

CAFCA

Chapter 5

User-Tree Evaluation

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Aus 10000110011
Bus 10000110110
Cus 01000001100
Dus 01001001100
Eus 00100000100
Fus 00010100111
Gus 00010100001
Hus 00010110010
Ius 00101000110
Anc 00000000000

#NEXUS

begin trees; [Treefile saved Monday, June 8, 1992 6:04 PM]
[!>Heuristic search settings:
> Addition sequence: simple (reference taxon = Aus)
> 1 tree(s) held at each step during stepwise addition
> Tree-bisection-reconnection (TBR) branch-swapping performed
> MULPARS option in effect
> Steepest descent option not in effect
> Initial MAXTREES setting = 100
> Branches having maximum length zero collapsed to yield polytomies
> Topological constraints not enforced
> Trees are rooted
> Total number of rearrangements tried = 968
> Length of shortest tree found = 18
> Number of trees retained = 3
> Time used = 1.12 sec
]

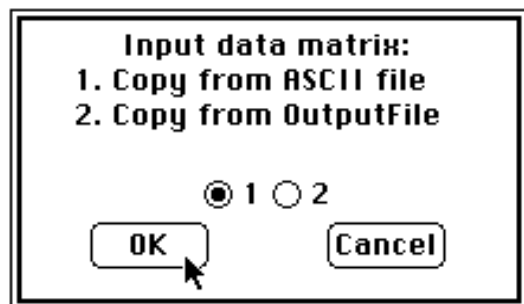
    translate
      1 Aus,
      2 Bus,
      3 Cus,
      4 Dus,
      5 Eus,
      6 Fus,
      7 Gus,
      8 Hus,
      9 Ius,
     10 Anc
    ;
tree PAUP_1 = (((1,2),((6,7),8)),((3,4),(5,9))),10);
tree PAUP_2 = (((((1,2),8),(6,7)),((3,4),(5,9))),10);
tree PAUP_3 = ((((((1,2),8),6),7),((3,4),(5,9))),10);
endblock;

```

Table 5.1 Example of a data matrix as **exported** by PAUP (top) and a tree file (bottom) resulting from a **save trees to file** operation in PAUP, both based on the data matrix as used in chapter 4 on secondary analyses in CAFCA.

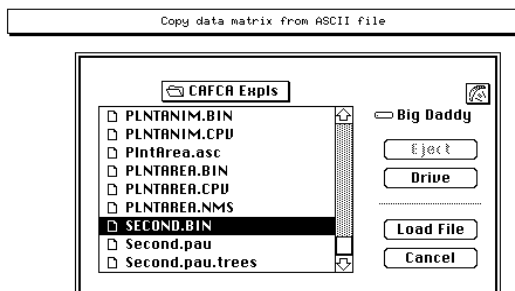
TUTORIAL

1. Select **User-tree Evaluation** from the **Run** menu.
2. We will assume that there is no data matrix present in your workspace. That's why the following dialog appears. If, however, there is a data matrix present because you did first run another analysis, either primary, secondary or biogeographic, CAFCA continues with step 6.

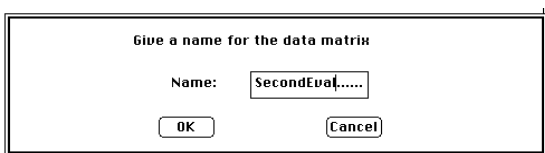


Click **OK** for the default value 1 (Copy from ASCII file).

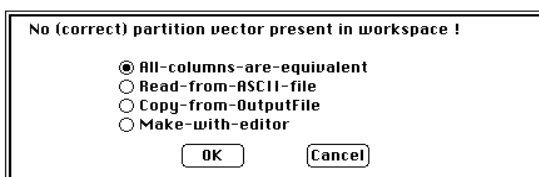
- In the next file selector box select **Second.bin** from the example data on your distribution disk and click **Load File**.



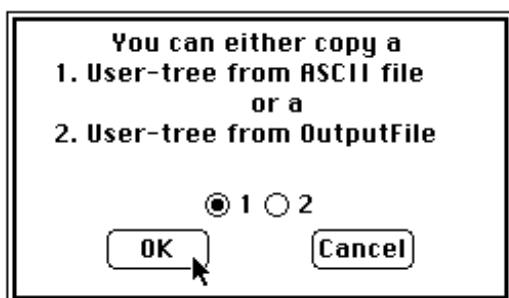
- Enter **'SecondEval'** (without quotation marks!), for example, as a name for your data matrix in the next dialog box.



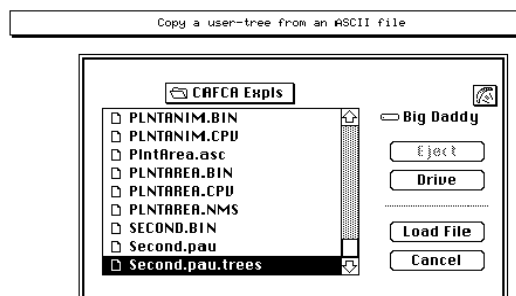
- Take the first option (default) in the next dialog for entering a partitioning vector for the columns in your data matrix.



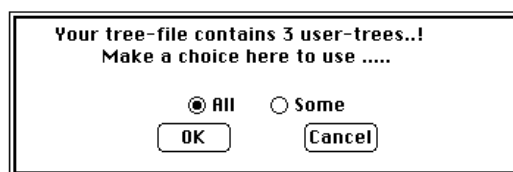
- The basic elements (data matrix, partitioning vector, taxon namelist) are present. Now all that is needed is the user-tree. The next dialog prompts for the source of this user-tree. Click **OK** for the default value **1 (User-tree from ASCII file)**.



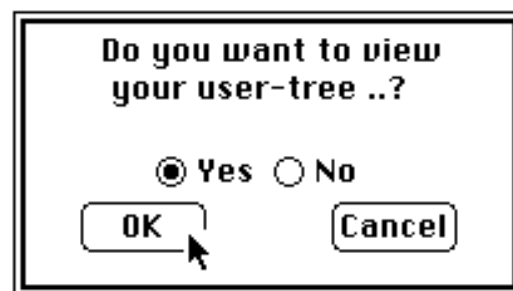
- Select the appropriate file name for the user-tree (**Second.pau.trees** in this example) and click **Load File** in the next dialog.



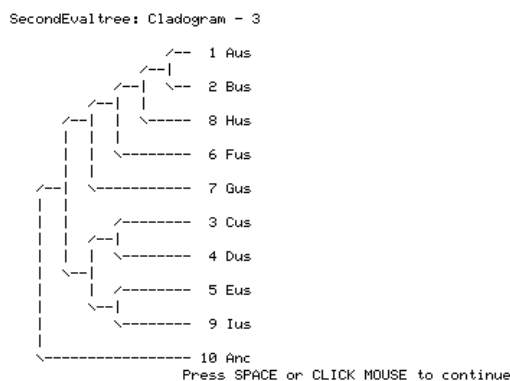
- As your tree file contains more than one tree (see table 5.1) CAFCA asks whether you want to use all the trees or just some of them.



- Click **Yes** (default) and **OK** in the dialog prompting for a view of the user-tree. Do **not** do this if you have many trees to evaluate (say, 10 or more).

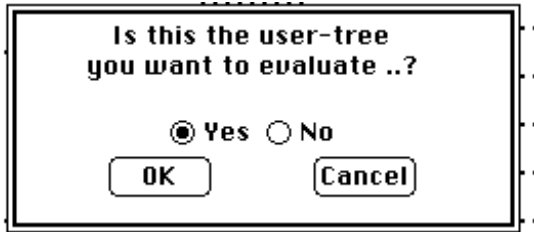


- In the CAFCA window a text (non-graphic) representation of the user-tree(s) will appear. You can use the scroll bar to view them all. Press the **space bar** or **click the mouse** to continue.

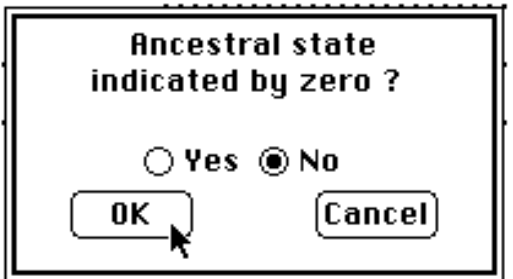


- After pressing the **SPACE** bar a dialog appears prompting to confirm the correctness

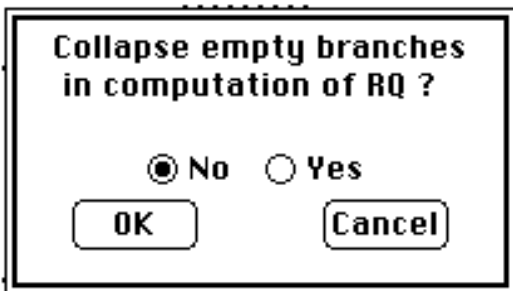
of the user-tree on display. Click **OK** for the default **Yes**.



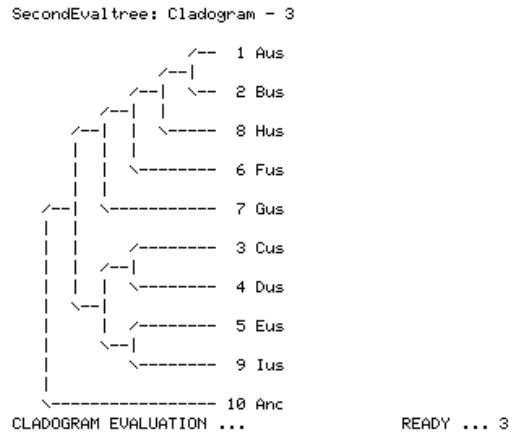
- You will not see the standard CAFCA parameter dialog as most entries are irrelevant now. However, you must indicate whether zero's in the data matrix are to be interpreted as ancestral or not. Click **OK** for the **NO** in the dialog, as we did not interpret zero's to be forced on the root in the primary and secondary analysis either.



- You must also indicate whether empty branches must be collapsed in the computation of the Redundancy Quotient. We take the default **No** here, as in the standard primary or secondary analysis empty branches were not collapsed either.



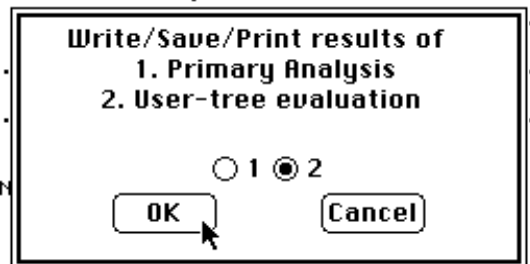
- Evaluation of the user-tree will now start. Its progress is indicated on the screen.



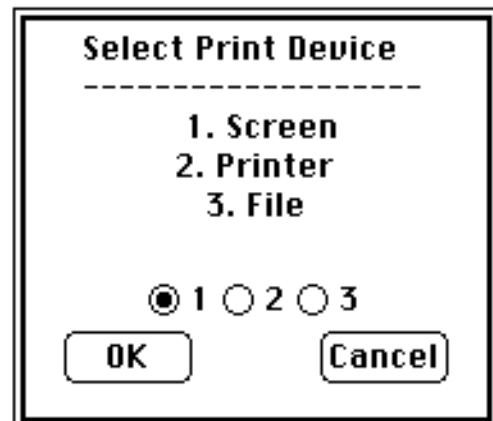
When the evaluation of the user-tree is finished, **READY** will appear on the screen. You can now print the results.

- Select **Diagram Evaluation...** from the **Print** menu.

As a data matrix etc.. is present in the workspace, CAFCA can not know whether you want to print the results of a primary analysis you could have been running, or the results of a user-tree evaluation. Click **OK** for **2 (User-tree evaluation)** in the next dialog.



- Click **1 (Screen)** or **3 (File)** in the **Select Print Device** dialog box.



DISCUSSION OF RESULTS

There is not much to discuss as the output of the cladogram evaluation looks the same as in a primary analysis. Note, however, that you can recognize by the name of the data matrix that these results are from a user-tree evaluation. This name is identical with the name you entered in the dialog (tutorial step 4), except for the addendum **tree**.

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Selection criteria for cladograms of: Secondtree
Column numbers refer to numbers of cladograms
-----
Row 1 : Total number of homoplasous events
Row 2 : Total number of single origins (Support)
Row 3 : Corrected Extra Length (x1000; CEL: Turner + Zandee)
Row 4 : Total number of state changes (S: Steps)
Row 5 : Redundancy Quotient (x1000; RQ: Zandee + Geesink)
Row 6 : Rescaled Redundancy Quotient (x1000; RQc)
Row 7 : Consistency Index (x1000; CI), with autapomorphy correction
Row 8 : Rescaled Consistency Index (x1000; RC: Farris)
Row 9 : Average Unit Character Consistency (x1000; AUCC: Sang)
Row 10: Homoplasly Distribution Ratio (x1000; HDR: Sang)
Row 11: Compatible Character State Index (x1000; CCSI: Zandee)

      1      2      3
-----
1 |      6      6      6
2 |      6      6      6
3 |    7197    7197    7220
4 |      18     18     18
5 |     521     521     512
6 |     147     147     133
7 |     611     611     611
8 |     417     417     417
9 |     742     742     742
10|     338     338     338
11|     273     273     273

No-Order Limit for Steps, Extra Steps, RQ, and CI:

      S      ES      RQ      CI
-----
    33     22    438    333
    
```

Table 5.2 Result of the evaluation of the user-trees from the file **Second.pau.trees**

Looking at the result of the cladogram evaluation listed in table 5.2 we notice that cladograms number 1 and 2 (fig 5.1) have the highest value of RQ and the lowest for CEL. Comparing this result with that obtained in the secondary analyses we also notice that all cladograms from the PAUP analysis are among the cladograms generated by CAFCA in its primary and secondary analyses on the same data matrix, as shown in chapter 5. PAUP, however, finds these different most parsimonious solutions very quickly and direct (contrary to the indirect nature of the secondary analysis by CAFCA) with either the branch & bound or the exhaustive search option.

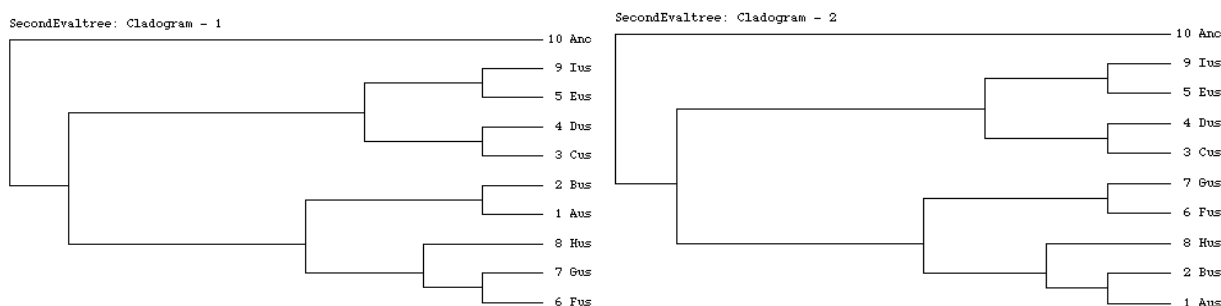


Figure 5.1. Two cladograms from PAUP analysis, used as user-trees, with highest RQ.

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