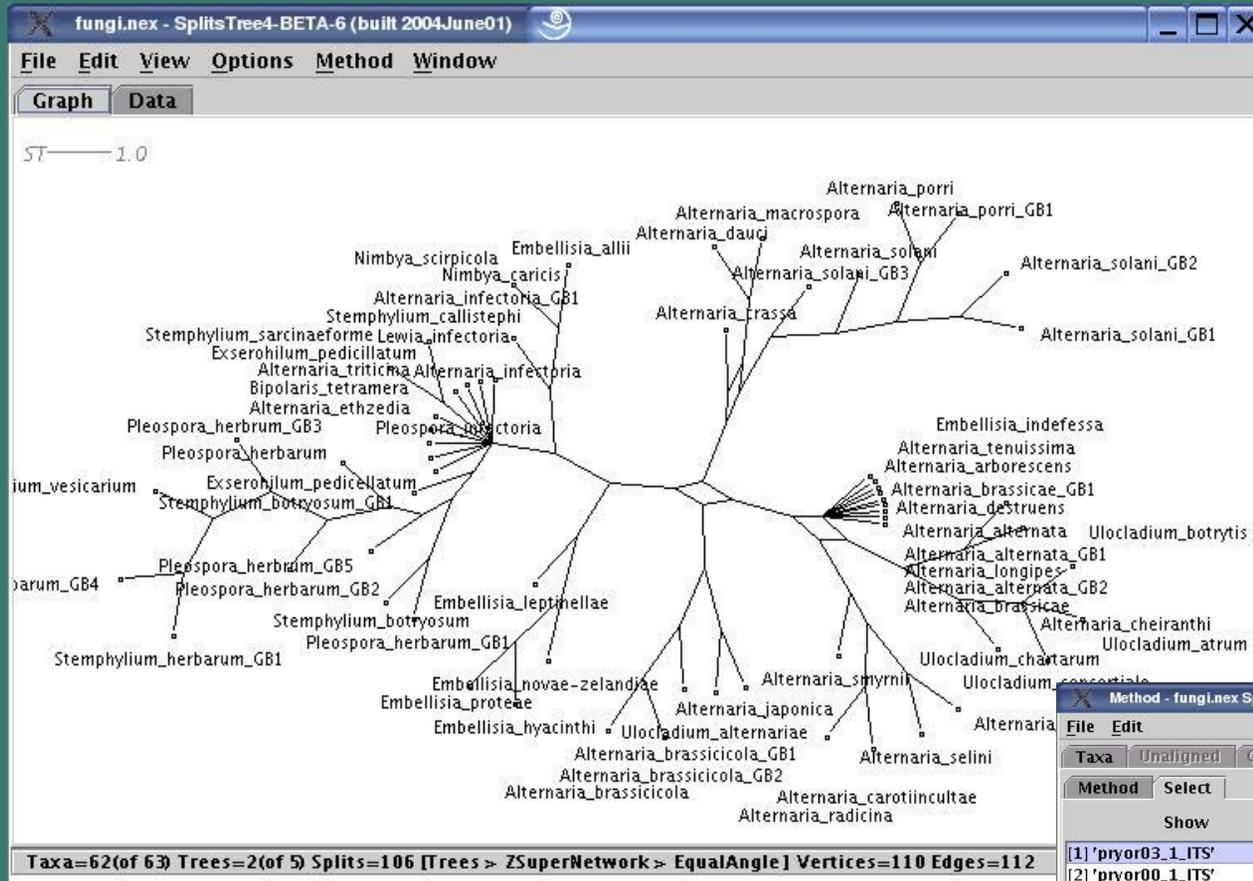
Gene Trees as Super Network



Z-closure: a fast super-network method (WABI 2004) 17

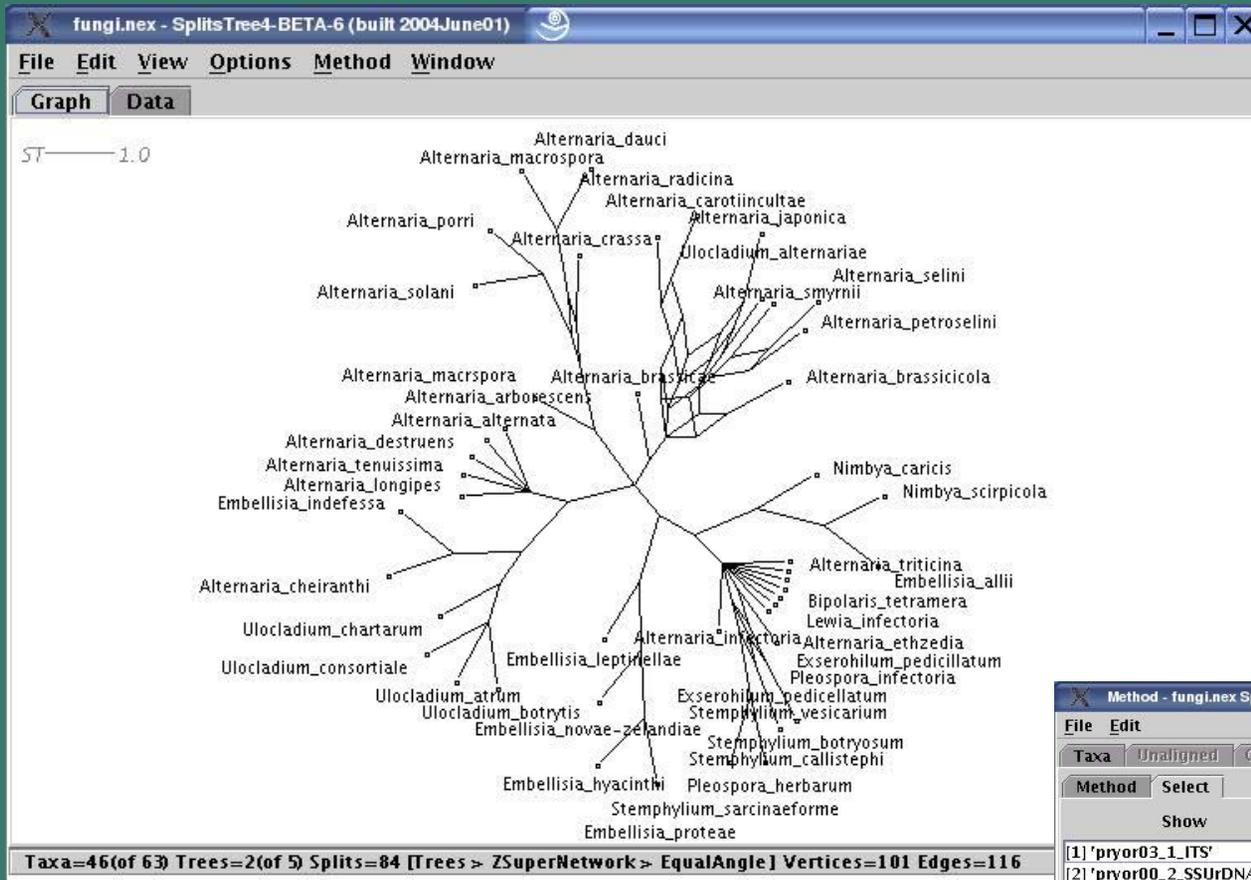


Gene Trees as Super Network



ITS00+
ITS03

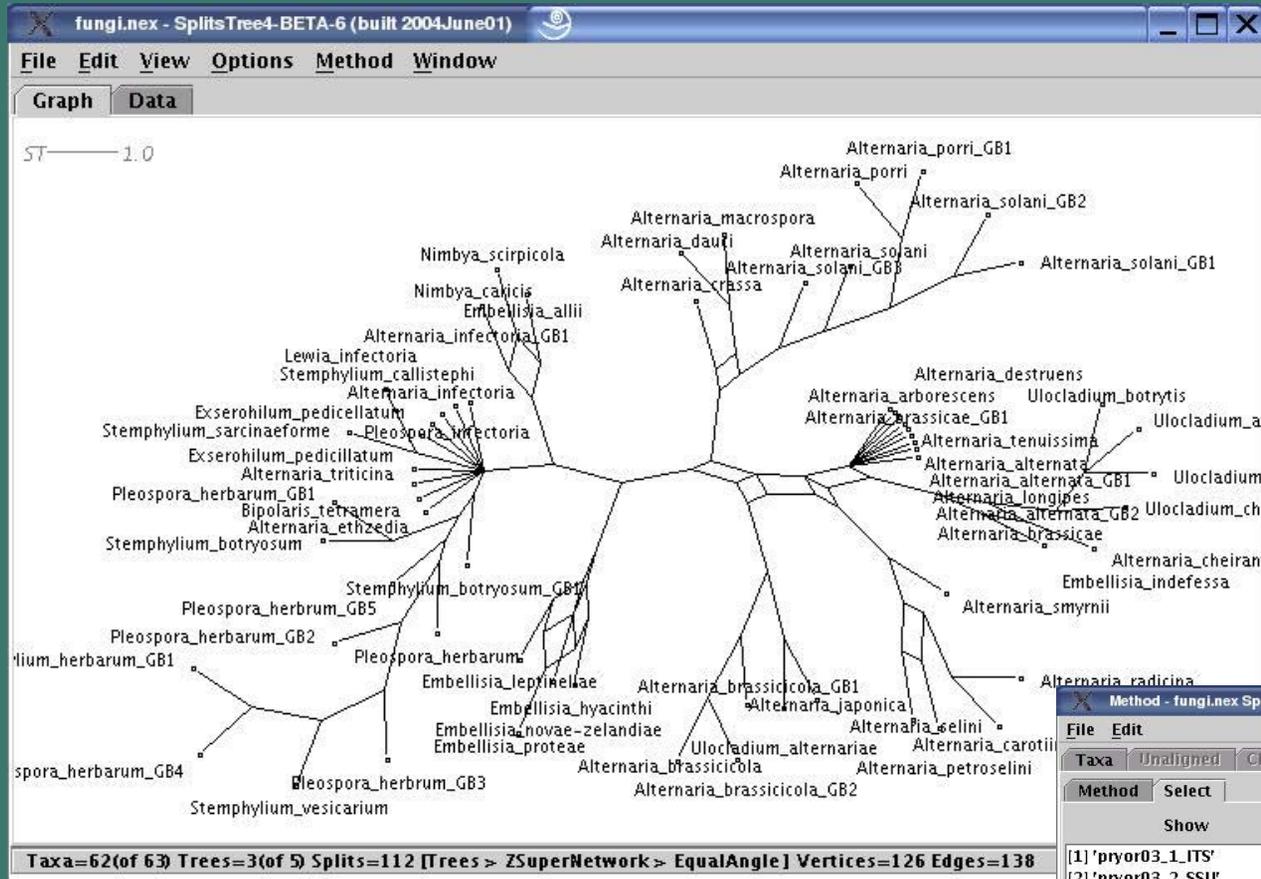
Gene Trees as Super Network



ITS03+
SSU00



Gene Trees as Super Network



ITS00+
ITS00+
SSU03

Method - fungi.nex SplitsTree4-BETA-6 (built 2004.June01)

File Edit

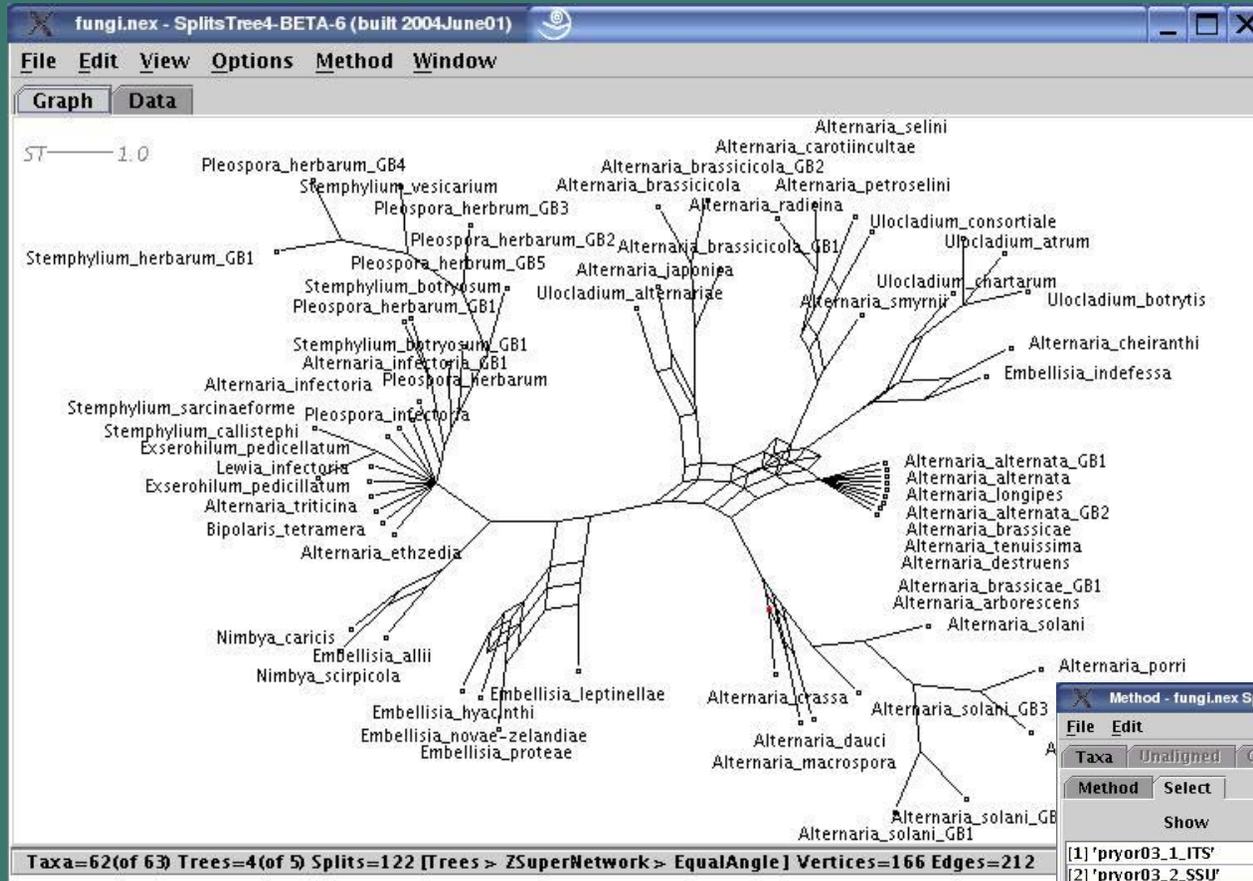
Taxa Unaligned Characters Distances Quartets Trees Splits

Method Select

Show	Hide	Apply
[1] 'pryor03_1_ITS'	'pryor03_3_gpd'	< Show
[2] 'pryor03_2_SSSU'	'pryor00_2_SSSUDNA'	
[3] 'pryor00_1_ITS'		Hide >
		Show all
		Hide all

nTrees= 3 (2 of 5 hidden)

Gene Trees as Super Network



ITS00+
ITS03+
SSU03+
Gpd03

Method - fungi.nex SplitsTree4-BETA-6 (built 2004.June01)

File Edit

Taxa Unaligned Characters Distances Quartets Trees Splits

Method Select

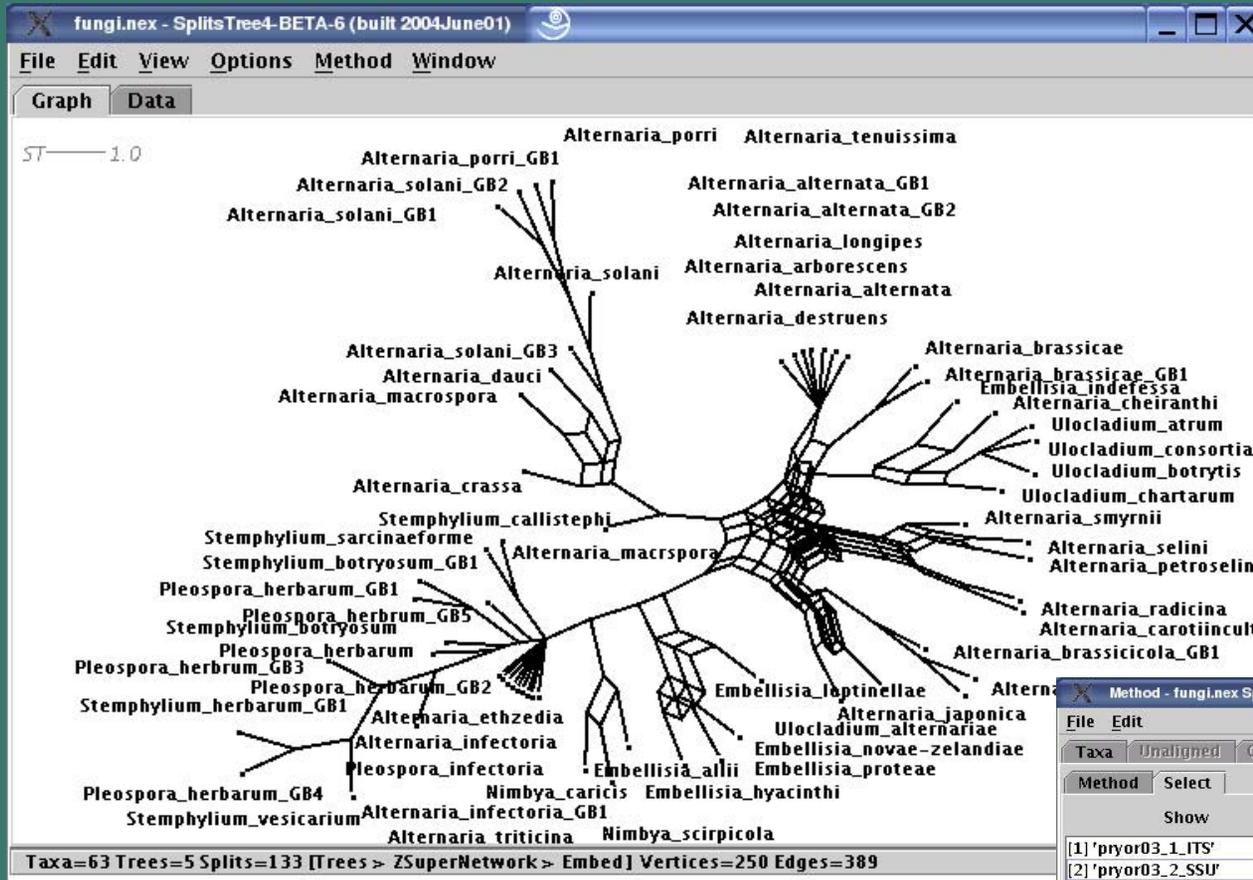
Show	Hide
[1] 'pryor03_1_ITS'	pryor00_2_SsuDNA'
[2] 'pryor03_2_Ssu'	
[3] 'pryor03_3_gpd'	
[4] 'pryor00_1_ITS'	

< Show Hide > Show all Hide all

nTrees= 4 (1 of 5 hidden)



Gene Trees as Super Network



ITS00+
ITS03+
SSU00+
SSU03+
Gpd03

Method - fungi.nex SplitsTree4-BETA-6 (built 2004June01)

File Edit

Taxa Unaligned Characters Distances Quartets Trees Splits

Method Select

Show	Hide	Apply
[1] 'pryor03_1_ITS'	<input type="checkbox"/>	<input type="button" value="Apply"/>
[2] 'pryor03_2_SSU'	<input type="checkbox"/>	<input type="button" value="Apply"/>
[3] 'pryor03_3_gpd'	<input type="checkbox"/>	<input type="button" value="Apply"/>
[4] 'pryor00_1_ITS'	<input type="checkbox"/>	<input type="button" value="Apply"/>
[5] 'pryor00_2_SSuDNA'	<input type="checkbox"/>	<input type="button" value="Apply"/>

nTrees= 5 (0 of 5 hidden)



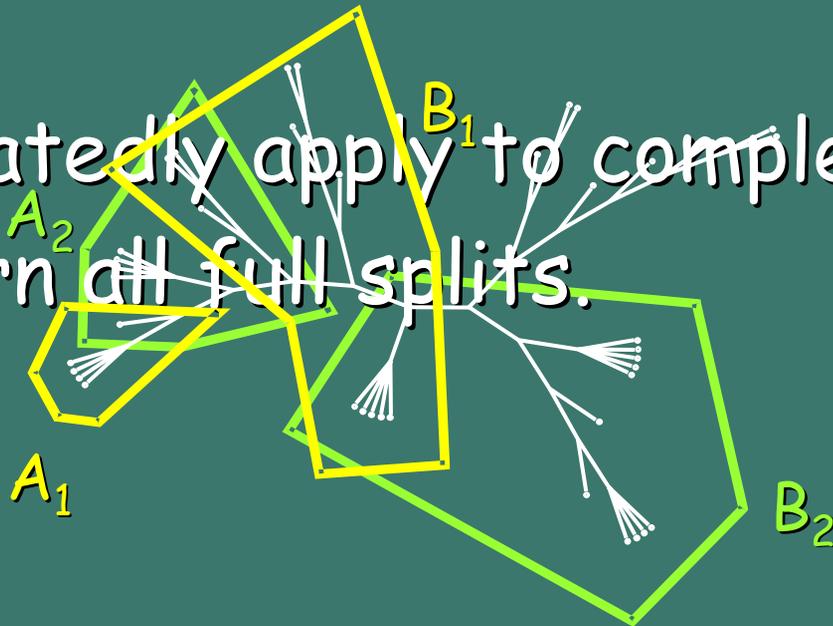
Z-Super Network

- Idea: Extend partial splits.

Z-rule:

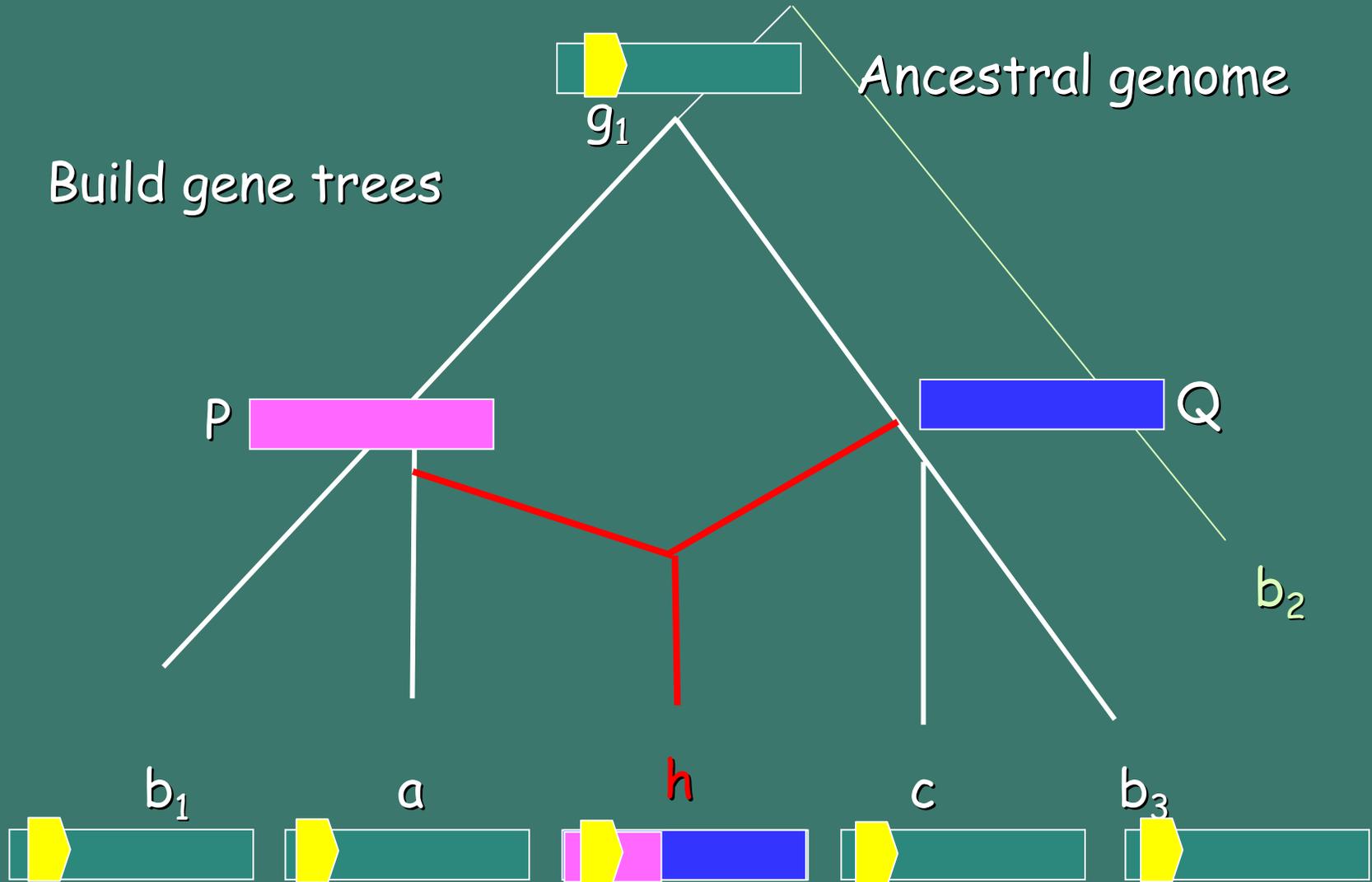
$$\begin{array}{ccc}
 A_1 & \overset{n}{\text{Z}} & A_2 \\
 \text{---} & & \text{---} \\
 B_1 & & B_2
 \end{array}
 \longrightarrow
 \begin{array}{cc}
 A_1 & A_1 \cup A_2 \\
 \text{---} & \text{---} \\
 B_1 \cup B_2 & B_2
 \end{array}$$

- Repeatedly apply to completion.
- Return all full splits.



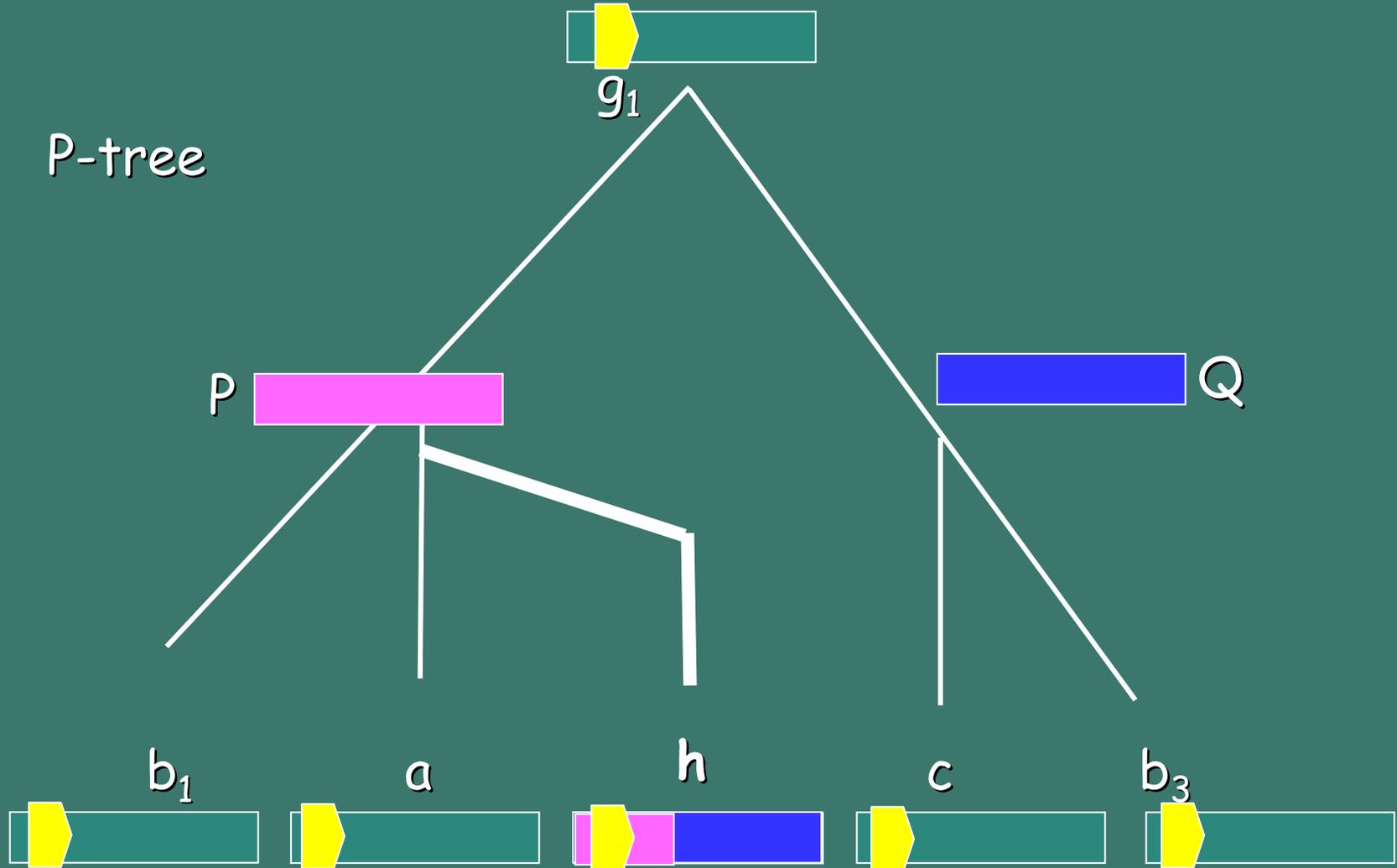


Reticulation Networks



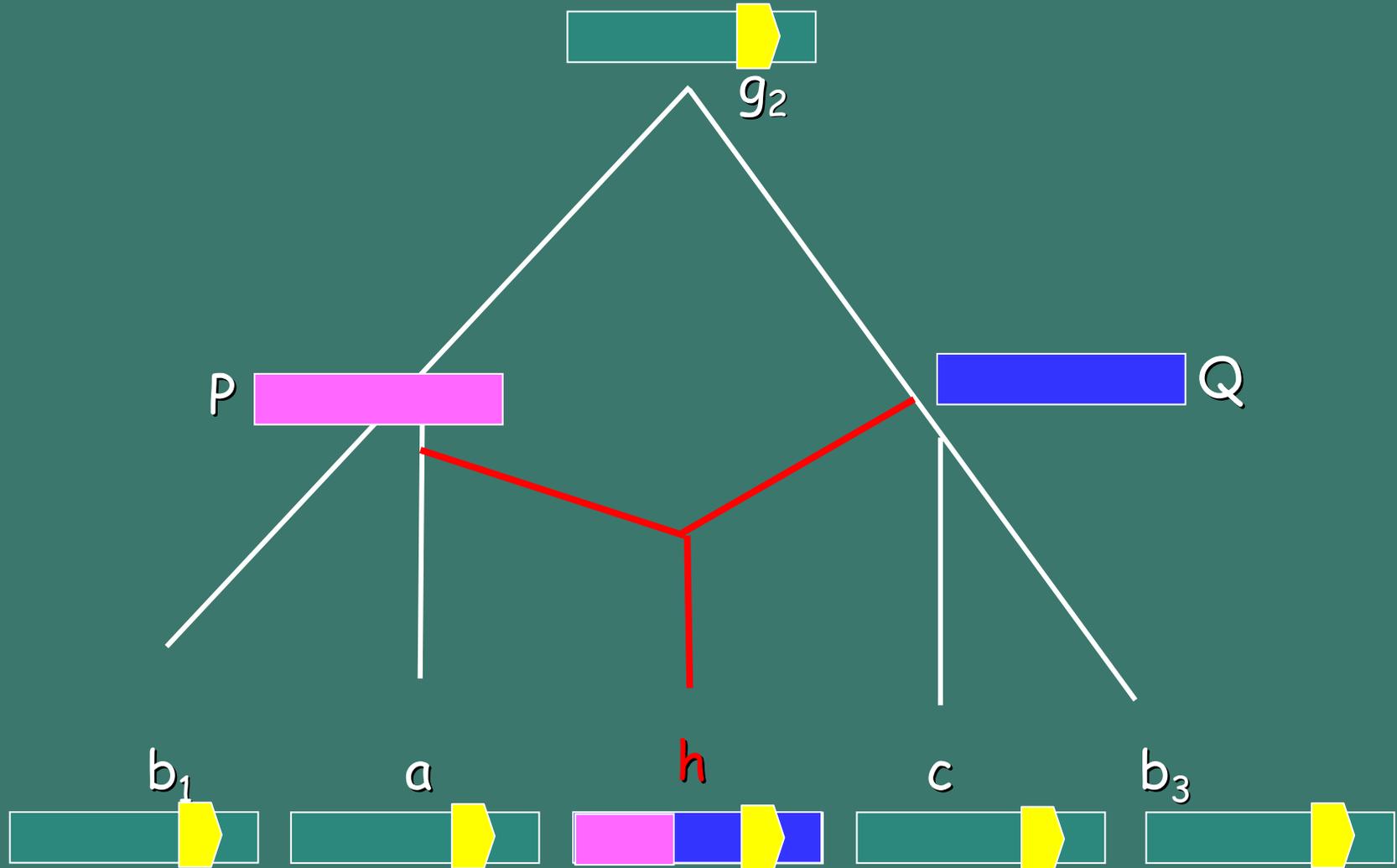


Reticulation Networks



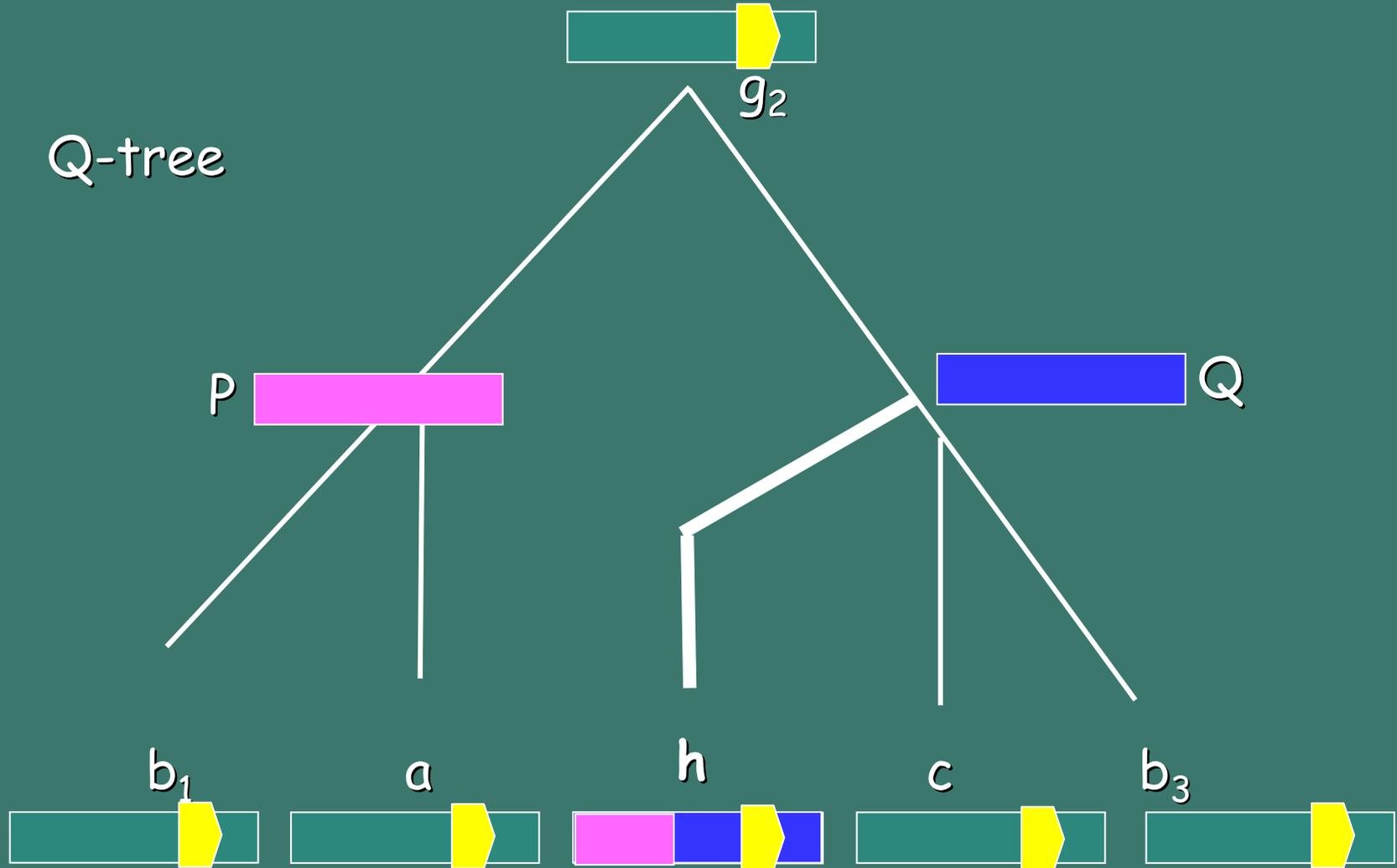


Reticulation Networks



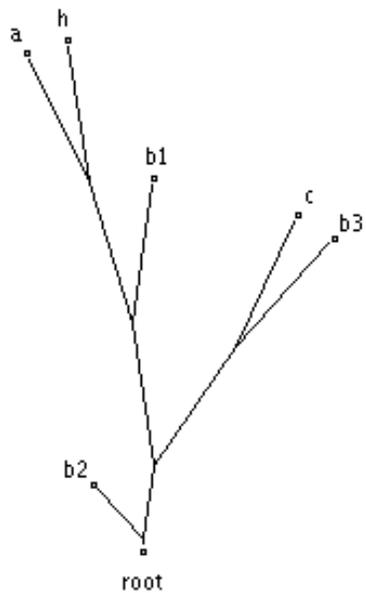


Reticulation Networks

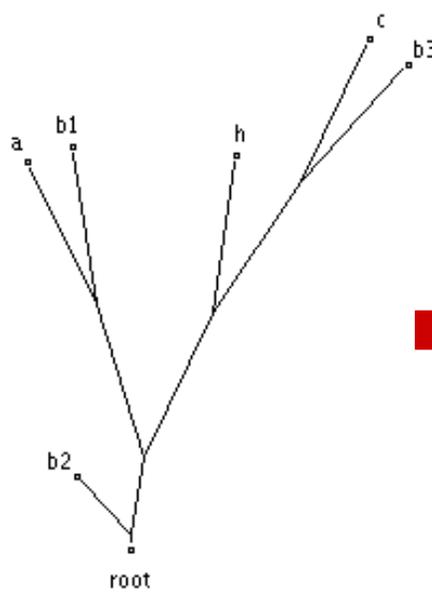




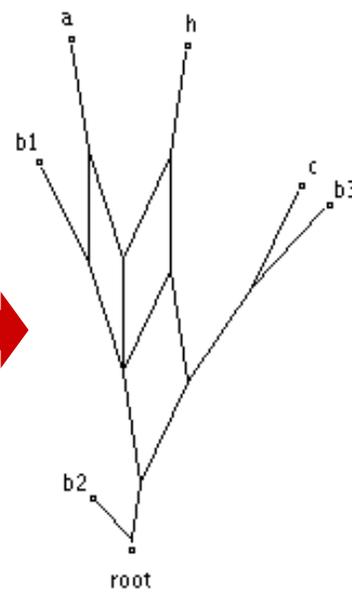
From Gene Trees to Reticulation Graphs



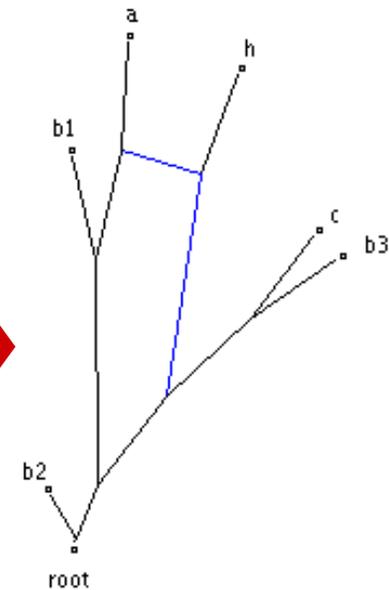
gene tree1



gene tree2



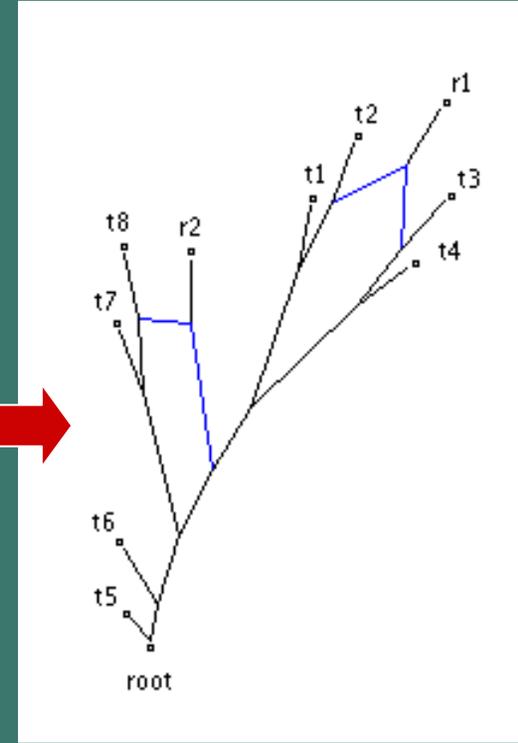
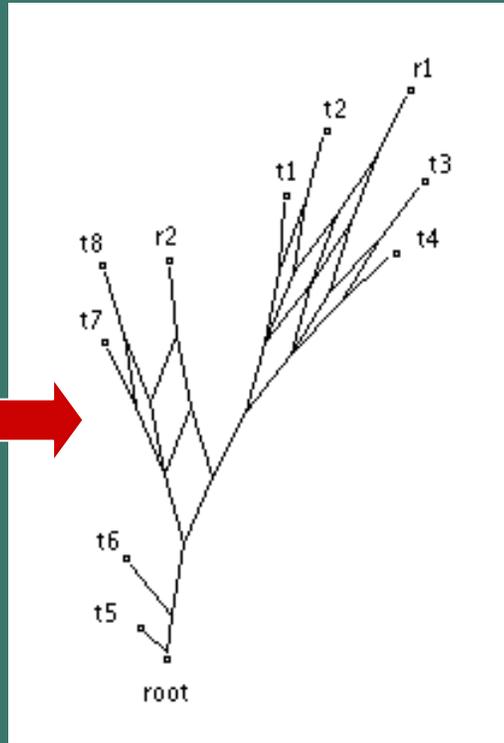
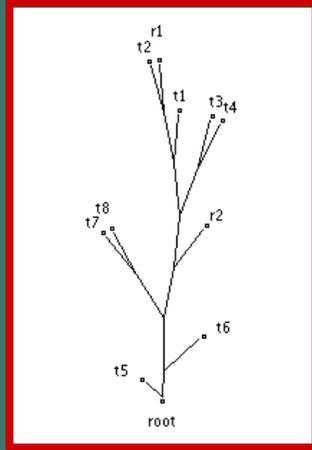
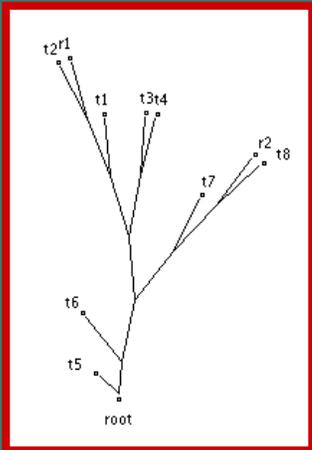
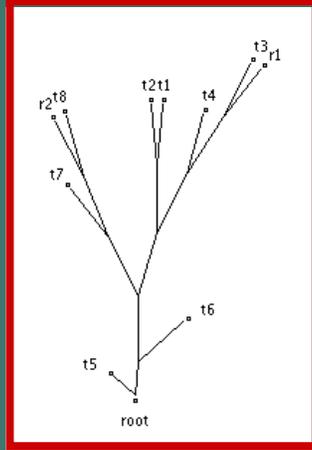
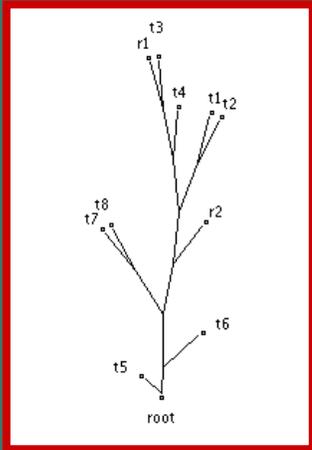
combined
splits



reticulation
graph



Multiple Independent Reticulations



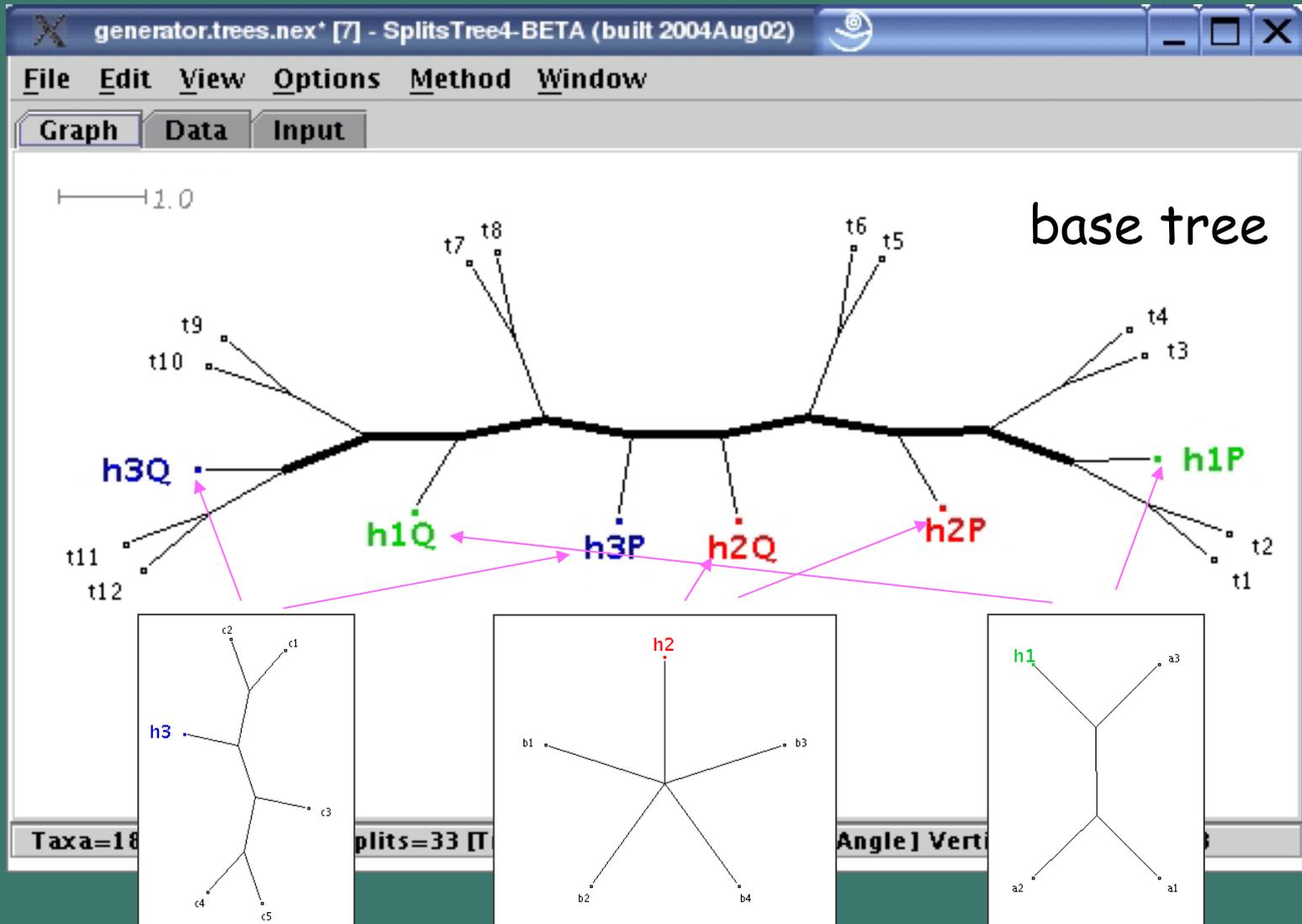
Two hybridizations \Rightarrow
four different gene trees

all splits

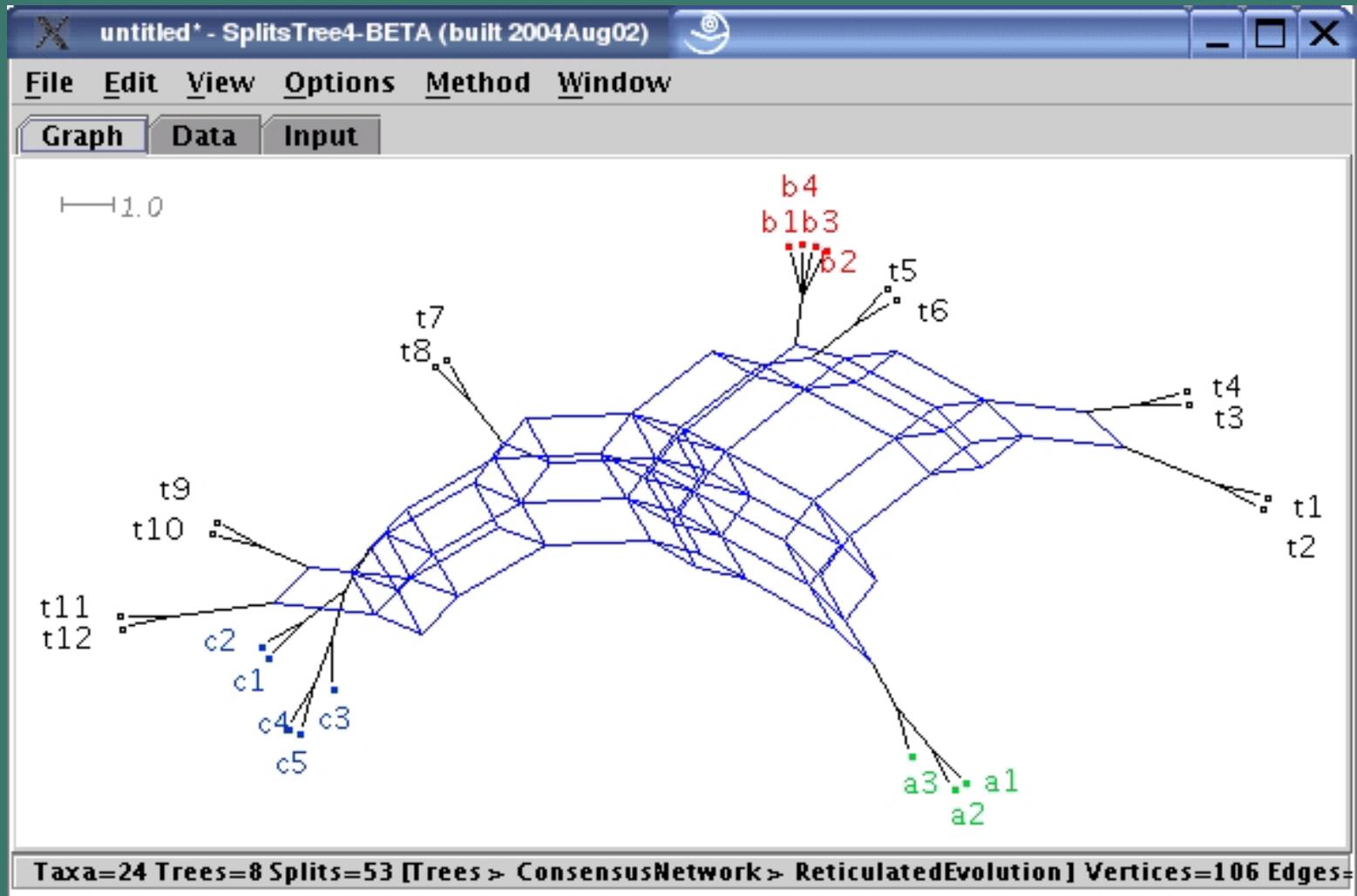
reconstructed
reticulations



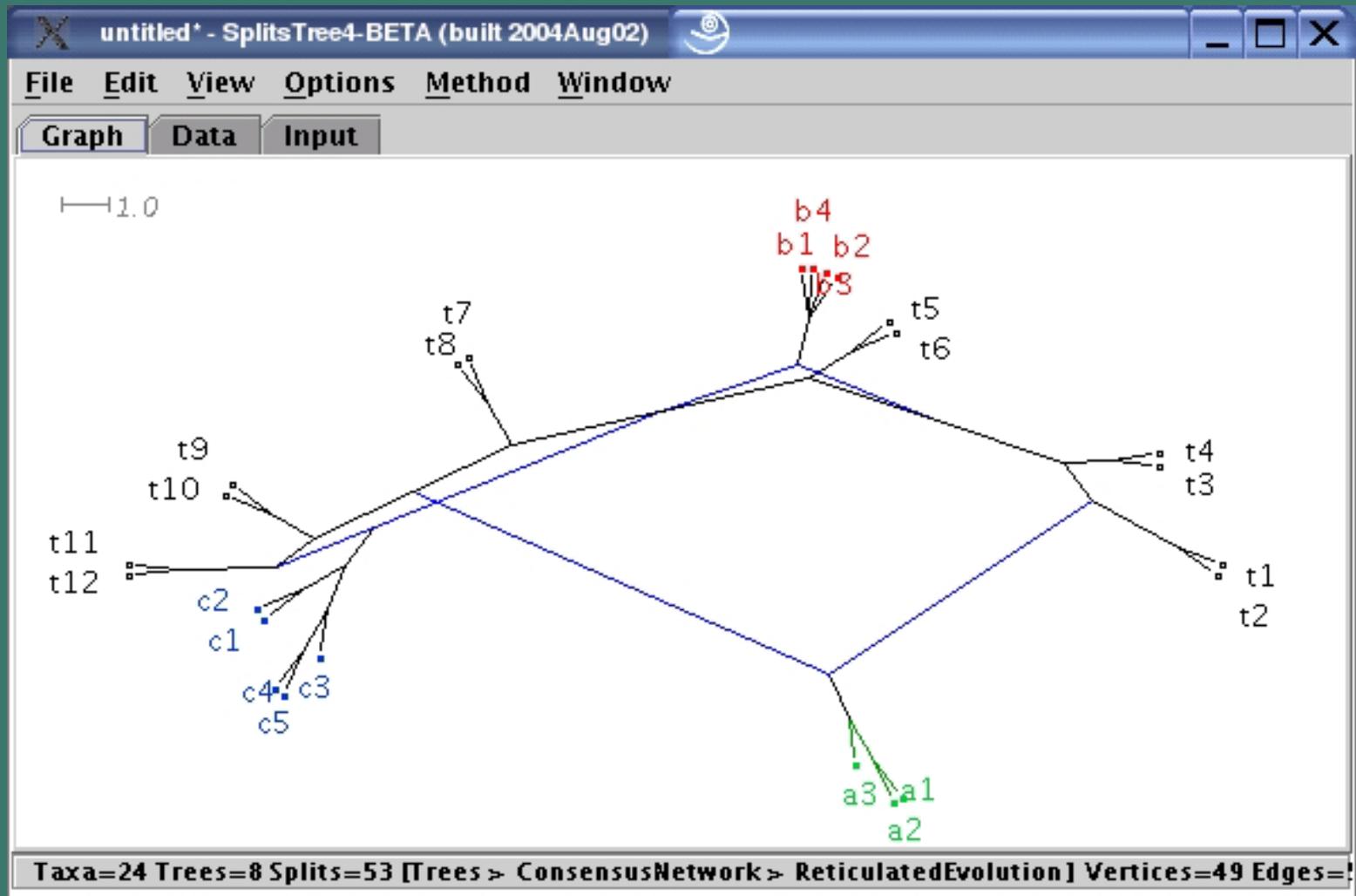
Non-Independent Reticulation Events



Splits Graph

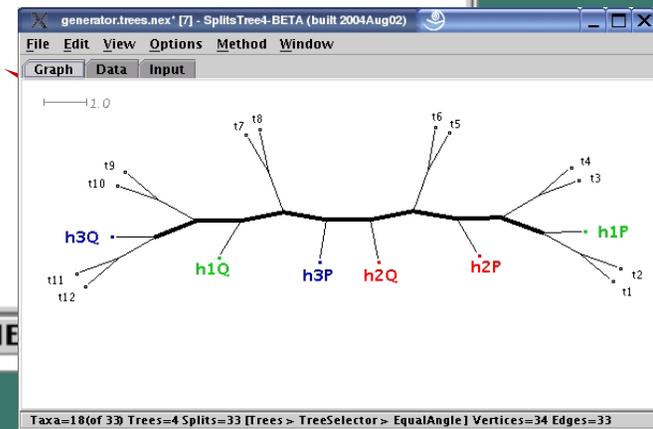
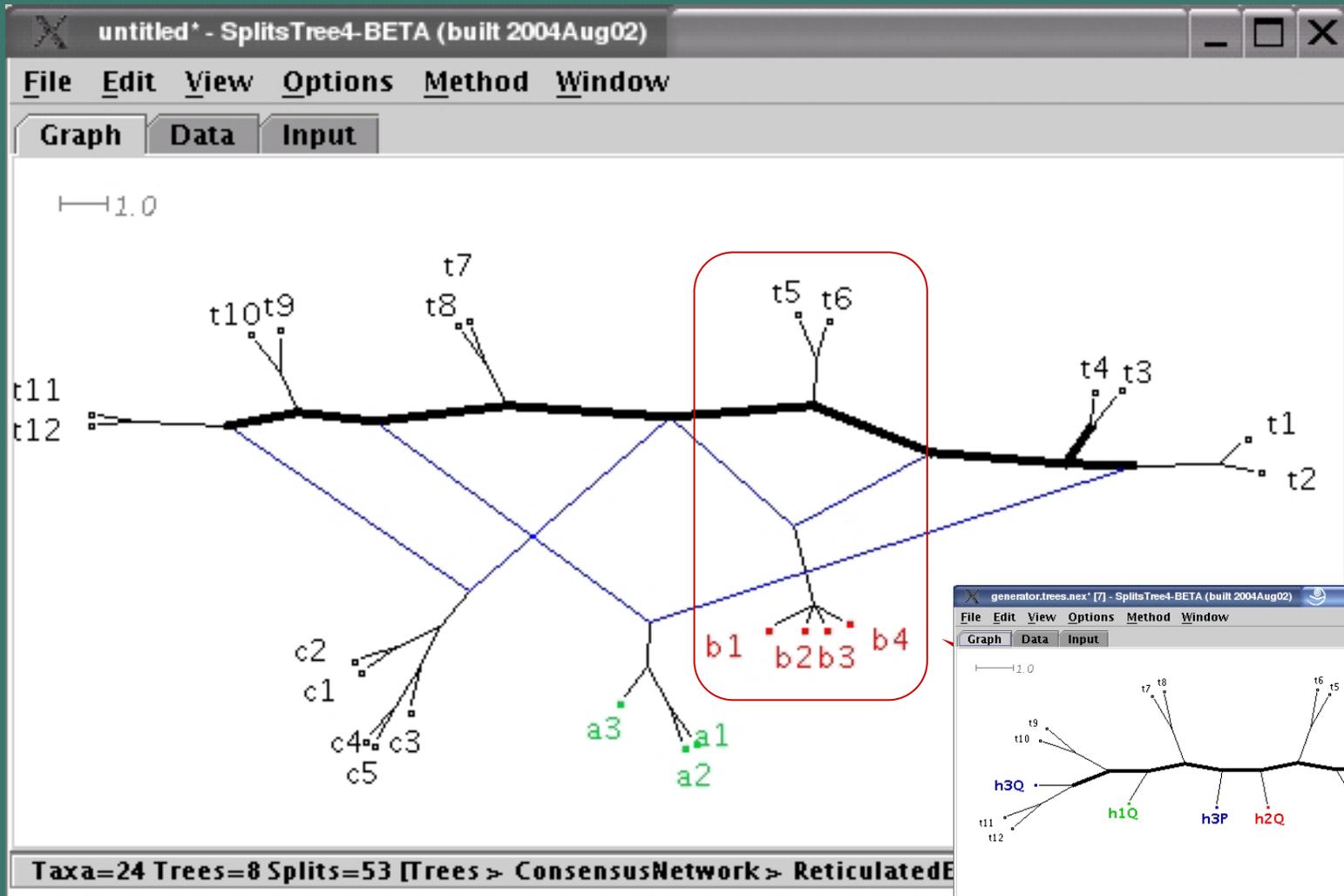


Reticulation Graph

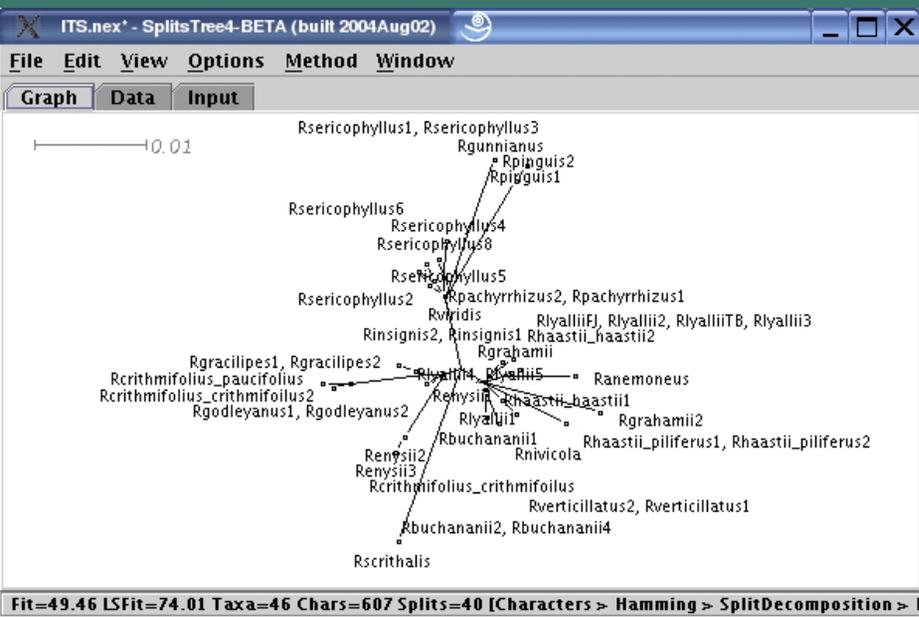




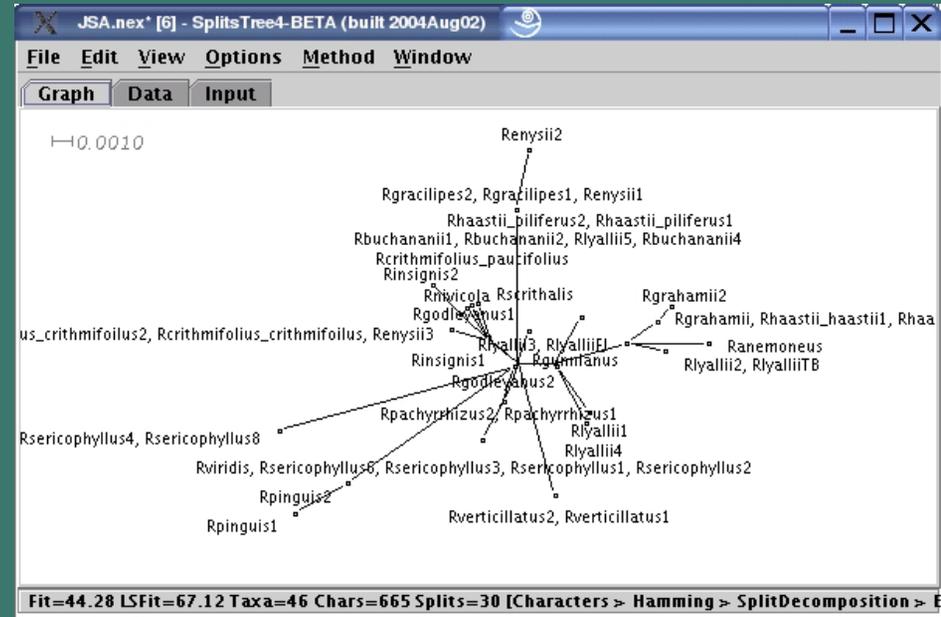
Reticulation Graph



Application to Real Data: Buttercups

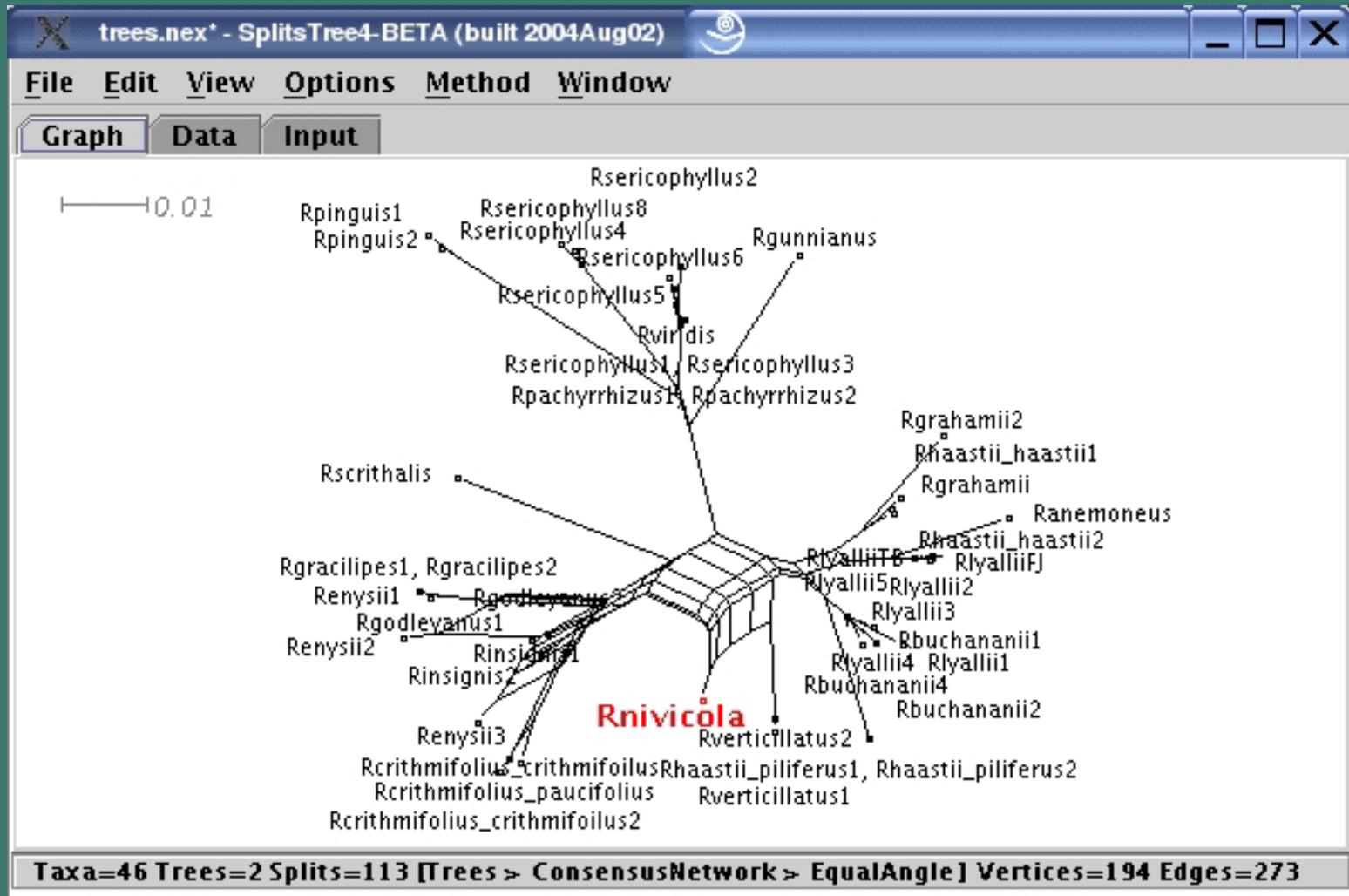


ITS (nuclear genome)

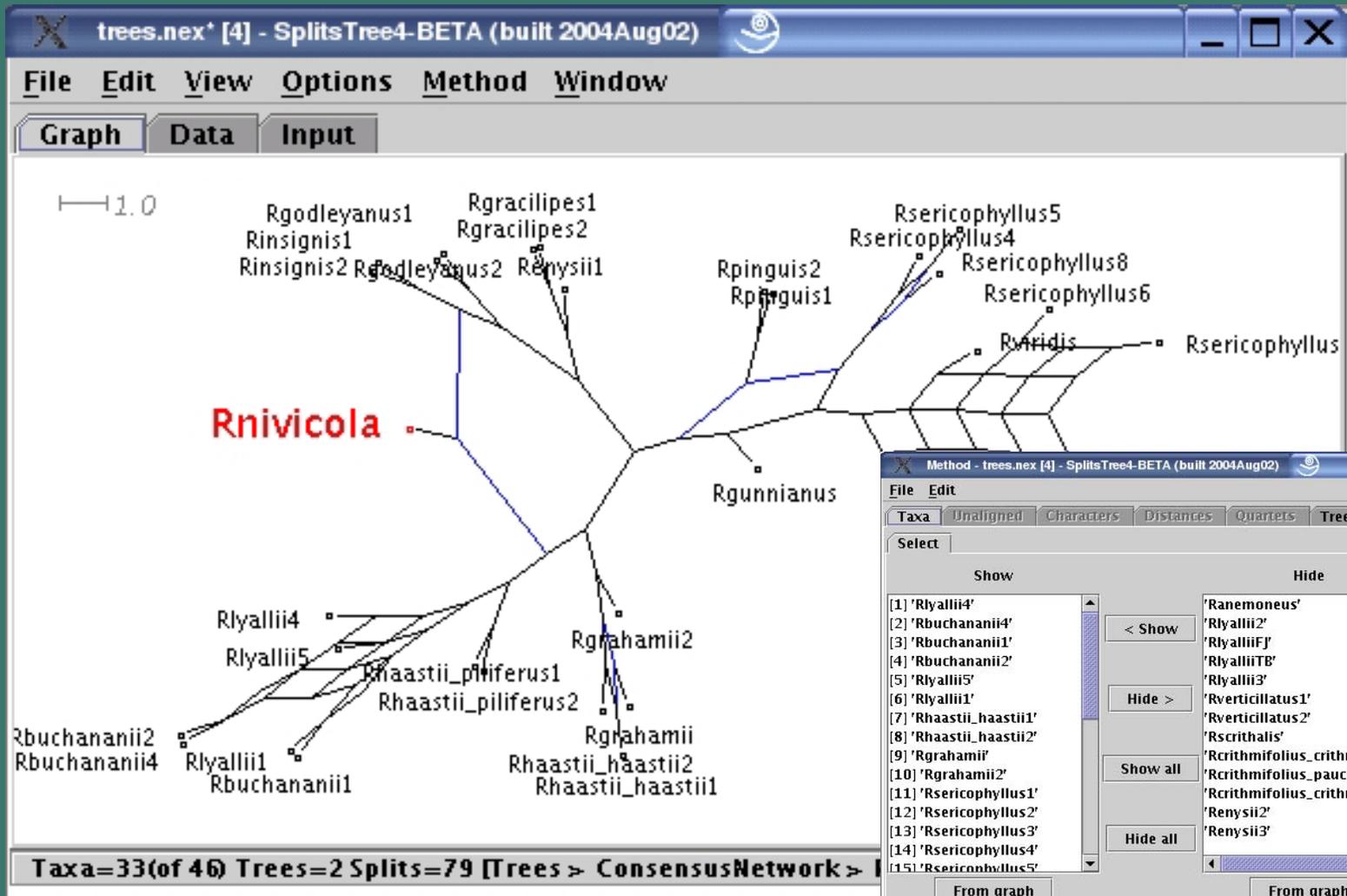


JSA (chloroplast genome)

Application to Real Data: Buttercups



Application to Real Data: Buttercups



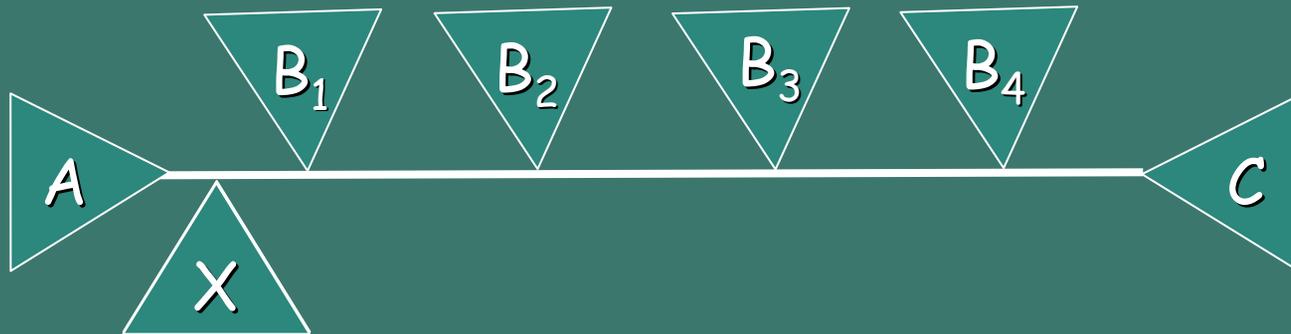
Taxa=33(of 46) Trees=2 Splits=79 [Trees > ConsensusNetwork >

nTaxa= 33 (13 of 46 hidden)

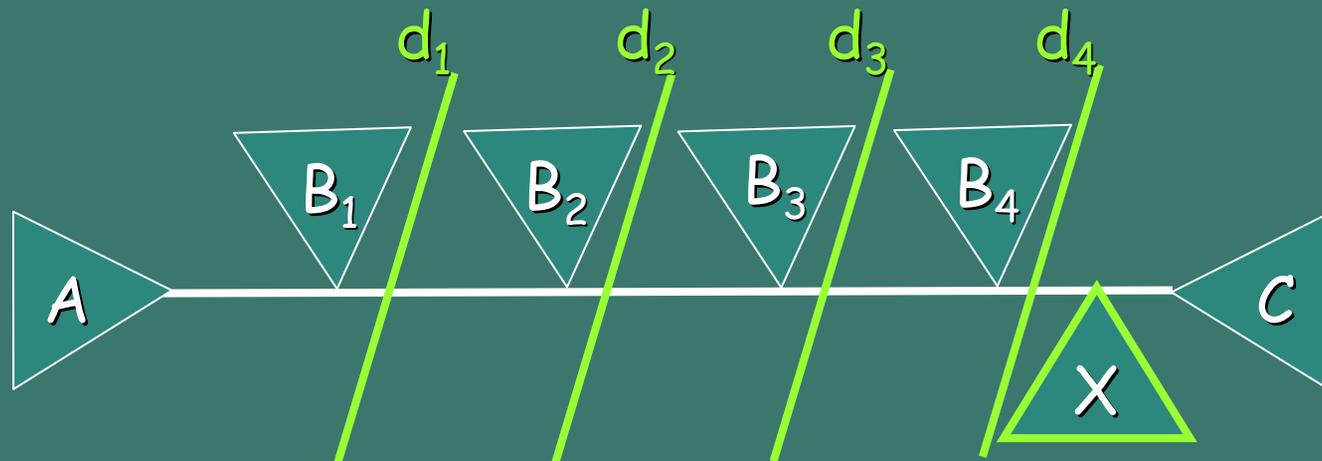
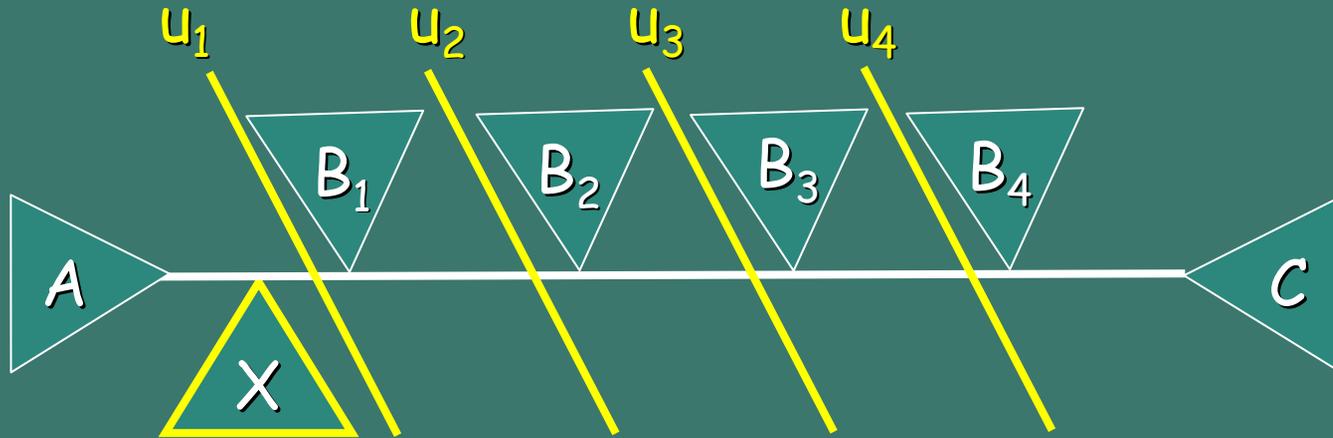
Algorithm to Detect Reticulation

- Input: set of splits Σ
- Process each component of the incompatibility graph $IG(\Sigma)$ separately
- Generate all possible "linear" reticulation scenarios
- Check necessary conditions on splits
- Check sufficient conditions on splits
- Modify splits graph to display detected reticulations

Splits Graphs and Reticulations

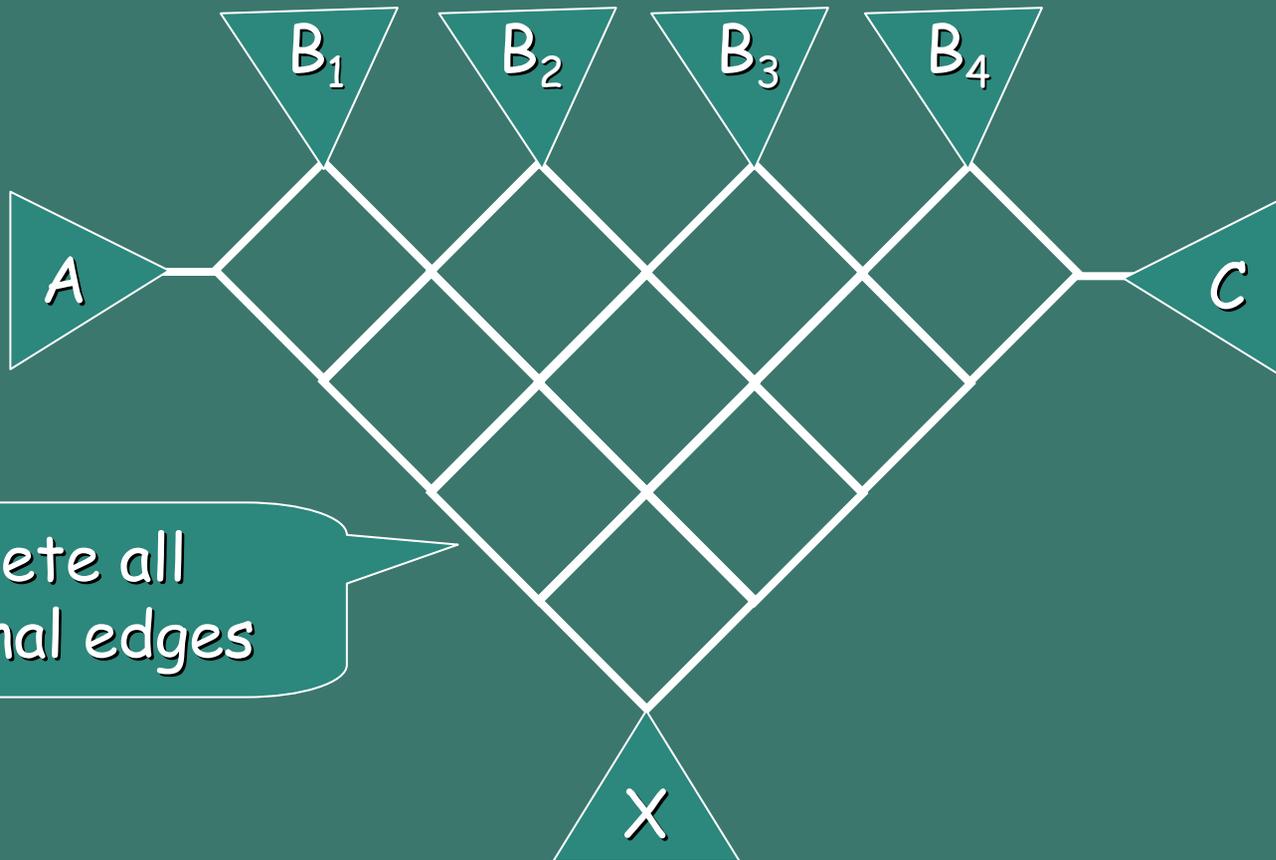


Recognizing an Isolated Reticulation



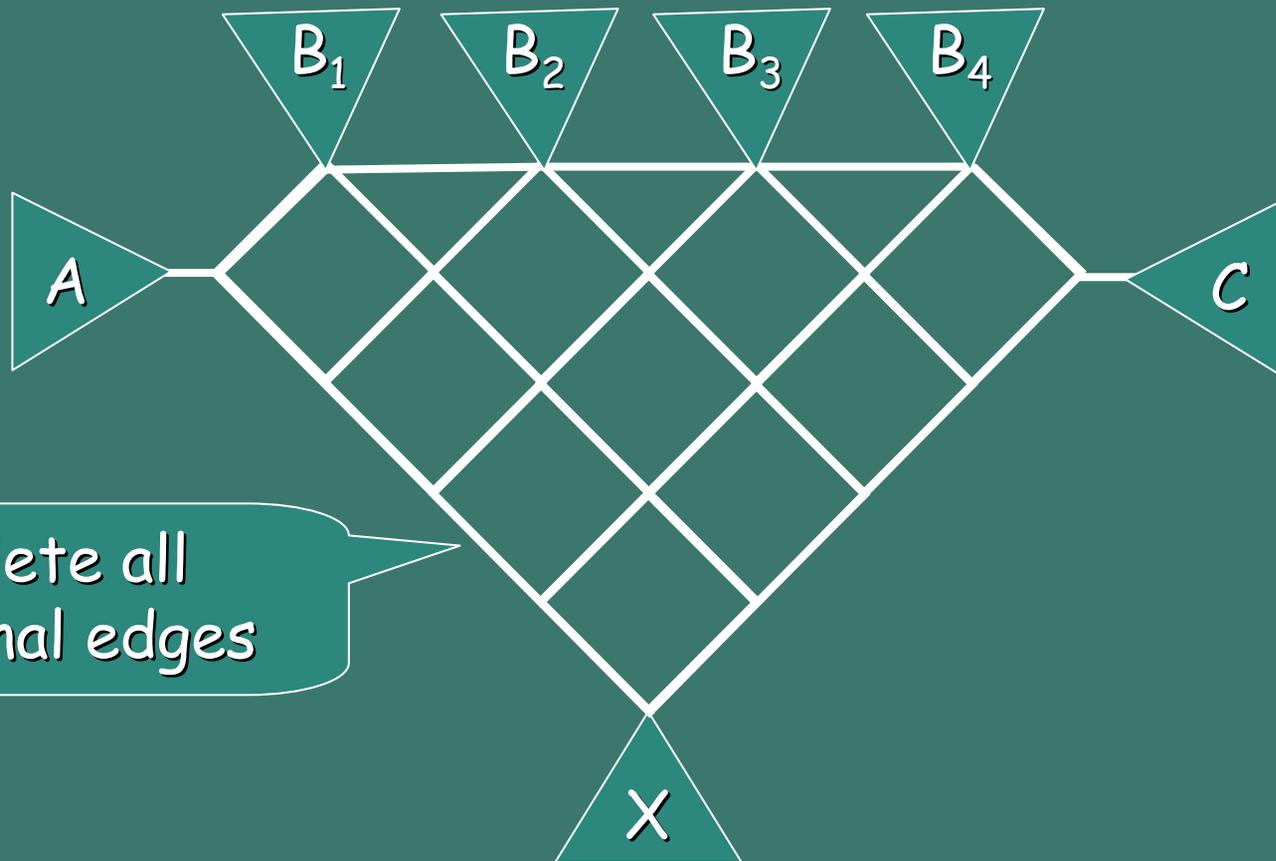
Splits Graph to Reticulation Graph

The associated splits graph...



Splits Graph to Reticulation Graph

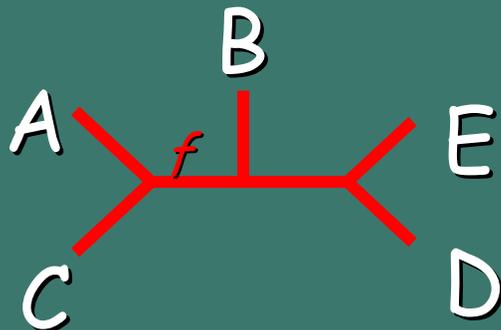
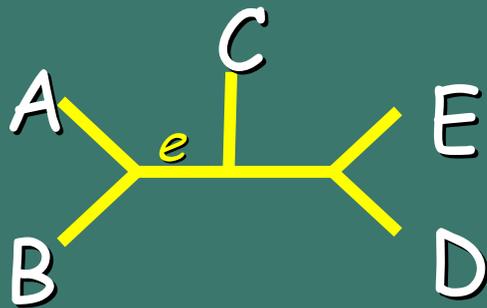
The associated splits graph... & the reticulation graph



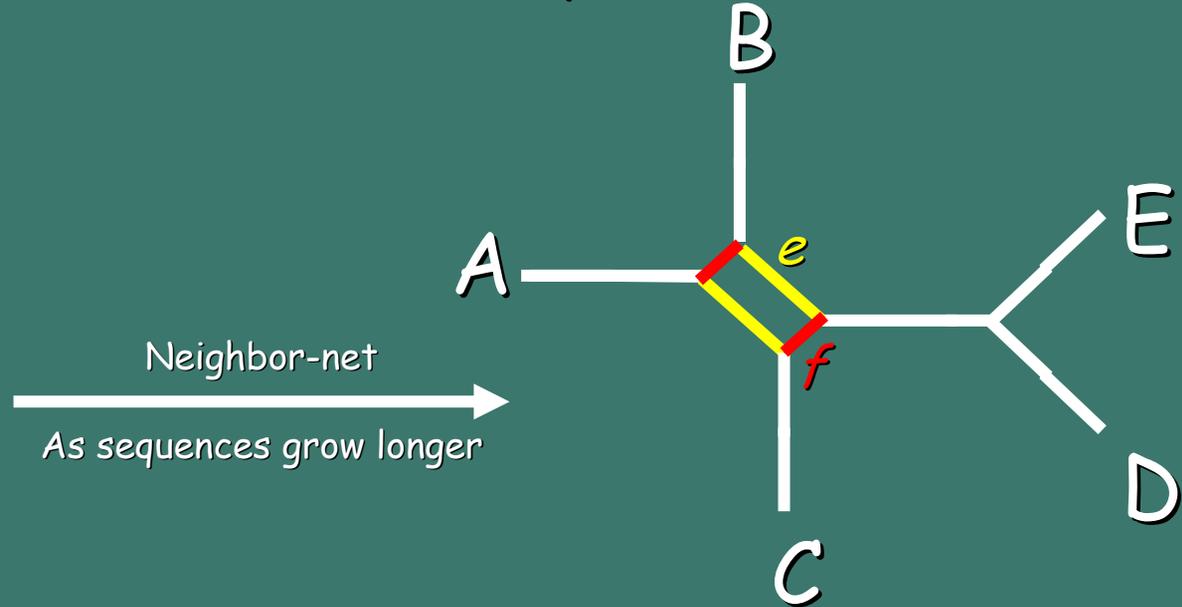


Reconstruction From Mosaic Sequences

Mosaic sequences evolving along two different trees



Splits graph containing the splits of both trees



Neighbor-net consistent on circular distances
Galled trees always circular

Summary

- Splits graphs and reticulation networks are different, but related types of phylogenetic networks
- Based on this, algorithms for detecting and visualizing "linear" reticulation scenarios can be developed
- Implementations exist and will be made available in SplitsTree

Acknowledgements

- Tobias Kloeppe and Mike Steel (hybridization detection algorithms)
- Pete Lockhart (application to plants)
- Dave Bryant (SplitsTree4)

