# **Sequence to Sequence Parsing**

#### **CODE STRUCTURE**

The entire project is submitted in the folder *project4*, which has two subdirectories:

- *nmt* the sequence2sequence code, taken from <a href="https://github.com/tensorflow/nmt#introduction">https://github.com/tensorflow/nmt#introduction</a>
  - o <u>nmt</u> folder containing the actual code
  - o <u>tmp</u> folder containing the prepared data (prepared using code in *data* directory and manually placed in *tmp/parse data*):
    - EXPERIMENTS stores results of previous runs
    - *parse\_data*: stores the required data with corresponding extensions (files were prepared by *prepare\_input.py* code and transferred here):
      - dev.en
      - dev.parse
      - test.en
      - test.parse
      - train.en (and train 150000 sentences.en)
      - train.parse (and train 150000 sentences.parse)
      - vocab.en
      - vocab.parse
- data this contains packages and scripts for processing and evaluating data (and data itself):
  - o train, dev, test folders with gold data
  - o dev sents single text file with all dev sentences (used for EVALB)
  - test sents single text file with all test sentences (used for EVALB)
  - EVALB bracket scoring code, taken from https://nlp.cs.nyu.edu/evalb/
  - o obsolete this contains my unfinished attempt at setting up a seq2seq model
  - o prepare input.py code for converting parsed data into linearized format presented in class slides (actual words removed), which is then used in seq2seq model:
    - e.g. (S (NP (N John)) (VP (VBD sneezed)))  $\rightarrow$  (S (NP N )NP (VP VBD )VP )S
  - o post process.py code for reconverting the linearized output of the seq2seq model into standard parse trees (including inserting the vocabulary from corresponding sentence)
  - o <u>seq2seq\_output</u> folder storing output parses of test data from the nmt model, transferred manually from the *parse model* folder that is created during the run of *nmt*
  - postprocessed\_output folder with the outputs from seq2seq\_output converted to the standard parsed format – PLEASE RUN EVALB ON THE FILES IN THIS FOLDER!!!

## Running the *nmt* sequence to sequence program

Navigate inside the outer *nmt* directory, and run the following command (hyperparameters can be modified as desired):

In the process a folder named *parse\_model* will be created in *tmp* (as specified in settings above), inside which the predicted *output\_dev* and *output\_test* files will appear after training. After the program terminates, transfer these files to *seq2seq\_output* inside the *data* directory (I have only done this for *output\_test*, which I evaluated).

#### Running post process.py

When running *post\_process.py*, you must provide the filepath to the output of the *nmt*, located in  $seq2seq\_output$ , as well as the filepath to a file in  $postprocessed\_output$  where an empty file of the corresponding waits to be written to. [Since I ran the program from PyCharm, I changed the filepaths right in the main method instead of providing sys.argv (this can be easily modified).] The resulting post-processed file will be used by EVALB.

Some notes on *post\_process.py*: this code reconverts a sequence such as (*S* (*NP N* )*NP* (*VP VBD* )*VP* )*S* back to a normal tree for the corresponding sentence (i.e. *John sneezed*). While it is always possible to remove the labels from the closing brackets, the output doesn't always give the correct number of parts of speech (such as *VBD*) to match the number of words in the corresponding sentence. Therefore my code simply iterates simultaneously over the parts of speech in the output parse and the corresponding words in

the original sentence, and inserts a word where possible (i.e.  $VBD \rightarrow (VBD \ sneezed)$ ). If there are more words than parts of speech, the extra words don't get inserted. If there are more parts of speech than words in the sentence, my code inserts a dummy '-' character as the word for the POS.

### **Evaluating Accuracy Using EVALB**

Navigate inside EVALB and run:

```
./evalb -e 50000 ../test sents ../postprocessed output/postprocessed output test default
```

where we provide the [relative] path first to the file with all the test sentences (*test\_sents* – the first argument) and then the post-processed output of the seq2seq model (the second argument). Please provide a high maximum error threshold (e.g. 50000, as in the command above) to avoid EVALB stalling after a high number of invalid sentences.