

## Instructions for running CLAN MLU analysis on Brown's Adam data

These instructions assume that you have downloaded the CLAN software and the Brown corpus from the CHILDES website, and decompressed them into a directory on your computer. The instructions are also written for the Mac version of the CLAN software. I hope and assume the PC version works the same way.

You'll probably need to change some of the program's default settings.

I needed to change the default LIB directory before clicking the HELP button did anything useful. On the Commands window, click the LIB button, then select the appropriate directory (in my case one folder deeper: CLAN: LIB), open this directory, then click Select Current Directory. You'll see the change noted next to the button on the Commands window.

You'll also need to change the WORKING directory to whatever directory you have Brown's data for Adam in. On my machine its in the directory brown corpus: adam. On the Commands window, click the WORKING button, then navigate to the directory in which you have the data, then click the Select Current Directory button.

In the Commands window, typing "dir" should now produce (in the CLAN Output window) a listing of all the adam data files:

```
> dir
adam01.cha  adam02.cha  adam03.cha  adam04.cha  adam05.cha  adam06.cha
adam07.cha  adam08.cha  adam09.cha  adam10.cha  adam11.cha  adam12.cha
adam13.cha  adam14.cha  adam15.cha  adam16.cha  adam17.cha  adam18.cha
adam19.cha  adam20.cha  adam21.cha  adam22.cha  adam23.cha  adam24.cha
adam25.cha  adam26.cha  adam27.cha  adam28.cha  adam29.cha  adam30.cha
adam31.cha  adam32.cha  adam33.cha  adam34.cha  adam35.cha  adam36.cha
adam37.cha  adam38.cha  adam39.cha  adam40.cha  adam41.cha  adam42.cha
adam43.cha  adam44.cha  adam45.cha  adam46.cha  adam47.cha  adam48.cha
adam49.cha  adam50.cha  adam51.cha  adam52.cha  adam53.cha  adam54.cha
adam55.cha
```

```
55 files, 0 directories
```

```
>
```

And at this point clicking HELP should produce this listing in the CLAN Output window:

```
=====
>help

You can run any of the following CLAN programs:
chains      check      chip      columns   combo
compound    cooccur   dates     dist      dss
```

|              |           |          |         |          |
|--------------|-----------|----------|---------|----------|
| flo          | freq      | freqmerg | freqpos | gem      |
| gemfreq      | gemlist   | keymap   | kwal    | lines    |
| makedata     | makemod   | maxwd    | mlt     | mlu      |
| modrep       | mor       | phonfreq | post    | postlist |
| postmodrules | posttrain | rely     | rtfin   | saltin   |
| statfreq     | textin    | timedur  | vocd    | wklen    |

Or any of the following CLAN Plug-in programs:  
SNDBoolets

Or any of the following CLAN utility programs:

|          |          |       |       |    |          |         |
|----------|----------|-------|-------|----|----------|---------|
| chstring | combtier | delim | fixit | id | longtier | lowcase |
| repeat   | retrace  | uniq  |       |    |          |         |

Supplementary commands available:

|        |        |    |       |     |      |      |
|--------|--------|----|-------|-----|------|------|
| accept | batch  | cd | copy  | del | dir  | info |
| list   | rename | rm | rmdir | ty  | type |      |

| Command                           | Function                                    |
|-----------------------------------|---|
| accept TEXT                       | allow TEXT type input files                 |
| accept ALL                        | allow any type of input file                |
| batch FILENAME                    | runs a batchfile                            |
| cd ..                             | move up one directory                       |
| cd FolderName                     | change to a folder within current directory |
| cd HardDiskName:                  | move to top level                           |
| copy [-luctqr] source destination | copy files                                  |
|                                   | -l changes filenames to lowercase           |
|                                   | -u changes filenames to uppercase           |
|                                   | -cMSWD changes creator to MSWD, etc.        |
|                                   | -tTEXT changes file type to TEXT            |
|                                   | -q verification                             |
|                                   | -r recursive                                |
| del [-qr] filename                | delete file                                 |
|                                   | -q verification                             |
|                                   | -r recursive                                |
| dir [-rl]                         | show contents of current directory          |
|                                   | -r recursive                                |
|                                   | -l long format                              |
| info                              | list all current CLAN settings              |
| list                              | lists the files currently under the @ sign  |
| page filename                     | open up files for editing                   |
| ren [-luctqr] oldfile newfile     | rename file                                 |
|                                   | -l changes filenames to lowercase           |
|                                   | -u changes filenames to uppercase           |

Word,  
etc.

-cMCED changes creator to MCED for CLAN, -cMSWD for  
-tTEXT changes file type to TEXT  
-f rename even if the new file does already exist  
-q verification  
-r recursive

rmdir [-qr] dir delete directory, if empty  
-q verification  
-r recursive

Left and right arrows move the cursor left and right on the command line.

Up and down arrows rotate through the previous commands.

>

=====

Now we'll get ready to run a "mean length of utterance" analysis. Let's get the instructions first. Type MLU into the Command window:

The CLAN Output window will show the instructions for the MLU analysis:

=====

```
> mlu
MLU- Mean Length Utterance computes the number of utterances, morphemes
and their ratio.
Usage: mlu [bS cS gF dN fS k pF rN re sS tS u yN zN ] filename(s)
+bS: make all S characters morpheme delimiters (default: -#~)
-bS: do not consider all S characters to be morpheme delimiters
+cS: look for unit marker S
+gF: exclude utterance consisting solely of specified words
+d : output in STATFREQ format. Must include speaker specifications
+d1: output data ONLY.
+fS: send output to file (program will derive filename)
-f : send output to the screen or pipe
+k : treat upper and lower case as different
+pF: define punctuation set according to file F
+rN: if N = 1 then "get(s)" goes to "gets", 2- "get(s)", 3- "get"
4- recognize prosodic symbols in words, 5- no text replacement: [:
*]
6- include repetitions: </> and <\/>
+re: run program recursively on all sub-directories.
+sS: either word S or words in file @S to search for in a given input
file
-sS: either word S or words in file @S to be exclude from a given input
file
+tS: include tier code S
-tS: exclude tier code S
+u : merge all specified files together.
-u : compute result for each turn separately.
+y : work on TEXT format files one line at the time
+y1: work on TEXT format files one utterance at the time
+zN: compute statistics on a specified range of input data
```

>

Now we'll run this analysis on the first file of data from Adam. Doubleclick the file adam01.cha. This will open a new Clan window, showing the transcript. This begins:

```

=====
@Begin
@Participants:   CHI Adam Target_Child, MOT Mother, URS Ursula_Bellugi
                 Investigator, RIC Richard_Cromer Investigator, COL
                 Colin_Fraser Investigator
@ID:  en|brown|CHI|2;3.4|Male|normal|middle-class|Target_Child||
@ID:  en|brown|MOT|||Mother||
@ID:  en|brown|URS|||Investigator||
@ID:  en|brown|RIC|||Investigator||
@ID:  en|brown|COL|||Investigator||
=====

```

Now you are ready to conduct an analysis. We won't set any parameters except the -f parameter, which sends output directly to the screen instead of to a file.

In the Command window, type:

```
mlu -f adam01.cha
```

The CLAN Output window will report the results:

```

=====
> mlu -f adam01.cha
mlu -f adam01.cha
Wed Jun 27 11:20:58 2001
mlu (13-Apr-2001) is conducting analyses on:
  ALL speaker tiers
*****
From file <Macintosh HD: Work More:CHILDES:brown
corpus:adam:adam01.cha>
MLU for Speaker: *RIC:
  MLU (xxx and yyy are EXCLUDED from the utterance and morpheme
counts):
    Number of: utterances = 5, morphemes = 17
    Ratio of morphemes over utterances = 3.400
    Standard deviation = 1.020

MLU for Speaker: *COL:
  MLU (xxx and yyy are EXCLUDED from the utterance and morpheme
counts):
    Number of: utterances = 0, morphemes = 0

MLU for Speaker: *URS:
  MLU (xxx and yyy are EXCLUDED from the utterance and morpheme
counts):
    Number of: utterances = 14, morphemes = 73
    Ratio of morphemes over utterances = 5.214
    Standard deviation = 2.932

MLU for Speaker: *MOT:

```

MLU (xxx and yyy are EXCLUDED from the utterance and morpheme counts):

Number of: utterances = 447, morphemes = 1862  
Ratio of morphemes over utterances = 4.166  
Standard deviation = 2.274

MLU for Speaker: \*CHI:

MLU (xxx and yyy are EXCLUDED from the utterance and morpheme counts):

Number of: utterances = 1239, morphemes = 2600  
Ratio of morphemes over utterances = 2.098  
Standard deviation = 1.043

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If you run the same analysis on the file adam55.cha, you'll find that MLU has increased from 1.043 (at age 2;3.4) to 2.555 (at age 4;10.0):

=====

MLU for Speaker: \*CHI:

MLU (xxx and yyy are EXCLUDED from the utterance and morpheme counts):

Number of: utterances = 935, morphemes = 4240  
Ratio of morphemes over utterances = 4.535  
Standard deviation = 2.555