

How to use PYRE Classic

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How to create a new data file with an external editor

File...Save as...xls or .txt

Determine the characters in the first row
(if there are more than 256 characters use instead
the first column)

Determine the objects in the first column
(if there are more than 256 characters use instead
the first row)

Use matrioshka coding

String1[string2]

A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T
Species / characters																			
Aix galericulata (3)	A[]	B[A]	0[]																
Anas spp. (10)	B[A]	B[A]	1[0]																
Anser spp. (19)	D[A]	0[]	0[]																
Branta spp. (20)	D[A]	0[]	0[]																
Cairina moschata (1)	A[]	0[]	0[]																
Casarca ferruginea (18)	A[]	A[0]	0[]																
Chaulelasmus strepera (6)	C[B]	B[A]	1[0]	0[]	0[]	B[0]	0[]	C[B]	C[B]	B[A]	C[B]	A[0]	C[A]	0[]	A[0]	A[]	0[]	0[]	0[]
Dafila acuta (12)	A[]	C[B]	1[0]	0[]	0[]	B[0]	0[]	A[]	C[B]	A[0]	F[C]	A[0]	C[A]	0[]	A[0]	C[B]	0[]	1[0]	1[0]
Dafila spinicauda (11)	A[]	C[B]	1[0]	0[]	0[]	B[0]	0[]	B[A]	C[B]	A[0]	F[C]	A[0]	C[A]	0[]	A[0]	C[B]	0[]	1[0]	1[0]
Lampronessa sponsa (2)	A[]	B[A]	0[]	0[]	A[0]	0[]	0[]	D[C]	D[B]	B[A]	B[A]	A[0]	B[A]	0[]	A[0]	A[]	0[]	0[]	1[0]
Mareca penelope (5)	C[B]	B[A]	1[0]	0[]	0[]	B[0]	0[]	B[A]	B[A]	B[A]	C[B]	0[]	A[]	0[]	A[0]	A[]	0[]	0[]	1[0]
Mareca sibilatrix (4)	C[B]																0[]	0[]	0[]
Nettion crecca (7)	B[A]																0[]	0[]	1[0]
Nettion flavirostre (8)	B[A]																0[]	0[]	1[0]
Poecilonetta bahamensis (13)	A[]																0[]	1[0]	1[0]
Poecilonetta erythrorhyncha (14)	A[]																0[]	1[0]	1[0]
Querquedula querquedula (15)	A[]																0[]	1[0]	0[]
Spatula clypeata (16)	A[]	E[A]	0[]	0[]	0[]	B[0]	0[]	E[A]	B[A]	0[]	G[F]	A[0]	C[A]	0[]	A[0]	A[]	0[]	1[0]	0[]
Tadorna tadorna (17)	A[]	A[0]	0[]	0[]	0[]	0[]	C[0]	A[]	E[A]	0[]	B[A]	0[]	A[]	0[]	A[0]	A[]	1[0]	0[]	0[]
Virago castanea (9)	B[A]	B[A]	1[0]	0[]	0[]	B[0]	0[]	B[A]	C[B]	A[0]	D[C]	A[0]	C[A]	B[A]	B[A]	A[]	0[]	0[]	1[0]

PYRE Classic uses either Excel (.xls) or tabulator delimited textfiles (.txt). The latter can be created by any editor.

If your matrix has less than 256 characters, species determination should occur in the first column, character determination in the first row. You have to use matrioshka coded data. Use any string to define a character state. If the state is not known use „?“.

How to use PYRE Classic to open a file

The screenshot shows the PYRE Classic application window. The 'File/Data' menu is open, and the 'Open' option is selected, which has opened a file selection dialog titled 'Öffnen'. The dialog shows a list of files in the 'matroschka' directory, with 'Lorenz41Korr' selected. The 'Dateiname' field is set to 'Lorenz41Korr' and the 'Dateityp' is set to 'Excel'. The 'Öffnen' button is highlighted with a blue callout box. A yellow callout box on the right explains the process of selecting a file type and the role of the protocol. A red callout box at the bottom right points to the 'Save' button, indicating where to save the protocol after file selection.

Choose `File/Data...Open...`

Choose `File/Data...Open...` of the main menu to select an Excel- or a textfile. If you use a .xls file, the data are loaded from the first worksheet. The main window contains a protocol that follows the processing and gives some advices. The protocol can be saved.

Press here after file selection

Save the protocol

First steps

Data from C:\AlphaEgo\Forschung\Aktuelle Forschung\Parsimony\2008\Tab2 of AppendixI.xls

Focus

Row 7 **Chaulelasmus strepera (6)** Col 7 **VII**

C[B] **Transpose**

Species / characters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV	XVI	XVII	XVIII
Aix galericulata (3)	A[]	B[A]	O[]	O[]	A[0[]]	D	A[0]	C[A]	B[A]	O[]	B[A]	O[]	A[0]	A[]	O[]	O[]	O[]	1[0]
Anas spp. (10)	B[A]	B[A]									C[A]	B[A]	B[A]	A[]	O[]	O[]	O[]	1[0]
Anser spp. (19)	D[A]	O[]									A[]	O[]						
Branta spp. (20)	D[A]	O[]	O[]	O[]	C[0]	A	O[]	O[]	A[]	O[]	A[]	O[]						
Cairina moschata (1)	A[]	O[]	O[]	O[]	A[0[]]	A[]	O[]	O[]	B[A]	O[]	A[]	O[]						
Casarca ferruginea (18)	A[]	A[0]	O[]	O[]	C[0]	A	O[]	O[]	B[A]	O[]	A[]	O[]						
Chaulelasmus strepera (6)	C[B]	B[A]	1[0]	O[]	B[0]	C[B]	C[B]	B[A]	C[B]	A[0]	C[A]	O[]						
Dafila acuta (12)	A[]	C[B]	1[0]	O[]	B[0]	A[]	O[B]	A[0]	F[C]	A[0]	C[A]	O[]						
Dafila spinicauda (11)	A[]	O[]	O[]	O[]	B[0]	B	C[B]	A[0]	F[C]	A[0]	C[A]	O[]						
Lampronessa sponsa (2)	A[]		O[]	A[0[]]	D[C]	E[B]	B[A]	B[A]	A[0]	B[A]	O[]							
Mareca penelope (5)	C[B]	B[A]	1[0]	O[]	B[0]	B	B[A]	B[A]	C[B]	O[]	A[]	O[]						
Mareca sibilatrix (4)	C[B]	B[A]	1[0]	O[]	B[0]	B[A]	B[A]	B[A]	C[B]	O[]	A[]	O[]						
Nettion crecca (7)	B[A]	B[A]	1[0]	O[]	B[0]	B[A]	C[B]	A[0]	E[D]	A[0]	C[A]	A[0]						
Nettion flavirostre (8)	B[A]	B[A]	1[0]	O[]	B[0]	B	C[B]	A[0]	E[D]	A[0]	C[A]	A[0]						
Poecilonetta bahamensis (13)	A[]	D[C]	1[0]	O[]	B[0]	B	B[A]	A[0]	G[F]	A[0]	C[A]	O[]						
Poecilonetta erythrorhyncha (14)	A[]	A[0]	1[0]	O[]	B[0]	A[]	B[A]	A[0]	G[F]	A[0]	C[A]	O[]	A[0]	B[A]	O[]	1[0]	1[0]	1[0]
Querquedula querquedula (15)	A[]	E[A]	1[0]	O[]	B[0]	E[A]	B[A]	A[0]	G[F]	B[A]	C[A]	O[]	A[0]	A[]	O[]	1[0]	O[]	1[0]
Spatula clypeata (16)	A[]	E[A]	O[]	O[]	B[0]	E	B[A]	O[]	G[F]	A[0]	C[A]	O[]	A[0]	A[]	O[]	1[0]	O[]	1[0]
Tadorna tadorna (17)	A[]	A[0]	O[]	O[]	C[0]	A[]	D[A]	O[]	B[A]	O[]	A[]	O[]	A[0]	A[]	1[0]	O[]	O[]	1[0]
Vireo castaneus (9)	B[A]	B[A]	1[0]	1[0]	B[0]	B	C[B]	A[0]	D[C]	A[0]	C[A]	B[A]	B[A]	A[]	O[]	O[]	O[]	1[0]

Exchange rows and columns

Focus

The „Data“ – window shows the data, allows to set the focus to a cell of the grid and to transpose the matrix (this means it exchanges rows and columns). This may be necessary, because an Excel – worksheet has only 256 columns and maybe you want to work with more characters. Press „Path“ to go on.

Path

First steps

Data from C:\AlphaEgo\Forschung\Beendete Forschung\Parsimony\Lorenz41Korr.xls

Focus

Row 8 **Nettion flavirostre** Col 9 **VII** **Transpose**

C[B[A[0]]]

	I	II	III	IV	V-1	V-2	V-3	VI	VII	VIII	IX
Cairina moschata	A[]	O[]	O[]	O[]	A[0[]]	O[]	O[]	A[]	O[]	O[]	B[A[]]
Lampronessa sponsa	A[]					O[]	O[]	D[C[B[A[]]]]	D[B[A[0[]]]]	B[A[0[]]]	B[A[]]
Aix galericulata	A[]					O[]	O[]	D[C[B[A[]]]]	A[0[]]	C[A[0[]]]	B[A[]]
Mareca sibilatrix	C[B[A[]]]					B[0[]]	O[]	B[A[]]	B[A[0[]]]	B[A[0[]]]	C[B[A[]]]
Mareca penelope	C[B[A[]]]					B[0[]]	O[]	B[A[]]	B[A[0[]]]	B[A[0[]]]	C[B[A[]]]
Chaulelasmus strepera	C[B[A[]]]					B[0[]]	O[]	C[B[A[]]]	C[B[A[0[]]]]	B[A[0[]]]	C[B[A[]]]
Nettion crecca	B[A[]]					B[0[]]	O[]	B[A[]]	C[B[A[0[]]]]	A[0[]]	E[D[C[B[A[]]]]]
Nettion flavirostre	B[A[]]					B			C[B[A[0[]]]]	A[0[]]	E[D[C[B[A[]]]]]
Virago castanea	B[A[]]					B			C[B[A[0[]]]]	A[0[]]	D[C[B[A[]]]]
Anas spp.	B[A[]]					B			C[B[A[0[]]]]	A[0[]]	C[B[A[]]]
Dafila spinicauda	A[]					B			C[B[A[0[]]]]	A[0[]]	F[C[B[A[]]]]
Dafila acuta	A[]	C[B[A[0[]]]]	1[0[]]	O[]	O[]	B			C[B[A[0[]]]]	A[0[]]	F[C[B[A[]]]]
Poecilonetta bahamensis	A[]	D[C[B[A[0[]]]]]	1[0[]]	O[]	O[]	B			C[B[A[0[]]]]	A[0[]]	G[F[C[B[A[]]]]]
Poecilonetta erythrorhyncha	A[]	A[0[]]	1[0[]]	O[]	O[]	B			C[B[A[0[]]]]	A[0[]]	G[F[C[B[A[]]]]]
Querquedula querquedula	A[]	E[A[0[]]]	1[0[]]	O[]	O[]	B			C[B[A[0[]]]]	A[0[]]	G[F[C[B[A[]]]]]
Spatula clypeata	A[]	E[A[0[]]]	O[]	O[]	O[]	B			C[B[A[0[]]]]	O[]	G[F[C[B[A[]]]]]
Tadorna tadorna	A[]	A[0[]]	O[]	O[]	O[]	O			E[A[0[]]]	O[]	B[A[]]
Casarca ferruginea	A[]	A[0[]]	O[]	O[]	O[]	O			O[]	O[]	B[A[]]
Anser spp.	D[A[]]	O[]	O[]	O[]	O[]	O[]			O[]	O[]	A[]

The „Data“ – window now shows the reconstructed paths. All paths of a column (a character) must have the same root!

The character state tree of the selected column is presented.

Press „Continue“ to go on.

Character stat...

```

graph TD
    A --> B
    A --> C
    B --> D
    B --> E
  
```

Save Path Continue

Data check

If data are valid, continue here

The check message if errors occur

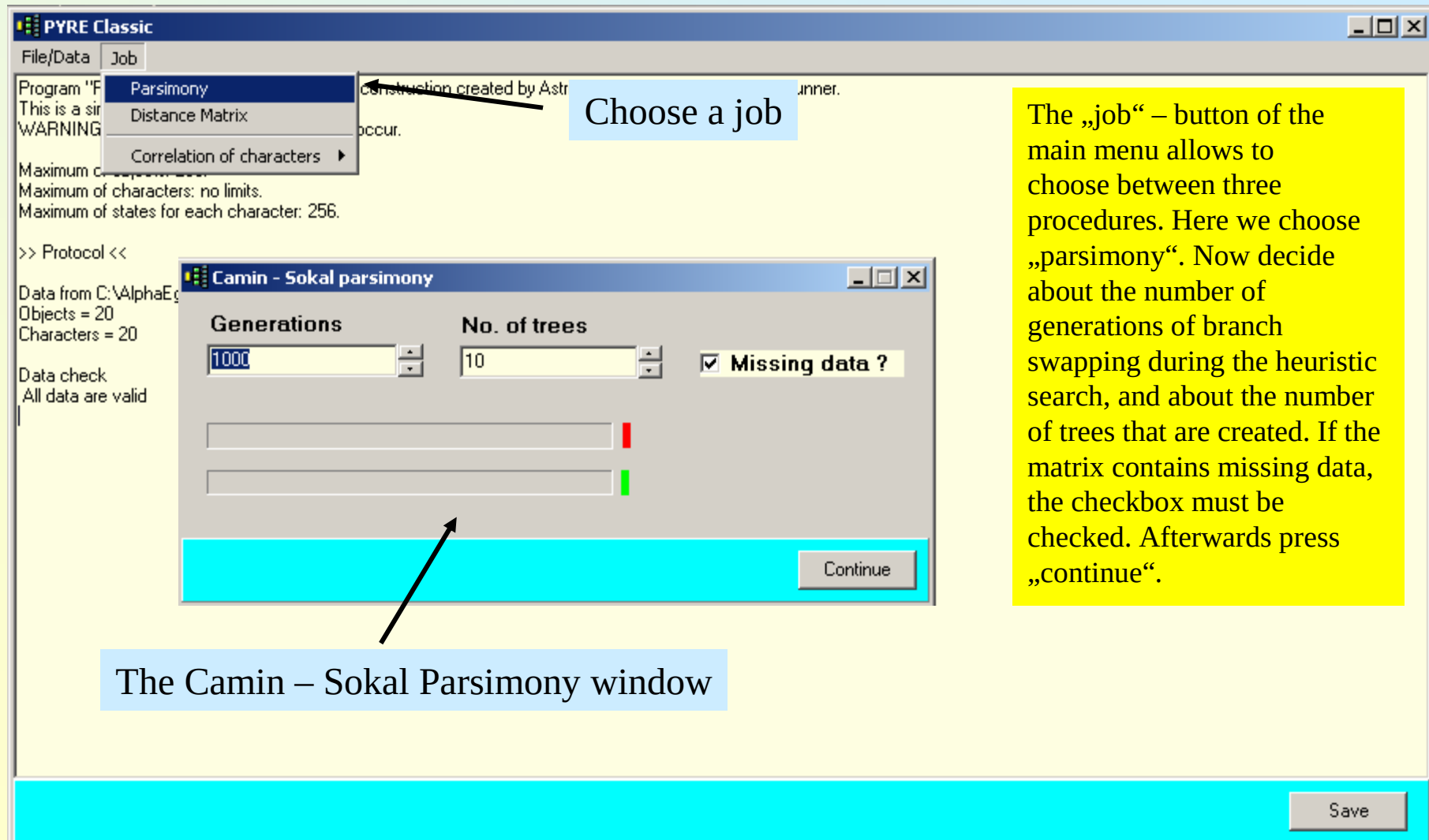
Correct data

The check message if data are valid

Automatic data check:
All strings with „?“ are treated as missing data. It is Controlled whether there is exactly one root per character. If data have to be corrected, press the „Start Excel“ button. Excel is used as external editor, the file is loaded automatically. After editing and saving, close Excel to return to Pyre Classic. The „open file dialogue“ window is presented, reopen the corrected file.

Program "PYRE Classic" for PhYlogenetic REconstruction created by Astrid, Martin & Wolfgang Tiefenbrunner.
This is a sin
WARNING
Maximum of objects: 255.
Maximum of characters: no limits.
Maximum of states for each character: 256.
>> Protocol <<
Check data
Only matroschka - coded data are allowed
Data check:
All data are valid
Continue using main menu
No root in character IV
No root in character V-1
More than one root in character V
CORRECT DATA!
Use the "Start excel" button to edit data
Back Start Excel
Back Start Excel
Save

Choose and proceed a job



A Camin – Sokal Parsimony Cladogram

Trees

a: change tip to tip; b: change tip to node c: change node to node

	add - fit	swap - fit
1 11b	74	70
2	71	
3	70	
4 2c	73	70
5	70	
6 11b	75	70
7	71	
8	72	
9	70	
10 11b	73	70

Click on a row to load a tree

Total length of the tree

Optimum = Minimum = 70

	Tips	T-fit	Nodes	N-fit
Cairina moschata (1)	1[1]	1	1[9]	3
Querquedula querquedula (15)	2[11]	3	2[8]	3
Mareca sibilatrix (4)	3[13]	0	3[2]	5
Anas spp. (10)	4[7]	0	4[10]	2
Nyroca americana (1)	5[2]		5[2]	4
Scolopax minor (1)	6[4]		6[4]	2
Nyroca americana (1)	7[4]		7[4]	2
Villula (1)	8[17]		8[17]	1
Aythya (1)	9[1]		9[1]	0
Branta (1)	10[3]		10[3]	3
Clarus (1)	11[5]		11[5]	3
Podiceps (1)	12[8]		12[8]	7
Larus (1)	13[3]		13[3]	2
Mareca (1)	14[9]		14[9]	2
Anas (1)	15[5]		15[5]	4
Dendrocygna (1)	16[15]		16[15]	2
Podiceps (1)	17[1]		17[1]	1
Ca...	18[16]		18[16]	2
Dallia spinicoda (11)	19[18]	1	19[17]	2
Tadorna tadorna (17)	20[19]	2	Fitness	70

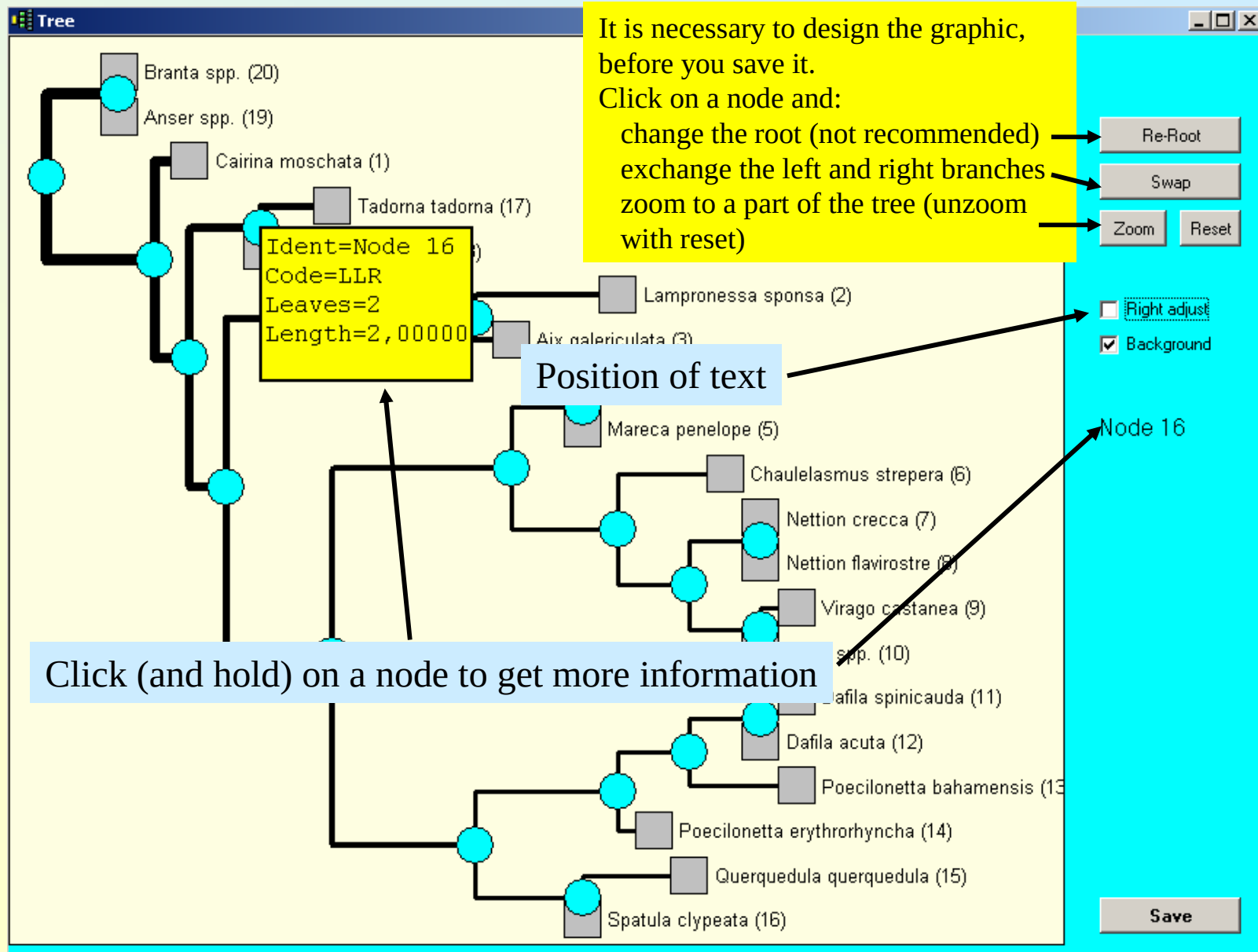
You can choose one of the proceeded trees by clicking on a row of the left grid. The right grid shows the structure of the chosen cladogram and the length of the branches. „Fitness“ gives the total lentgh of the tree. The smaller, the better. For more information press the „graphic“ or the „tree compatibility“ button

Additional information to the selected tree

Tree compatibility

Grafic

The graphic



The tree compatibility

Compatibility of characters				
Characters	No of states	Evolutionary steps	Compatibility	Homoplasy
I	4	4	no	yes
II	6	7	no	yes
III	2	3	no	yes
IV	2	1	yes	no
V1	2	2	no	yes
V2	2	1	yes	no
V3	2	2	no	yes
VI	5	8	no	yes
VII	6	8	no	yes
VIII	4	8	no	yes
IX	7	9	no	yes
X	3	4	no	yes
XI	3	3	no	yes
XII	3	2	yes	no
XIII	3	2	yes	no
XIV	3	2	yes	no
XV	2	1	yes	no

Start Excel Save

The tree compatibility window tells you, which character is compatible with the cladogram and whether homoplasy is predicted. The number of evolutionary steps should be number of states -1. If there are missing data, you can see it in the „no. of states“ column. If you decide to delete or change some characters, press the „start Excel“ button.

More about phylogenetic reconstruction using character state trees:

Tiefenbrunner, A., Tiefenbrunner, M. & W. Tiefenbrunner, NEW TOOLS FOR PHYLOGENETIC RECONSTRUCTION USING CHARACTER STATE TREES, Linzer biologische Beiträge 43/1, 99-117, 2011.