

Instructions for Making Cladograms using Fluxus Software

I. Choosing which haplotypes to include in your Fluxus datafile

All haplotypes you process must be run on the same number of markers.

- (1) To maximize the number of people you include in your cladogram, use only the markers that all of them have in common, or
- (2) To maximize the number of markers you include in your cladogram, eliminate the people who have not tested on the maximum number of markers, or
- (3) To maximize the number of markers while not sacrificing too many people, include the highest number of markers that most people have tested on, and eliminate the people who have tested on fewer markers.

For example, if you have 10 people in your study and

2 tested on 43 markers

7 tested on 26 markers

1 tested on 12 markers

- (1) would produce a cladogram based on all 10 people tested on only 12 markers. Markers 13 through 43 would be eliminated,
- (2) would produce a cladogram with only the 2 people tested on 43 markers, and
- (3) would produce a cladogram with 9 people tested on 26 markers. The last person who tested on only 12 would be eliminated.

I suggest you do (3).

	19	385a	385b	388	389i	389ii	390	391	392	393	426	437	438	439	441	442	444	445	446	447	448	452	454	455	456	458
M2	14	13	14	14	13	29	22	10	11	13	11	16	10	11	17	17	12	11	13	23	20	31	11	8	14	15
C4	14	11	15	12	13	30	24	11	13	13	12	15	13	12	14	16	12	12	13	26	19	30	11	11	15	17
J9	14	11	15	12	13	30	24	11	13	13	12	15	13	12	14	16	12	12	13	25	19	30	11	11	15	
F5	14	11	14	12	13	30	24	11	13	13	12	15	13	11	14	16	12	12	13	25	19	30	11	11	15	
V9	14	11	15	12	13	30	24	11	13	13	12	15	13	12	14	16	12	12	13	25	19	30	11	11	15	
V1	14	11	15	12	13	30	24	11	13	13	12	15	13	12	14	16	12	12	13	25	19	30	11	11	15	
F9	14	11	15	12	13	30	24	11	13	13	12	15	13	12	14	16	12	12	13	25	19	30	11	11	15	
R5	14	11	15	12	13	30	24	11	13	13	12	15	13	12	14	16	12	12	13	25	19	30	11	11	15	
D3	14	11	15	12	13	30	24	11	13	13	12	15	13	12	14	16	12	12	13	25	19	30	11	11	15	
A1	14	11	15	12	13	30	24	11	13	13	12	15	13	12	14	16	12	12	13	25	19	30	11	11	15	
K1	14	11	15	12	13	30	24	11	13	13	12	15	13	12	14	16	12	12	13	25	19	30	11	11	15	
U9	14	11	15	12	13	30	24	11	13	13	12	15	13	12	14	16	12	12	13	25	19	30	11	11	15	
PK	14	13	14	14	13	29	22	11	11	13	11	16	10	11	17	17	12	11	13	23	20	31	11	8	14	
QQ	15	11	15	12	13	29	25	11	13	13	11															

Note: The first two rows of the table are too long to fit on the page. These rows actually go out to 43 markers.

→ You wind up with

	19	385a	385b	388	389i	389ii	390	391	392	393	426	437	438	439	441	442	444	445	446	447	448	452	454	455	456
M2	14	13	14	14	13	16	22	10	11	13	11	16	10	11	17	17	12	11	13	23	20	31	11	8	14
C4	14	11	15	12	13	17	24	11	13	13	12	15	13	12	14	16	12	12	13	26	19	30	11	11	15
J9	14	11	15	12	13	17	24	11	13	13	12	15	13	12	14	16	12	12	13	25	19	30	11	11	15
F5	14	11	14	12	13	17	24	11	13	13	12	15	13	11	14	16	12	12	13	25	19	30	11	11	15
V9	14	11	15	12	13	17	24	11	13	13	12	15	13	12	14	16	12	12	13	25	19	30	11	11	15
V1	14	11	15	12	13	17	24	11	13	13	12	15	13	12	14	16	12	12	13	25	19	30	11	11	15
F9	14	11	15	12	13	17	24	11	13	13	12	15	13	12	14	16	12	12	13	25	19	30	11	11	15
R5	14	11	15	12	13	17	24	11	13	13	12	15	13	12	14	16	12	12	13	25	19	30	11	11	15
D3	14	11	15	12	13	17	24	11	13	13	12	15	13	12	14	16	12	12	13	25	19	30	11	11	15
A1	14	11	15	12	13	17	24	11	13	13	12	15	13	12	14	16	12	12	13	25	19	30	11	11	15
K1	14	11	15	12	13	17	24	11	13	13	12	15	13	12	14	16	12	12	13	25	19	30	11	11	15
U9	14	11	15	12	13	17	24	11	13	13	12	15	13	12	14	16	12	12	13	25	19	30	11	11	15
PK	14	13	14	14	13	16	22	11	11	13	11	16	10	11	17	17	12	11	13	23	20	31	11	8	14

There are two ways to generate a datafile for Fluxus. For smaller files, it's easier to do it by hand. For larger files, it is easier to use the McGee Y-Utility at <http://www.mymcgee.com/tools/yutility.html>

II. To generate your input file manually

2. Format your Excel spreadsheet to like this:

Row 1: Marker names

Rows 2 & 3: Blank

Row 4: First taxa (participant ID)

Row 5: Marker values

Row 6: 1

Row 7: Second taxa

Row 8: Marker values

Row 9: 1

Continue for all the haplotypes in your dataset. The very last character in the file should be a 1. (Not a space or an extra line.) If you have several people with the same haplotype, you can substitute how many you have for the number "1".

19 385a 385b 388 389i 389ii 390 391 392 393 426 437 438 439 441 442 444 445 446 447 448 449 452 454 455 456

M2

14 13 14 14 13 16 22 10 11 13 11 16 10 11 17 17 12 11 13 23 20 29 31 11 8 14
1

C4

14 11 15 12 13 17 24 11 13 13 12 15 13 12 14 16 12 12 13 26 19 29 30 11 11 15
1

J9

14 11 15 12 13 17 24 11 13 13 12 15 13 12 14 16 12 12 13 25 19 29 30 11 11 15
1

F5

14 11 14 12 13 17 24 11 13 13 12 15 13 11 14 16 12 12 13 25 19 29 30 11 11 15
1

V9

14 11 15 12 13 17 24 11 13 13 12 15 13 12 14 16 12 12 13 25 19 29 30 11 11 15
1

V1

14 11 15 12 13 17 24 11 13 13 12 15 13 12 14 16 12 12 13 25 19 29 30 11 11 15
1

F9

14 11 15 12 13 17 24 11 13 13 12 15 13 12 14 16 12 12 13 25 19 29 30 11 11 15
1

R5

14 11 15 12 13 17 24 11 13 13 12 15 13 12 14 16 12 12 13 25 19 29 30 11 11 15
1

D3

14 11 15 12 13 17 24 11 13 13 12 15 13 12 14 16 12 12 13 25 19 29 30 11 11 15
1

A1

14 11 15 12 13 17 24 11 13 13 12 15 13 12 14 16 12 12 13 25 19 29 30 11 11 15
1

K1

14 11 15 12 13 17 24 11 13 13 12 15 13 12 14 16 12 12 13 25 19 29 30 11 11 15
1

U9

14 11 15 12 13 17 24 11 13 13 12 15 13 12 14 16 12 12 13 25 19 29 30 11 11 15
1

PK

14 13 14 14 13 16 22 11 11 13 11 16 10 11 17 17 12 11 13 23 20 28 31 11 8 14
1

3. Save your spreadsheet in .csv (DOS) format.

4. In Windows Explorer, right click on your .csv file.

5. From the drop-down menu, click on “Open With”, and open the file with Notepad. It will look like the file to the right, except that it might have extra commas all over the place.

Notes:

(a) Get rid of any extra commas between or at the end of lines that show up.

(b) The last item in the entire file should be a “1”, not a space or a blank line.

(c) If the last haplotype has more than one person associated with it, the last item can be the number of people that haplotype represents, if it is not 1.

If you generate an error message:

(a) Check that each taxa has a different name.

(b) Check that the names of the taxa are at most five letters long (the shorter the better).

(c) Check that the names of the markers are at most five letters long (the shorter the better).

(d) Check that all haplotypes have the same number of markers.

(e) Check that there are no marker values = 0 or that an empty cell has a hyphen in it.

(f) Check for extra commas, extra spaces or lines at the end of the file.

(7) If you used Word to generate your datafile, go back and follow the instructions to use Notepad. Word includes hidden control characters even in the text files it generates. These hidden characters will cause errors.

6. Open the Network.exe program that you downloaded from www.fluxus-engineering.com.

```
File Edit Format View Help
19,385a,385b,388,389i,389ii,390,391,392,393,394
VC4
14,11,15,12,13,17,24,11,13,13,12,15,13
1
AJ9
14,11,15,12,13,17,24,11,13,13,12,15,13
1
VF5
14,11,14,12,13,17,24,11,13,13,12,15,13
1
BV9
14,11,15,12,13,17,24,11,13,13,12,15,13
1
SV1
14,11,15,12,13,17,24,11,13,13,12,15,13
1
XF9
14,11,15,12,13,17,24,11,13,13,12,15,13
1
ER5
14,11,15,12,13,17,24,11,13,13,12,15,13
1
XD3
14,11,15,12,13,17,24,11,13,13,12,15,13
1
RA1
14,11,15,12,13,17,24,11,13,13,12,15,13
1
CK1
14,11,15,12,13,17,24,11,13,13,12,15,13
1
YU9
14,11,15,12,13,17,24,11,13,13,12,15,13
1
ZQQ
15,11,15,12,13,16,25,11,13,13,11,15,12
1
JPK
14,13,14,14,13,16,22,11,11,13,11,16,10
1
UM2
14,13,14,14,13,16,22,10,11,13,11,16,10
1
```

7. Follow these steps to run the Fluxus software.

III. To generate your input file using the McGee Utility at <http://www.mymcgee.com/tools/yutility.html>

1. Set the switches for the markers you are using.
2. Set the options you want to use in the Generate Tables box. Typical values are shown in the figure.
3. Check the box marked “Generate Fluxus phylogenetic network .ych file”.
3. Copy and paste contents of Excel spreadsheet into empty box.
4. Click on Execute.

Status:

Ysearch Database Configuration - DNA Results Comparison

ID	D393	D390	D394	D391	D385a	D385b	D426	D388	D389-1	D392	D389B	D437
modal	24	13	14	11	11	15	12	12	13	13	30	15
M2	22	13	14	10	13	14	11	14	13	11	29	16
C4	24	13	14	11	11	15	12	12	13	13	30	15
J9	24	13	14	11	11	15	12	12	13	13	30	15
F5	24	13	14	11	11	14	12	12	13	13	30	15
V9	24	13	14	11	11	15	12	12	13	13	30	15
V1	24	13	14	11	11	15	12	12	13	13	30	15
F9	24	13	14	11	11	15	12	12	13	13	30	15
R5	24	13	14	11	11	15	12	12	13	13	30	15
D3	24	13	14	11	11	15	12	12	13	13	30	15
A1	24	13	14	11	11	15	12	12	13	13	30	15
K1	24	13	14	11	11	15	12	12	13	13	30	15
U9	24	13	14	11	11	15	12	12	13	13	30	15
PK	22	13	14	11	13	14	11	14	13	11	29	16
QQ	25	13	15	11	11	15	11	12	13	13	29	15

Distance from reference: Zero One Two Three+

Fluxus data - paste into a .ych file

```
D393, D390, D394, D391, D385a, D385b, D426, D388, D389-1, D392, D389B, D437

modal
24, 13, 14, 11, 11, 15, 12, 12, 13, 13, 17, 15
1
M2
22, 13, 14, 10, 13, 14, 11, 14, 13, 11, 16, 16
1
C4
```

SMGF Database Configuration - DNA Results Comparison

ID	D393	D390	D394	D391	D385a	D385b	D426	D388	D389-1	D392	D389B	D437	D393	D390	D394	D391	D385a	D385b	D426	D388	D389-1	D392	D389B	D437	D393	D390	D394	D391	D385a	D385b	D426	D388	D389-1	D392	D389B	D437		
modal	11-15	12	13	30	13	11	13	24	14	12	15																											
M2	13-14	14	13	29	13	10	11	22	14	11	16																											
C4	11-15	12	13	30	13	11	13	24	14	12	15																											
J9	11-15	12	13	30	13	11	13	24	14	12	15																											
F5	11-14	12	13	30	13	11	13	24	14	12	15																											
V9	11-15	12	13	30	13	11	13	24	14	12	15																											
V1	11-15	12	13	30	13	11	13	24	14	12	15																											
F9	11-15	12	13	30	13	11	13	24	14	12	15																											
R5	11-15	12	13	30	13	11	13	24	14	12	15																											

Output from McGee will open in a new window.
Copy and paste the .ych file into Notepad.

In Windows Explorer, change the extension of the file to .ych.

