## LING 570: Hw4 Due date: 11:45pm on Oct 27

As usual, the example files are stored under ~/dropbox/10-11/570/hw4/examples/.

**Note:** In this assignment, "FSM" (finite state machine) means an FSA or an FST. You can decide which one you want to use.

**Q1** (**20 points**): Write **expand\_fsm1.sh**, which builds an expanded FSM given a lexicon and morphotactic rules expressed by an FSA.

- The command line: **expand\_fsm1.sh** lexicon morph\_rules output\_fsm
- Lexicon and morph\_rules are input files; output\_fsm is the output file.
- The lexicon file has the format "word classLabel". A sample file is **examples/lexicon\_ex**.
- The morph\_rules file is an FSA (in the Carmel format) that encodes the morphotactic rules; that is, the input symbols in the FSA are class labels (e.g., regular\_verb\_stem). An example is **examples/morph\_rules\_ex**, which represents the same FSA as the one on Slide #23 of 10\_13\_morph.pdf except that the hyphens in class labels are replaced with underlines and there is only one final state.
- The output\_fsm file is the expanded FSM (in the Carmel format), where the labels of the arcs in the morph\_rule FSA are replaced by the words in the lexicon. See slide #19-21 in 10\_13\_morph.pdf as an example.

**Q2** (**20 points**): Write **morph\_acceptor1.sh**, which checks whether the input words are accepted by the FSM created in Q1.

- The command line: morph\_acceptor1.sh fsm word\_list output\_file
- fsm and word\_list are input files; output\_file is the output file
- "word list" is a list of words, one word per line (e.g., examples/wordlist ex)
- "fsm" is the FSM (in the Carmel format) created in Q1
- "output\_file" has the format "word => answer" for each word in the word\_list, where "answer" is "yes" if the word is accepted by the morph acceptor, or "no" otherwise (e.g., examples/q2\_result\_ex)

Q3 (35 points): Write expand\_fsm2.sh and morph\_acceptor2.sh so that the "output" file produced by morph\_acceptor2.sh has the format "word => answer", where "answer"

is "morph1/label1 morph2/label2 ..." if the word is accepted by the morph acceptor, or "\*NONE\*" otherwise (e.g., examples/q3\_result\_ex).

- The command line formats of **expand\_fsm2.sh** and **morph\_acceptor2.sh** are the same as **expand\_fsm1.sh** and **morph\_acceptor1.sh**, respectively.
- In your note file, explain briefly how the fsm produced by expand\_fsm1.sh differs from the one produced by expand\_fsm2.sh.

Q4 (10 points) Run the following commands and store the results under hw4\_dir/q4/expand\_fsm1.sh lexicon\_ex morph\_rules\_ex hw4\_dir/q4/q4\_expand\_fsm
morph\_acceptor1.sh hw4\_dir/q4/q4\_expand\_fsm wordlist\_ex hw4\_dir/q4/q4\_result

Q5 (15 points) Run the following commands and store the results under hw4\_dir/q5/expand\_fsm2.sh lexicon\_ex morph\_rules\_ex hw4\_dir/q5/q5\_expand\_fsm
morph\_acceptor2.sh hw4\_dir/q5/q5\_expand\_fsm wordlist\_ex hw4\_dir/q5/q5\_result

Note: The example files (e.g., q2 result ex) under examples/ are meant to show the format of the files. They are not meant to serve as the gold standard.

The submission should include:

- The hw4 note file that includes answers to Q3.
- The source and shell scripts in Q1, Q2, Q3: **expand\_fsm1.sh**, **morph\_acceptor1.sh**, **expand\_fsm2.sh**, **morph\_acceptor2.sh**, and any scripts called by them.
- Hw4\_dir/q4/, which includes q4\_expand\_fsm and q4\_result.
- Hw4\_dir/q5/, which include q5\_expand\_fsm and q5\_result.

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