## RUNNING BASELINE MODEL

We are preprocessing the data, basically tokenizing the raw medical reports files into sentences and further tokenizing the sentences into words. So, ultimately the raw medical report files are converted into list of list of words with their corresponding NER type tags (BIO format). There are 29 tags/labels for the task which we mentioned in Milestone 2.

## Step 1. How to preprocess the raw text files -

Training files -

\$python preprocessing data.py --dataDir ./train/gold/ --train

After this pre-processing step, a pickle file - train\_word\_ner\_startidx\_dict.pickle - is created which has the data in the NER type tag format (BIO) which is used for building the model.

Dev files -

\$python preprocessing data.py --dataDir ./dev/gold/ --dev

After this pre-processing step, a pickle file - dev\_word\_ner\_startidx\_dict.pickle - is created which has the data in the NER type tag format (BIO) which is used for building the model.

Test files -

\$python preprocessing data.py --dataDir ./test/gold/ --test

After pre-processing step, a pickle file - test\_word\_ner\_startidx\_dict.pickle - is created which has the data in the NER type tag format (BIO) which is used for building the model.

## Step 2. How to run baseline model (baseline.py)

baseline.py assumes that the data should be in the current working directory in the same folder hierarchy as is submitted with this Milestone 3.

\$python baseline.py

## How to evaluate -

Evaluation on Training Data -

\$ python evaluate.py brat ner ./train/gold/ ./train/system

Report (SYSTEM: system):

SubTrack 1 [NER] Measure Micro
Total (401 docs) Precision 0.9792

Recall 0.9408 F1 0.9597

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Evaluation on Dev Data -

\$ python evaluate.py brat ner ./dev/gold/ ./dev/system

Report (SYSTEM: system):

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F1 0.852

Evaluation on Test Data -

\$ python evaluate.py brat ner ./test/gold/ ./test/system

Report (SYSTEM: system):

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SubTrack 1 [NER] Measure Micro

Total (156 docs) Precision 0.8918

Recall 0.8337 F1 0.8618

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