AI4M C3 M2 lecture notebook negbio

September 13, 2021

0.1 AI for Medicine Course 3 Week 1 lecture notebook

0.2 Using BioC format and the NegBio Library

Welcome to this lecture notebook! You'll be exploring some of the uses of the NegBio library, a tool for biomedical text mining, which you will use in the graded assignment at the end of the week.

You'll be using the same dataset as in the assignment, so this is a good opportunity to become more familiar with it. - This dataset consists of 1,000 X-ray reports that have been manually labeled by a board-certified radiologist. - The reports indicate the presence or absence of several different pathologies. - You'll also have access to the extracted "Report Impression" section of each report, which is the summary provided for each X-ray.

0.2.1 Import Pandas and Load Dataset

```
[1]: import pandas as pd

# Read the data from file
df = pd.read_csv("stanford_report_test.csv")

# Check the num of rows, columns
print(f"dataset has shape: {df.shape}")
df.head()
```

dataset has shape: (1000, 18)

	•	•	•			
[1]:	SimpleTestRe	eportID		Rep	oort Impressi	on \
0		1.0	\n \n1.mild pulmonary ed	ema, and ca	ardiomegaly	
1		2.0	\n \n1.unremarkable card	iomediastin	nal silhouet	
2		3.0	\n1. lines and tubes are	unchanged	in position	
3		4.0	\n1. postoperative portal	ble film wi	ith a right	
4		6.0	\n \n1.single frontal vio	ew of the c	chest demons	
	No Finding	Enlarge	. Cardiomediastinum Card	iomogalu I	ung Legion	\
	NO PINGING	Tiltarge	. Cardiomediastinum Card.	Tomegary L	rung repron	\
0	NaN		NaN	1.0	NaN	
1	NaN		0.0	NaN	NaN	
2	NaN		NaN	NaN	NaN	

```
3
               NaN
                                           {\tt NaN}
                                                         NaN
                                                                      NaN
     4
               NaN
                                           {\tt NaN}
                                                         NaN
                                                                      NaN
        Airspace Opacity
                          Edema
                                 Consolidation Pneumonia Atelectasis \
     0
                     NaN
                            1.0
                                          -1.0
                                                      NaN
                                           0.0
                                                     -1.0
     1
                     1.0
                            NaN
                                                                   NaN
     2
                     1.0
                                                      NaN
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                                           NaN
                                                                   NaN
     3
                     1.0
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                                           {\tt NaN}
                                                      NaN
                                                                   1.0
     4
                     1.0
                                                      NaN
                            NaN
                                           NaN
                                                                   NaN
       Pneumothorax Pleural Effusion Pleural Other Fracture
                                                                 Support Devices \
     0
                NaN
                                   1.0
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     1
                 0.0
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     2
                -1.0
                                   {\tt NaN}
                                                  NaN
                                                            NaN
                                                                              1.0
     3
                 1.0
                                   NaN
                                                  NaN
                                                            NaN
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                 0.0
                                   1.0
     4
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                                 Report Impression Parsed \
       ['(S1 (S (S (S (LST (LS 1.)) (NP (JJ mild) (JJ...
     1 ['(S1 (S (NP (LST (LS 1.)) (NN unremarkable...
     2 ['(S1 (S (S (LST (LS 1.)) (NP (NP (NNS lines))...
     3 ['(S1 (S (LST (LS 1.)) (NP (NP (JJ postoper...
     4 ['(S1 (S (S (NP (NP (LST (LS 1.)) (JJ single) ...
                               Report Impression DG Paths
     0 ['/data3/CXR-CHEST/dgs/GL66832b_GL6dd686/0.pkl...
     1 ['/data3/CXR-CHEST/dgs/GL6f51db_GL6f51dd/0.pkl...
     2 ['/data3/CXR-CHEST/dgs/GL666dde_GL6b021a/0.pkl...
     3 ['/data3/CXR-CHEST/dgs/GL6a8d08_GL6d5d21/0.pkl...
     4 ['/data3/CXR-CHEST/dgs/GL675b56_GL6f4eb9/0.pkl...
[2]: # Get a better view of the report impression column
     for i in range(3):
         print("#################"")
         print(f"Report number: {i+1}")
         print(df.loc[i, 'Report Impression'])
```

Report number: 1

- 1.mild pulmonary edema, and cardiomegaly. trace pleural fluid effusions.
- 2.low lung volumes with minimal basilar atelectasis.
- 3.no new focal consolidation.

4.interval placement of defibrillation pads.

####################################

Report number: 2

- 1.unremarkable cardiomediastinal silhouette
- 2.diffuse reticular pattern, which can be seen with an atypical infection or chronic fibrotic change. no focal consolidation.
- 3.no pleural effusion or pneumothorax
- 4.mild degenerative changes in the lumbar spine and old right rib fractures.

####################################

Report number: 3

- 1. lines and tubes are unchanged in position.
- 2. increasing retrocardiac opacity and left midlung zone opacity.
- 3. there is a deep left costophrenic sulcus which is increased when compared with prior films. no definite evidence of left pneumothorax. clinical correlation is recommended. if clinically indicated, consider film in expiration or decubitus views.
- 4. the icu team was informed of these results at 10 am on 05 02 2005.

0.2.2 Introducing BioC

Let's get started by looking at the BioC module. You'll be using BioC to convert your clinical data into a standard format that can be leveraged on more specialized libraries. This module is used for many other NLP tasks as well, such as serialization or deserialization of data. You can read more about it here.

For your purposes, you're interested in the BioCCollection object, which represents a collection of documents for a project. The collection might be an entire corpus, or a partial one.

```
[3]: import bioc

collection = bioc.BioCCollection()
print(f"attributes with value: \n\n{collection.__dict__}\n")
print(f"methods and attributes: \n\n{dir(collection)}\n")
print(f"documents within collection: {collection.documents}")
```

```
attributes with value:
{'encoding': 'utf-8', 'version': '1.0', 'standalone': True, 'source': '',
  'date': '2021-09-13', 'key': '', 'infons': {}, 'documents': []}

methods and attributes:

['__class__', '__delattr__', '__dict__', '__dir__', '__doc__', '__eq__',
  '__format__', '__ge__', '__getattribute__', '__gt__', '__hash__', '__init__',
  '__init_subclass__', '__le__', '__lt__', '__module__', '__ne__', '__new__',
  '__reduce__', '__reduce_ex__', '__repr__', '__setattr__', '__sizeof__',
  '__str__', '__subclasshook__', '__weakref__', 'add_document', 'clear_infons',
  'date', 'documents', 'encoding', 'infons', 'key', 'source', 'standalone',
  'version']
```

documents within collection: []

0.2.3 Preparing the Text for BioC

When working with collections, you're mostly interested in the documents attribute and the add_document() method.

The BioC module gives you a standard format that allows you to apply other, more specialized libraries. Before seeing BioC in action, let's introduce NegBio, a tool that distinguishes negative or uncertain findings in radiology reports. It accomplishes this by using patterns on universal dependencies, instead of using rule-based methods. If you'd like to know more, check out the official github repo, or the official documentation.

You'll be using the NegBioSSplitter object to split your text into sentences. However, in order to do this, you'll first need to convert your text into a format that BioC supports. For this you'll use the text2bioc() function, which transforms the text into a BioC XML file. You can go even further and convert the text into documents with the text2document() function.

[5]: collection.documents

```
[5]: [BioCDocument[id=0,infons=[],passages=[BioCPassage[offset=0,text='\n \n1.mild pulmona ... lation pads. \n \n',infons=[],sentences=[BioCSentence[offset=0,text='\n \n1.mild pulmona ... and cardiomegaly.',infons=[],annotations=[],relations=[],],BioCSentence[offset=46,text=46]
```

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oCSentence[offset=80,text='2.low lung volume ... ilar atelectasis.',infons=[],an
notations=[],relations=[],],BioCSentence[offset=135,text='3.no new focal consoli
dation.',infons=[],annotations=[],relations=[],BioCSentence[offset=168,text='4
.interval placem ... ibrillation pads.',infons=[],annotations=[],relations=[],]]
,annotations=[],relations=[],]],annotations=[],relations=[],],
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\n1.unremarkable ... b \nfractures. \n
\n',infons=[],sentences=[BioCSentence[offset=0,text='\n \n1.unremarkable ...
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tence[offset=179,text='3.no pleural effu ... t rib \nfractures.',infons=[],annot
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tub ... m on
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otations=[],relations=[],],BioCSentence[offset=288,text='if clinically\nind ...
decubitus
views.',infons=[],annotations=[],relations=[],],BioCSentence[offset=361,text='4.
the icu team w ... am on 05_02_2005.',infons=[],annotations=[],relations=[],]],a
nnotations=[],relations=[],]],annotations=[],relations=[],],
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postoperative ... table
technique.\n',infons=[],sentences=[BioCSentence[offset=0,text='\n1.
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CSentence[offset=97,text='2. left basilar o ... kely atelectasis.',infons=[],ann
otations=[],relations=[],],BioCSentence[offset=142,text='recommend attenti ...
ion or infection.',infons=[],annotations=[],relations=[],],BioCSentence[offset=2
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ions=[],]],annotations=[],relations=[],]],annotations=[],relations=[],],
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\n',infons=[],sentences=[BioCSentence[offset=0,text='\n \n1.single front ...
the \nprior exam.',infons=[],annotations=[],relations=[],],BioCSentence[offset=1
57, text='2.stable redemons ... o the prior exam.', infons=[], annotations=[], relat
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],annotations=[],relations=[],],annotations=[],relations=[],],annotations=[],r
elations=[],],
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mild pe ... solidation. \n \n
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ronchiolitis.',infons=[],annotations=[],relations=[],],BioCSentence[offset=85,te
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[],]],annotations=[],relations=[],],annotations=[],relations=[],],
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from
prior.',infons=[],annotations=[],relations=[],],BioCSentence[offset=261,text='3.
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osteopenia.\n',infons=[],sentences=[BioCSentence[offset=0,text='\n1. interval
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ioCSentence[offset=394,text='atherosclerotic aorta.',infons=[],annotations=[],re
lations=[],],BioCSentence[offset=417,text='osteopenia.',infons=[],annotations=[]
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\n', infons=[], sentences=[BioCSentence[offset=0,text='\n \n1.
                                                               no eviden ... or
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[],],BioCSentence[offset=146,text='2. the cardiomed ... in normal limits.',info
ns=[],annotations=[],relations=[],],BioCSentence[offset=210,text='3. no acute
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ions=[],]],annotations=[],relations=[],],
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\n',infons=[],sentences=[BioCSentence[offset=0,text=' \n \n1.stable lef ...
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',infons=[],sentences=[BioCSentence[offset=0,text=' \n \n 1. low lung ...
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nce[offset=38,text='no focal consolid ... pleural effusion.',infons=[],annotatio
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lines and ... leural
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nnotations=[],relations=[],]],annotations=[],relations=[],],
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```

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6,text='thoracic aortic g ... xation \nhardware.',infons=[],annotations=[],relat
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,infons=[],annotations=[],relations=[],]],annotations=[],relations=[],]],annotat
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interval r ... effusions.\n \n \n
```

\n',infons=[],sentences=[BioCSentence[offset=0,text='\n \n1. interval r ... cal

```
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[],]],annotations=[],relations=[],]],annotations=[],relations=[],],
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\n1.cardiomedias ... the skeleton.\n
\n',infons=[],sentences=[BioCSentence[offset=0,text='\n \n1.cardiomedias ... s
thoracic aorta.',infons=[],annotations=[],relations=[],],BioCSentence[offset=102
,text='lungs appear
clear.',infons=[],annotations=[],relations=[],],BioCSentence[offset=123,text='no
\nconsolidation ... pulmonary edema.',infons=[],annotations=[],relations=[],],B
ioCSentence[offset=190,text='mild \ndegenerativ ... of the skeleton.',infons=[]
,annotations=[],relations=[],]],annotations=[],relations=[],]],annotations=[],re
lations=[],],
 BioCDocument[id=24,infons=[],passages=[BioCPassage[offset=0,text='\n1. interval
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12 25 2014
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            mastogleticieneck..the first neestomach.', infons=[], annotations=[], relations=[],], Bio
[7]: collection.documents[0]
[7]: BTGCBtelmshtfid=0;inf8Hs=[];BTBStationEstationBtelmshtfid=0,inf8Hs=[];BTBStationBtelmshtfid=0,inf8Hs=[];BTBStationBtelmshtfid=0,inf8Hs=[];BTBStationBtelmshtfid=0,inf8Hs=[];BTBStationBtelmshtfid=0,inf8Hs=[];BTBStationBtelmshtfid=0,inf8Hs=[];BTBStationBtelmshtfid=0,inf8Hs=[];BTBStationBtelmshtfid=0,inf8Hs=[];BTBStationBtelmshtfid=0,inf8Hs=[];BTBStationBtelmshtfid=0,inf8Hs=[];BTBStationBtelmshtfid=0,inf8Hs=[];BTBStationBtelmshtfid=0,inf8Hs=[];BTBStationBtelmshtfid=0,inf8Hs=[];BTBStationBtelmshtfid=0,inf8Hs=[];BTBStationBtelmshtfid=0,inf8Hs=[];BTBStationBtelmshtfid=0,inf8Hs=[];BTBStationBtelmshtfid=0,inf8Hs=[];BTBStationBtelmshtfid=0,inf8Hs=[];BTBStationBtelmshtfid=0,inf8Hs=[];BTBStationBtelmshtfid=0,inf8Hs=[];BTBStationBtelmshtfid=0,inf8Hs=[];BTBStationBtelmshtfid=0,inf8Hs=[];BTBStationBtelmshtfid=0,inf8Hs=[];BTBStationBtelmshtfid=0,inf8Hs=[];BTBStationBtelmshtfid=0,inf8Hs=[];BTBStationBtelmshtfid=0,inf8Hs=[];BTBStationBtelmshtfid=0,inf8Hs=[];BTBStationBtelmshtfid=0,inf8Hs=[];BTBStationBtelmshtfid=0,inf8Hs=[];BTBStationBtelmshtfid=0,inf8Hs=[];BTBStationBtelmshtfid=0,inf8Hs=[];BTBStationBtelmshtfid=0,inf8Hs=[];BTBStationBtelmshtfid=0,inf8Hs=[];BTBStationBtelmshtfid=0,inf8Hs=[];BTBStationBtelmshtfid=0,inf8Hs=[];BTBStationBtelmshtfid=0,inf8Hs=[];BTBStationBtelmshtfid=0,inf8Hs=[];BTBStationBtelmshtfid=0,inf8Hs=[];BTBStationBtelmshtfid=0,inf8Hs=[];BTBStationBtelmshtfid=0,inf8Hs=[];BTBStationBtelmshtfid=0,inf8Hs=[];BTBStationBtelmshtfid=0,inf8Hs=[];BTBStationBtelmshtfid=0,inf8Hs=[];BTBStationBtelmshtfid=0,inf8Hs=[];BTBStationBtelmshtfid=0,inf8Hs=[];BTBStationBtelmshtfid=0,inf8Hs=[];BTBStationBtelmshtfid=0,inf8Hs=[];BTBStationBtelmshtfid=0,inf8Hs=[];BTBStationBtelmshtfid=0,inf8Hs=[];BTBStationBtelmshtfid=0,inf8Hs=[];BTBStationBtelmshtfid=0,inf8Hs=[];BTBStationBtelmshtfid=0,inf8Hs=[];BTBStationBtelmshtfid=0,inf8Hs=[];BTBStationBtelmshtfid=0,inf8Hs=[];BTBStationBtelmshtfid=0,inf8Hs=[];BTBStationBtelmshtfid=0,inf8Hs=[];BTBStationBtelmshtfid=0,inf8Hs=[];BTBStationBtelmshtfid=0,inf8Hs=[];BTBStationBtelmshtfid=0,inf8Hs=[]
              Puterta Left Tretpagardien ... us \nconsolidation. , infons=[], annotations=[], rela
              tions=[]nnetations=[hirelations=[hirelations=[]nfelations=[]nfelations=[]nfelations=[]n. and
              cBiaCDacyment Lida457sinfonandtapasasees-leiaCPaasaseeloffseesentexteloffsetalaa
              singlease pothrkidneysd \heffusions.',infons=[],annotations=[],relations=[],],Bi
              deseinfore defreet enceste in continue loffunt of the land of the 
              ribatlans=q]; Yelainfons=T;; qanotations=d{offlations=text=B30fSentenfelaffsen=321
              datexta: i;ladefiaefd, anastatiefisiefs, fenausions=[];nf,enscsenaunceatiesetilesetatie-4
              nsaterla Ripssentence of first 240 ptast = 12 nr 8 ng ey math 8 raxi dissidentified on sinfons = [
              ]annotations=[],relations=[]]],BinCSentence[offset=275stext='3.contrast is see
                      of both kidneys.',infons=[],annotations=[],relations=[],]],annotations=[],r
            Each double of has an attribute called passages in which the sentences are stored. Notice that passages used is the constant of the case of of th
              portable up … ural\neffusions.\n
              ',infons=[],sentences=[BioCSentence[offset=0,text='\n 1. portable up ...
              tube.',infons=[],annotations=[],relations=[],],BioCSentence[offset=94,text='2.
              persistent lo ... or consolidation.',infons=[],annotations=[],relations=[],],Bio
              CSentence[offset=194,text='possible bilateral pleural\neffusions.',infons=[],ann
              otations=[],relations=[],]],annotations=[],relations=[],]],annotations=[],relati
```

... p not visualized.',infons=[],annotations=[],relations=[],],BioCSentence[offs

```
[8]: collection.documents[0].passages[0].sentences
[8]: [BioCSentence[offset=0,text='\n \n1.mild pulmona ... and
     cardiomegaly.',infons=[],annotations=[],relations=[],],
      BioCSentence[offset=46,text='trace pleural fluid
     \neffusions.',infons=[],annotations=[],relations=[],],
      BioCSentence[offset=80,text='2.low lung volume ... ilar
     atelectasis.',infons=[],annotations=[],relations=[],],
      BioCSentence[offset=135,text='3.no new focal
     consolidation.',infons=[],annotations=[],relations=[],],
      BioCSentence[offset=168,text='4.interval placem ... ibrillation
    pads.',infons=[],annotations=[],relations=[],]]
    Each sentence stores information about the text, offset, relations and annotations. Let's check the
    sentences saved in the first document of our collection:
[9]: for i,s in enumerate(collection.documents[0].passages[0].sentences):
         print(f"sentence number {i + 1}: {s.text}\n")
         print("################"\n")
    sentence number 1:
    1.mild pulmonary edema, and cardiomegaly.
    sentence number 2: trace pleural fluid
    effusions.
    ###################################
    sentence number 3: 2.1ow lung volumes with minimal basilar atelectasis.
    ###################################
    sentence number 4: 3.no new focal consolidation.
    ####################################
    sentence number 5: 4.interval placement of defibrillation pads.
    ####################################
```

0.2.5 Cleaning up with the clean() function

Notice how the first report impression, which had two sentences, was split successfully. However, the newlines have not been trimmed. The clean() function from the previous lecture notebook will come in handy here. Let's bring it back out of the toolbox and apply it in this notebook!

```
import re
def clean(sentence):
    lower_sentence = sentence.lower()
    corrected_sentence = re.sub('and/or', 'or', lower_sentence)
    corrected_sentence = re.sub('(?<=[a-zA-Z])/(?=[a-zA-Z])', 'or ',u

corrected_sentence)
    clean_sentence = corrected_sentence.replace("..", ".")
    punctuation_spacer = str.maketrans({key: f"{key} " for key in ".,"})
    clean_sentence = clean_sentence.translate(punctuation_spacer)
    clean_sentence = ' '.join(clean_sentence.split())
    return clean_sentence</pre>
```

0.2.6 Exercise

Now that you've spent some time exploring how the NegBio library works, let's try it out on your data.

You'll determine whether a given report impression can tell you if a patient has an existing condition, while taking into account whether there was negation or uncertainty in the findings. For this task, you'll use these predetermined categories:

0.2.7 Import NegBio Dependencies

Next you'll import everything you need for this task. Don't be alarmed by the declared paths below the imports! They're just mapping the path to various files that NegBio relies on.

```
[12]: from pathlib2 import Path
from negbio.main_chexpert import pipeline
from negbio.pipeline.parse import NegBioParser
from negbio.chexpert.stages.load import NegBioLoader
from negbio.chexpert.stages.extract import NegBioExtractor
from negbio.chexpert.stages.classify import ModifiedDetector
from negbio.chexpert.stages.aggregate import NegBioAggregator
from negbio.pipeline.ptb2ud import NegBioPtb2DepConverter, Lemmatizer

PARSING_MODEL_DIR = "~/.local/share/bllipparser/GENIA+PubMed"
```

```
CHEXPERT_PATH = "NegBio/negbio/chexpert/"

MENTION_PATH = f"{CHEXPERT_PATH}phrases/mention"

UNMENTION_PATH = f"{CHEXPERT_PATH}phrases/"

NEG_PATH = f'{CHEXPERT_PATH}patterns/negation.txt'

PRE_NEG_PATH = f'{CHEXPERT_PATH}patterns/pre_negation_uncertainty.txt'

POST_NEG_PATH = f'{CHEXPERT_PATH}patterns/post_negation_uncertainty.txt'
```

The encoding of information within these files is beyond the scope of this notebook, but if you're really curious about the contents you could do something like this to see more:

!cat \$NEG_PATH

```
[13]: !cat $NEG PATH
     # No definite XXX
     ({} > {} {lemma:/definite/}) > {dependency:/neg/} {}
     # No obvious XXX
     ({} > {} {lemma:/obvious/}) > {dependency:/neg/} {}
     {} > {dependency:/amod|nsubj/} {lemma:/normal|unremarkable/}
     {} < {dependency:/amod|nsubj/} {lemma:/normal|unremarkable/}
     ({} > {} ) < {dependency:/nsubj|dobj/} {lemma:/unremarkable|normal/}
     {} < {} ({} > {dependency:/amod/} {lemma:/normal|unremarkable/})
     {} < {} ({} < {dependency:/nsubj/} {lemma:/normal|unremarkable/})
     {} < {dependency:/conj:no/} {}
     \{\} < \{\} (\{\} < \{dependency:/conj:or/\} (\{\} > \{\} \{lemma:/no/\}))
     {} < {dependency:/nsubj/} ({lemma:/limit.*/} > {} {lemma:/upper/} & >
     {dependency:/nmod:of/} {lemma:/normal/} & > {dependency:/case/}
     {lemma:/at|within/})
     \{\} < \{\} (\{dependency:/exclude/\} < \{\} (\{\} > \{\} \{lemma:/no/\}))
     ({lemma:/silhouette/} > {} {}) < {dependency:/dobj|nsubj/} {lemma:/obscure/}
     ({} > {dependency:/amod/} {lemma:/normal|unremarkable/}) <
     {dependency:/dobj|nsubj/} {lemma:/demonstrate.*|show|present|display/}
     {} < {dependency:/nmod:of/} ( {lemma:/appearance/} > {dependency:/amod/}
     {lemma:/normal/} & < {dependency:/dobj/}
     {lemma:/demonstrate.*|show|present|display/})
     {} < {dependency:/amod/} ({} < {dependency:/dep|nsubj/}
     {lemma:/normal|unremarkable/})
     {} < {dependency:/amod/} ({} > {dependency:/neg/} {lemma:/no/})
     {} < {dependency:/amod/}({lemma:/finding.*/} < {dependency:/dobj/}
     ({lemma:/acute/} > {dependency:/nsubj/} {lemma:/no/}))
     {} < {dependency:/amod/} ({lemma:/structure.*/} < {dependency:/dep|nsubj/}
```

```
({lemma:/appear/} > {dependency:/xcomp/} {lemma:/normal|unremarkable/}))
{} < {dependency:/compound/} ({} > {dependency:/neg/} {})
{} < {dependency:/nsubj/} {lemma:/absent/}</pre>
{} < {dependency:/amod/} ({} < {dependency:/nmod:of/} ({lemma:/evidence/} >
{dependency:/case/} {lemma:/without/}))
{} < {dependency:/amod/} ({} < {dependency:/nmod:of/} ({lemma:/evidence/} >
{dependency:/neg/} {}))
# XXX within normal limits
{} < {} ({} < {} ({lemma:/show|demonstrate|present/} >
{dependency:/nmod:within/} ({lemma:/limit.*/} > {} {lemma:/normal/})))
({} > {} ) > {dependency:/nmod:within/} {lemma:/limit.*/}
{} < {dependency:/nsubj/} ({lemma:/limit.*/} > {} {lemma:/upper/} & >
{dependency:/nmod:of/} {lemma:/normal/} & > {dependency:/case/}
{lemma:/at|within/})
\{\} < \{\} (\{\} < \{dependency:/nsubj/\} (\{lemma:/limit.*/\} > \{\} \{lemma:/upper/\} \& > \{\} \}
{dependency:/nmod:of/} {lemma:/normal/} & > {dependency:/case/}
{lemma:/at|within/}))
{} < {} ({} < {dependency:/nsubj/} ({lemma:/limit.*/} > {dependency:/amod/}
{lemma:/normal/} & > {dependency:/case/} {lemma:/at|within/}))
({lemma:/vascularity/} > {dependency:/amod/} {lemma:/pulmonary/}) >
{dependency:/amod/} {lemma:/normal/}
{} < {dependency:/dobj|nsubj/} ({} > {dependency:/nmod:within/}
({lemma:/limit.*/} > {} {lemma:/normal/}))
{} > {dependency:/nmod:within/} ({lemma:/limit.*/} > {dependency:/amod/}
{lemma:/normal/})
{} > {} ({lemma:/limit/} > {} {lemma:/normal/})
# XXX is/appears/are/appear/remain/remains (now, otherwise) normal/unremarkable
{} < {} ({lemma:/appear|remain/} > {} {lemma:/normal|unremarkable/})
# XXX is/appears/are/appear/remain/remains (now, otherwise) within normal limits
{} > {} ({lemma:/remain|appear/} > {} ({lemma:/limit/} > {} {lemma:/normal/}))
# rather than XXX
{} <{dependency:/conj:negcc/} {}</pre>
{} <{dependency:/nmod:without/} {}</pre>
{} <{dependency:/nmod:without|nmod:of/} {lemma:/clear|clearing/}=key
{} <{dependency:/nmod:out/} {lemma:/rule/}=key
# removal of XXX
{} <{dependency:/nmod:of/}
{lemma:/history|free|disappearance|resolution|drainage|resolution|removal/}
{} <{dependency:/nmod:for/} {lemma:/negative/}
```

```
# exclude XXX
{} <{} {lemma:/exclude/}</pre>
{} <{dependency:/advmod|dep|conj:or/} {lemma:/no/}
# XXX has resolved
{} <{dependency:/nsubj/} ({lemma:/resolve/}=key >{dependency:/aux/} {})
# there is no XXX
{} <{dependency:/nsubj/} ({lemma:/be/} >{} {lemma:/no/})
# without evidence|finding of|for XXX
{} <{dependency:/nmod:of|nmod:for/} ({lemma:/evidence|finding/}
<{dependency:/nmod:without/} {})
# without development of XXX
{} < {dependency:/nmod:of/} ({lemma:/development/} > {} {lemma:/without/})
# No development of XXX
{} < {dependency:/nmod:of/} ({lemma:/development/} > {} {lemma:/no/})
# no evidence of | for XXX
{} <{dependency:/nmod:of|nmod:for/} ({lemma:/evidence/} >{dependency:/neg/} {})
# without evidence|finding of|for XXX
{} <{dependency:/nmod:of|nmod:for/} ({lemma:/evidence|finding/} >{}
{lemma:/without/})
# no focus of XXX
{} <{dependency:/nmod:of/} ({lemma:/focus/} >{dependency:/neg/} {})
{} <{dependency:/nmod:of/} ({lemma:/focus/} >{} {lemma:/no/})
# no moderate to XXX
{} <{dependency:/nmod:to/} ({lemma:/moderate/} >{dependency:/neg/} {})
# no evidence of developing XXX
{} <{} ({lemma:/developing/} <{} ({lemma:/evidence/}</pre>
<{dependency:/nmod:without/} {}))
\{\} < \{\} (\{lemma:/developing/\} < \{\} (\{lemma:/evidence/\} > \{\} \{lemma:/no/\}))
# no focal XXX
{} <{dependency:/dobj/} ({} >{dependency:/nsubj/} {lemma:/no/})
# XXX is previously demonstrated/visualized
{} <{dependency:/dobj|nsubjpass/} ({lemma:/demonstrate|visualize/} >{}
{lemma:/previously/})
# there is no NN to suggest/explain XXX
```

```
\{\} < \{\} (\{lemma:/suggest|explain|diagnose/\} < \{\} (\{tag:/V.*/\} > \{\} (\{tag:/N.*/\} > \{\} (\{tag:/N.*/) > 
> {} {lemma:/no/})))
# no NN to suggest/explain XXX
\{\} < \{\} (\{lemma:/suggest|explain|diagnose/\} < \{\} (\{tag:/N.*/\} > \{\} \})
{lemma:/no/}))
# no area of XXX
{} < {dependency:/nmod:of/} ({lemma:/area/} > {dependency:/compound/}
{lemma:/no/})
# XXX is not enlarged
{} < {dependency:/nsubjpass/} ({lemma:/enlarge/} > {dependency:/neg/} {})
# without development of XXX
{} < {dependency:/nmod:of/} ({lemma:/development/} > {dependency:/case/}
{lemma:/without/})
# XXX removed
{} < {} {lemma:/remove/}
{} > {} {lemma:/remove/}
# XXX is no longer seen
{} < {dependency:/nsubjpass/} ({lemma:/see/} > {} ({} > {dependency:/neg/}
{lemma:/no/}))
{} < {dependency:/nsubjpass/} ({lemma:/see/} > {} {lemma:/no/})
# without evidence seen for XXX
\{\} < \{\} (\{lemma:/see/\} > \{\} (\{\} > \{\} (\{lemma:/evidence/\} > \{\} )\})
{lemma:/without/})))
\{\} < \{\} (\{lemma:/see/\} > \{\} (\{lemma:/evidence/\} > \{\} \{lemma:/without/\}))
# normal/unremarkable appearance of XXX
{} < {} ({lemma:/appearance/} > {} {lemma:/normal|unremarkable/})
# normal/unremarkable XXX | XXX is/appears normal/unremarkable
# make more general
{} > {} {lemma:/normal|unremarkable/}
{} < {} {lemma:/normal|unremarkable/}</pre>
# XXX has/have cleared
# cleared XXX
{} < {} {lemma:/clear/}
{} > {} {lemma:/clear/}
# no obvious associated XXX
{} < {} ({lemma:/associate.*/} > {} ({lemma:/obvious/} > {dependency:/neg/} {}))
\{\} > \{dependency:/neg/\} \{\} \& > \{\} \{lemma:/obvious/\} \& > \{\} \{lemma:/associate.*/\} \}
```

```
# XXX with interval resolution
{} > {} ({lemma:/resolution/} > {} {lemma:/interval/})

# no XXX / general negative case
{} >{dependency:/neg/} {}
{} >{} {lemma:/no/}
{} >{dependency:/case/} {lemma:/without/}
```

Running this process for the entire dataset is very slow (~1.5 hr on a fast laptop!) so let's slice it to showcase how NegBio works. Let's start with 50 random observations.

```
[14]: sampled_df = df.sample(50)
```

Also, let's recreate the code from the beginning of the notebook as a function, including the clean() function as well.

```
[15]: def get_bioc_collection(df):
    collection = bioc.BioCCollection()
    splitter = NegBioSSplitter()
    for i, report in enumerate(df["Report Impression"]):
        document = text2bioc.text2document(str(i), clean(report))
        document = splitter.split_doc(document)
        collection.add_document(document)
    return collection
```

Here, you'll repeat your process from earlier by converting the report impression strings into a BioC XML format which NegBio can read.

```
[16]: collection = get_bioc_collection(sampled_df)
```

Now let's instantiate NegBio's lemmatizer.

The process of lemmatization refers to returning the dictionary form of a word (or lemma) by removing inflectional endings. It's very cool and you can read more about it here.

```
[17]: lemmatizer = Lemmatizer()
```

Next you'll instantiate NegBio's converter to convert from parse tree to universal dependencies. This is done using the Stanford converter, which you can find more information about here.

The parse tree used here is the Penn Treebank. In general terms, a treebank is an annotated text corpus that includes analysis beyond part-of-speech tagging. They've become very valuable resources to NLP research in recent years.

Universal dependencies, or UD, provide a powerful framework for annotating grammar across different languages. Read more about them here.

```
[18]: ptb2dep = NegBioPtb2DepConverter(lemmatizer, universal=True)
```

You've already seen the splitter in action before, so you can skip it.

```
[19]: ssplitter = NegBioSSplitter(newline=True)
```

Now you'll instantiate the parser and the loader.

Under the hood, you're using the BLIPP reranking parser, which is a statistical natural language parser.

The loader, as you might imagine, loads the reports into memory.

Over all of this, the chexpert-labeler is used. This labeler extracts observations from radiology reports specifically, and can provide a vocabulary appropriate to the clinical context.

```
[20]: parser = NegBioParser(model_dir=PARSING_MODEL_DIR)
loader = NegBioLoader()
```

The extractor is what extracts the observations from the report impressions.

```
[21]: extractor = NegBioExtractor(Path(MENTION_PATH), Path(UNMENTION_PATH))
```

The negator will determine whether negation or uncertainty exists in the context of the observations provided by the extractor.

```
[22]: neg_detector = ModifiedDetector(PRE_NEG_PATH, NEG_PATH, POST_NEG_PATH)
```

The aggregator then aggregates these observations if they belong to the same category.

```
[23]: aggregator = NegBioAggregator(CATEGORIES)
```

0.2.8 Putting it all together

Finally, you'll put everything together using the pipeline function, which takes as arguments all of the objects you've instantiated so far. Then you'll get a nice, clean DataFrame with your result:

```
[24]: collection = pipeline(collection, loader, ssplitter, extractor, parser, ptb2dep, neg_detector, aggregator, u →verbose=True)
```

```
100% | 50/50 [00:57<00:00, 1.16s/it]
```

```
[25]: negbio_pred = pd.DataFrame()
    for doc in collection.documents:
        dictionary = {}
        for key, val in doc.infons.items():
            dictionary[key[9:]] = val
            negbio_pred = negbio_pred.append(dictionary, ignore_index=True)
        negbio_pred = negbio_pred.replace(
            "Positive", True).replace(
            "Negative", False).replace("Uncertain", False).fillna(False)
```

[26]: negbio_pred.head()

	Airspace Opacity	Atelectasis	Fracture	Cons	olidati	on P	neumonia	\
0	True	True	True		Fal	se	False	
1	True	False	False		Fal	se	True	
2	False	False	False		Fal	se	False	
3	False	False	False		Fal	se	False	
4	False	False	False		Fal	se	False	
	Pleural Effusion	Pneumothorax	Cardiomeg	aly	Edema	Lung	Lesion	\
0	False	False	Fa	lse	False		False	
1	False	False	Fa	lse	False		False	
2	True	True	Fa	lse	False		False	
3	False	False	Т	'rue	False		False	
4	False	False	Fa	lse	False		False	
	Pleural Other							
0	False							
1	False							
2	False							
3	False							
4	False							
	1 2 3 4 0 1 2 3 4	O True 1 True 2 False 3 False 4 False 4 False Pleural Effusion O False 1 False 2 True 3 False 4 False 4 False 5 False 5 False 1 False 1 False 2 False 3 False 5 False 5 False 7 False 7 False 7 False 8 False 9 False	True True True True True False False False False False False False Pleural Effusion Pneumothorax False False True True False	True True True True True False	True	True True True False True False False False False False False False Pleural Effusion Pneumothorax Cardiomegaly Edema False False False False False False False False False False True True False False False False False False Pleural Other False False	True True True False True False	$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$

Now you can check every entry in the report impressions for the presence of a condition, while knowing that negation has been taken into account. Really cool!

Congratulations on finishing this notebook!!! This was a very high-level explanation of everything that NegBio does and as you may have noticed, this library leverages many other great tools and libraries. Hopefully, it was a good introduction to how it works. Nice work, keep it up!