AI for Medicine Course 3 Week 1 lecture notebook

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.

Import Pandas and Load Dataset

In [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)
```

Out[1]:

	SimpleTestReportID	Report Impression	No Finding	Enlarged Cardiomediastinum	Cardiomegaly	Lung Lesion
0	1.0	\n \n1.mild pulmonary edema, and cardiomegaly....	NaN	NaN	1.0	NaN
1	2.0	\n \n1.unremarkable cardiomediastinal silhouet...	NaN	0.0	NaN	NaN
2	3.0	\n1. lines and tubes are unchanged in position...	NaN	NaN	NaN	NaN
3	4.0	\n1. postoperative portable film with a right-...	NaN	NaN	NaN	NaN
4	6.0	\n \n1.single frontal view of the chest demons...	NaN	NaN	NaN	NaN

In [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 whe
n
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_20
05.
```

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 (http://bioc.sourceforge.net/).

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.

In [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, 'sourc
e': '', 'date': '2021-02-03', 'key': '', 'infons': {}, 'documents'
: []}

methods and attributes:

['__class__', '__delattr__', '__dict__', '__dir__', '__doc__', '__
eq__', '__format__', '__ge__', '__getattribute__', '__gt__', '__ha
sh__', '__init__', '__init_subclass__', '__le__', '__lt__', '__mod
ule__', '__ne__', '__new__', '__reduce__', '__reduce_ex__', '__rep
r__', '__setattr__', '__sizeof__', '__str__', '__subclasshook__',
'__weakref__', 'add_document', 'clear_infons', 'date', 'documents'
, 'encoding', 'infons', 'key', 'source', 'standalone', 'version']

documents within collection: []
```

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 (https://github.com/ncbi-nlp/NegBio), or the official documentation (https://negbio.readthedocs.io/en/latest/index.html).

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.

In [4]:
```
from negbio.pipeline.ssplit import NegBioSSplitter
from negbio.pipeline import text2bioc

splitter = NegBioSSplitter()
for i, report in enumerate(df["Report Impression"]):
        document = text2bioc.text2document(str(i), report)
        document = splitter.split_doc(document)
        collection.add_document(document)
```

In [5]:
```
collection.documents
```

Out[5]:
```
[BioCDocument[id=0,infons=[],passages=[BioCPassage[offset=0,text='
\n \n1.mild pulmona ... lation pads.  \n \n',infons=[],sentences=[
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6,text='trace pleural fluid \neffusions.',infons=[],annotations=[]
,relations=[],],BioCSentence[offset=80,text='2.low lung volume ...
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tence[offset=135,text='3.no new focal consolidation.',infons=[],an
notations=[],relations=[],],BioCSentence[offset=168,text='4.interv
al placem ... ibrillation pads.',infons=[],annotations=[],relation
s=[],]],annotations=[],relations=[],]],annotations=[],relations=[]
,],
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\n \n1.unremarkable ... b \nfractures. \n \n',infons=[],sentences=
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nge.',infons=[],annotations=[],relations=[],],BioCSentence[offset=
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ons=[],],BioCSentence[offset=179,text='3.no pleural effu ... t rib
\nfractures.',infons=[],annotations=[],relations=[],]],annotations
=[],relations=[],]],annotations=[],relations=[],],
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\n1. lines and tub ... m on 05_02_2005.\n',infons=[],sentences=[Bi
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```

',infons=[],annotations=[],relations=[],],BioCSentence[offset=47,t
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ax.',infons=[],annotations=[],relations=[],],BioCSentence[offset=2
51,text='clinical correlation is recommended.',infons=[],annotatio
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ind ... decubitus views.',infons=[],annotations=[],relations=[],]
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',infons=[],annotations=[],relations=[],],BioCSentence[offset=97,t
ext='2. left basilar o ... kely atelectasis.',infons=[],annotation
s=[],relations=[],],BioCSentence[offset=142,text='recommend attent
i ... ion or infection.',infons=[],annotations=[],relations=[],],B
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e.',infons=[],annotations=[],relations=[],]],annotations=[],relati
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tations=[],relations=[],],BioCSentence[offset=293,text='3.no evide
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otations=[],relations=[],]],annotations=[],relations=[],],
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.',infons=[],annotations=[],relations=[],],BioCSentence[offset=136
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,BioCSentence[offset=261,text='3. there is bilat ... eural thicken
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tions=[],]],annotations=[],relations=[],],
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cified lymph nodes.',infons=[],annotations=[],relations=[],],BioCS
entence[offset=323,text='3. cardiac silhou ... ar\nconfiguration.'
,infons=[],annotations=[],relations=[],],BioCSentence[offset=394,t
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.',infons=[],annotations=[],relations=[],],BioCSentence[offset=48,
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eft.',infons=[],annotations=[],relations=[],],BioCSentence[offset=
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,infons=[],annotations=[],relations=[],],BioCSentence[offset=99,te
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m.',infons=[],annotations=[],relations=[],],BioCSentence[offset=80
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onia.',infons=[],annotations=[],relations=[],]],annotations=[],rel
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ter.',infons=[],annotations=[],relations=[],],BioCSentence[offset=
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ations=[],relations=[],],BioCSentence[offset=151,text='2.moderate
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],]],annotations=[],relations=[],]],annotations=[],relations=[],],
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horax.',infons=[],annotations=[],relations=[],],BioCSentence[offse
t=96,text='2. no significan ... leural effusions.',infons=[],anno
tations=[],relations=[],]],annotations=[],relations=[],]],annotati
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rta.',infons=[],annotations=[],relations=[],],BioCSentence[offset=
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[],],BioCSentence[offset=123,text='no \nconsolidation ... pulmona
ry edema.',infons=[],annotations=[],relations=[],],BioCSentence[of
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.',infons=[],annotations=[],relations=[],],BioCSentence[offset=112
,text='no evidence of\npu ... pleural effusion.',infons=[],annotat
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nfons=[],annotations=[],relations=[],],BioCSentence[offset=244,tex
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[],relations=[],]],annotations=[],relations=[],]],annotations=[],r
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' \n \n1. low lung ... ural effusion.\n \n',infons=[],sentences=

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ations=[],relations=[],],BioCSentence[offset=154,text='a dedicated
two v ... wo possibilities.',infons=[],annotations=[],relations=[]
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tations=[],relations=[],],BioCSentence[offset=314,text='three embo
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onia.',infons=[],annotations=[],relations=[],],BioCSentence[offset
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and tubes are unchanged.',infons=[],annotations=[],relations=[],],
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121,text='2. the cardiomed ... in normal limits.',infons=[],annot
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],]],annotations=[],relations=[],]],annotations=[],relations=[],],
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.',infons=[],annotations=[],relations=[],],BioCSentence[offset=56,
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,
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='\n \n1. a biventri ... \nseen.\n \n   \n \n \n',infons=[],sente
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in place.',infons=[],annotations=[],relations=[],],BioCSentence[of
fset=51,text='no pneumothorax is \nseen.',infons=[],annotations=[]
,relations=[],]],annotations=[],relations=[],]],annotations=[],rel
ations=[],],
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='\n1. no pneumothor ... cture\nlaterally.\n',infons=[],sentences=
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ied.',infons=[],annotations=[],relations=[],],BioCSentence[offset=
77,text='stable cardiomediastinal silhouette.',infons=[],annotatio
ns=[],relations=[],],BioCSentence[offset=114,text='2. redemonstrat
io ... acture\nlaterally.',infons=[],annotations=[],relations=[],]
],annotations=[],relations=[],]],annotations=[],relations=[],],
 BioCDocument[id=972,infons=[],passages=[BioCPassage[offset=0,text
='\n \n1.the lungs re ... is identified.\n \n',infons=[],sentences

=[BioCSentence[offset=0,text='\n \n1.the lungs re ... rity again n
oted.',infons=[],annotations=[],relations=[],],BioCSentence[offset
=103,text='2.cardiomediastin ... in normal limits.',infons=[],anno
tations=[],relations=[],],BioCSentence[offset=175,text='3.no osseo
us abnormality is identified.',infons=[],annotations=[],relations=
[],]],annotations=[],relations=[],]],annotations=[],relations=[],]
,
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='\n1. diffuse reti ... is recommended.\n',infons=[],sentences=[
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s.',infons=[],annotations=[],relations=[],],BioCSentence[offset=60
,text='these findings are nonspecific.',infons=[],annotations=[],r
elations=[],],BioCSentence[offset=92,text='main consideratio ...
pulmonary edema.',infons=[],annotations=[],relations=[],],BioCSent
ence[offset=180,text='clinical correlat ... s is recommended.',inf
ons=[],annotations=[],relations=[],]],annotations=[],relations=[],
]],annotations=[],relations=[],],
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='\n \n1. small to mo ... lidation. \n \n \n \n',infons=[],sentenc
es=[BioCSentence[offset=0,text='\n \n1. small to mo ... r \nconsol
idation.',infons=[],annotations=[],relations=[],]],annotations=[],
relations=[],]],annotations=[],relations=[],],
 BioCDocument[id=975,infons=[],passages=[BioCPassage[offset=0,text
='\n \n1. interval r ... 6_16_2014.\n \n \n \n',infons=[],sentenc
es=[BioCSentence[offset=0,text='\n \n1. interval r ... wer lung v
olumes.',infons=[],annotations=[],relations=[],],BioCSentence[offs
et=103,text='2. persistent le ... pleural effusion.',infons=[],an
notations=[],relations=[],],BioCSentence[offset=230,text='3. pers
istent pu ... d to \n06_16_2014.',infons=[],annotations=[],relatio
ns=[],]],annotations=[],relations=[],]],annotations=[],relations=[
],],
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='\n1. no significan ... pulmonary edema.\n',infons=[],sentences=[
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infons=[],annotations=[],relations=[],],BioCSentence[offset=36,tex
t='the volume of rig ... pleural effusion.',infons=[],annotations=
[],relations=[],],BioCSentence[offset=131,text='persistent bilater
al pulmonary edema.',infons=[],annotations=[],relations=[],]],anno
tations=[],relations=[],]],annotations=[],relations=[],],
 BioCDocument[id=977,infons=[],passages=[BioCPassage[offset=0,text
='\n \n1. post stern ... effusion.\n \n \n \n',infons=[],sentenc
es=[BioCSentence[offset=0,text='\n \n1. post stern ... pleural ef
fusion.',infons=[],annotations=[],relations=[],]],annotations=[],r
elations=[],]],annotations=[],relations=[],],
 BioCDocument[id=978,infons=[],passages=[BioCPassage[offset=0,text
='\n1. the tracheost ... t\nthe left base.\n',infons=[],sentences=
[BioCSentence[offset=0,text='\n1. the tracheost ... ficantly chang
ed.',infons=[],annotations=[],relations=[],],BioCSentence[offset=1
03,text='a right-sided pic ... has been removed.',infons=[],annota
tions=[],relations=[],],BioCSentence[offset=185,text='2. no defini
te pn ... een on the right.',infons=[],annotations=[],relations=[]
,],BioCSentence[offset=235,text='there is a\nmodera ... o the righ
t apex.',infons=[],annotations=[],relations=[],],BioCSentence[offs

et=312,text='3. as before, the ... at\nthe left base.',infons=[],a
nnotations=[],relations=[],]],annotations=[],relations=[],]],annot
ations=[],relations=[],],
 BioCDocument[id=979,infons=[],passages=[BioCPassage[offset=0,text
='\n \n1.stable confl ... g volumes.\n \n \n \n',infons=[],sentenc
es=[BioCSentence[offset=0,text='\n \n1.stable confl ... ly consoli
dation.',infons=[],annotations=[],relations=[],],BioCSentence[offs
et=111,text='stable blunting o ... pleural effusion.',infons=[],an
notations=[],relations=[],],BioCSentence[offset=207,text='no \npul
monary edema or pneumothorax.',infons=[],annotations=[],relations=
[],],BioCSentence[offset=246,text='2.stable right in ... sternotom
y wires.',infons=[],annotations=[],relations=[],],BioCSentence[off
set=335,text='3.interval slight ... appears widened.',infons=[],a
nnotations=[],relations=[],],BioCSentence[offset=434,text='interva
l decrease ... sed lung volumes.',infons=[],annotations=[],relatio
ns=[],]],annotations=[],relations=[],]],annotations=[],relations=[
],],
 BioCDocument[id=980,infons=[],passages=[BioCPassage[offset=0,text
='\n \n1. new left c ... \npneumothorax.\n \n',infons=[],sentence
s=[BioCSentence[offset=0,text='\n \n1. new left c ... al \npneumo
thorax.',infons=[],annotations=[],relations=[],]],annotations=[],r
elations=[],]],annotations=[],relations=[],],
 BioCDocument[id=981,infons=[],passages=[BioCPassage[offset=0,text
='\n1. ap view of t ... leural effusion.\n',infons=[],sentences=[
BioCSentence[offset=0,text='\n1. ap view of t ... low\nlung volum
es.',infons=[],annotations=[],relations=[],],BioCSentence[offset=8
6,text='there is left ret ... versus pneumonia.',infons=[],annotat
ions=[],relations=[],],BioCSentence[offset=184,text='2. cardiomeg
aly persists.',infons=[],annotations=[],relations=[],],BioCSentenc
e[offset=211,text='3. there is a le ... pleural effusion.',infons
=[],annotations=[],relations=[],]],annotations=[],relations=[],]],
annotations=[],relations=[],],
 BioCDocument[id=982,infons=[],passages=[BioCPassage[offset=0,text
='\n \n1.frontal and ... onary edema.\n \n \n',infons=[],sentence
s=[BioCSentence[offset=0,text='\n \n1.frontal and ... o the prior
exam.',infons=[],annotations=[],relations=[],],BioCSentence[offset
=134,text='2.there is no evi ... ediastinal shift.',infons=[],anno
tations=[],relations=[],],BioCSentence[offset=181,text='3.there is
no evidence or fracture.',infons=[],annotations=[],relations=[],],
BioCSentence[offset=219,text='4.there is no evi ... \npulmonary ed
ema.',infons=[],annotations=[],relations=[],]],annotations=[],rela
tions=[],]],annotations=[],relations=[],],
 BioCDocument[id=983,infons=[],passages=[BioCPassage[offset=0,text
='\n1. interval plac ... f the left lung.\n',infons=[],sentences=[
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x.',infons=[],annotations=[],relations=[],],BioCSentence[offset=12
4,text='no\nevidence of midline shift.',infons=[],annotations=[],r
elations=[],],BioCSentence[offset=154,text='prominent right-s ...
aneous\nemphysema.',infons=[],annotations=[],relations=[],],BioCSe
ntence[offset=200,text='2. interval devel ... of the left lung.',i
nfons=[],annotations=[],relations=[],]],annotations=[],relations=[
],]],annotations=[],relations=[],],
 BioCDocument[id=984,infons=[],passages=[BioCPassage[offset=0,text

='\n1. large left p ... cally warranted.\n',infons=[],sentences=[
BioCSentence[offset=0,text='\n1. large left p ... pleural effusio
n.',infons=[],annotations=[],relations=[],],BioCSentence[offset=67
,text='additionally, the ... nnot be excluded.',infons=[],annotati
ons=[],relations=[],],BioCSentence[offset=227,text='follow-up is r
eco ... ically warranted.',infons=[],annotations=[],relations=[],]
],annotations=[],relations=[],]],annotations=[],relations=[],],
 BioCDocument[id=985,infons=[],passages=[BioCPassage[offset=0,text
='\n \n1.increased di ... emonstrated.\n \n \n',infons=[],sentence
s=[BioCSentence[offset=0,text='\n \n1.increased di ... pulmonary
edema.',infons=[],annotations=[],relations=[],],BioCSentence[offse
t=130,text='there \nmaybe a ti ... pleural effusion.',infons=[],an
notations=[],relations=[],],BioCSentence[offset=176,text='2.multip
le healed ... s redemonstrated.',infons=[],annotations=[],relation
s=[],]],annotations=[],relations=[],]],annotations=[],relations=[]
,],
 BioCDocument[id=986,infons=[],passages=[BioCPassage[offset=0,text
='\n1. there has bee ... he\n aortic arch.\n',infons=[],sentences=
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le.',infons=[],annotations=[],relations=[],],BioCSentence[offset=1
47,text='2. there is no evidence of pneumothorax.',infons=[],annot
ations=[],relations=[],],BioCSentence[offset=188,text='3. no evide
nce of ... disease is seen.',infons=[],annotations=[],relations=[
],],BioCSentence[offset=239,text='4. there is re-de ... the\n aort
ic arch.',infons=[],annotations=[],relations=[],]],annotations=[],
relations=[],]],annotations=[],relations=[],],
 BioCDocument[id=987,infons=[],passages=[BioCPassage[offset=0,text
='\n1. minimal resid ... r on 11_19_2004.\n',infons=[],sentences=[
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x.',infons=[],annotations=[],relations=[],],BioCSentence[offset=48
,text='2. the left intra ... the lower thorax.',infons=[],annotati
ons=[],relations=[],],BioCSentence[offset=168,text='3. the nasogas
tri ... ave been removed.',infons=[],annotations=[],relations=[],]
,BioCSentence[offset=232,text='4. persistent loo ... hragmatic her
nia.',infons=[],annotations=[],relations=[],],BioCSentence[offset=
396,text='5. the findings w ... er on 11_19_2004.',infons=[],annot
ations=[],relations=[],]],annotations=[],relations=[],]],annotatio
ns=[],relations=[],],
 BioCDocument[id=988,infons=[],passages=[BioCPassage[offset=0,text
=' \n \nnormal heart ... ative changes.\n \n',infons=[],sentences
=[BioCSentence[offset=0,text=' \n \nnormal heart size.',infons=[],
annotations=[],relations=[],],BioCSentence[offset=24,text='interst
itial prom ... \npulmonary edema.',infons=[],annotations=[],relati
ons=[],],BioCSentence[offset=86,text='patchy consolidat ... on, or
pneumonia.',infons=[],annotations=[],relations=[],],BioCSentence[o
ffset=187,text='small bilateral \npleural effusions.',infons=[],an
notations=[],relations=[],],BioCSentence[offset=224,text='no pneum
othorax.',infons=[],annotations=[],relations=[],],BioCSentence[off
set=242,text='tortuous or ectat ... ic calcification.',infons=[],a
nnotations=[],relations=[],],BioCSentence[offset=315,text='left up
per extrem ... el of the carina.',infons=[],annotations=[],relatio
ns=[],],BioCSentence[offset=407,text='multilevel spine degenerativ
e changes.',infons=[],annotations=[],relations=[],]],annotations=[

],relations=[],]],annotations=[],relations=[],],
BioCDocument[id=989,infons=[],passages=[BioCPassage[offset=0,text
='\n1. ap erect ches ... cortical defect.\n',infons=[],sentences=[
BioCSentence[offset=0,text='\n1. ap erect ches ... tinal silhouett
e.',infons=[],annotations=[],relations=[],],BioCSentence[offset=82
,text='the lungs appear clear.',infons=[],annotations=[],relations
=[],],BioCSentence[offset=106,text='no rib\nfractures or pneumotho
rax.',infons=[],annotations=[],relations=[],],BioCSentence[offset=
140,text='2. ap and lateral ... e\nshoulder joint.',infons=[],anno
tations=[],relations=[],],BioCSentence[offset=281,text='there also
appear ... n the lower neck.',infons=[],annotations=[],relations=[
],],BioCSentence[offset=368,text='two paper clips p ... skin lacer
ations.',infons=[],annotations=[],relations=[],],BioCSentence[offs
et=453,text='no\nradiopaque foreign bodies.',infons=[],annotations
=[],relations=[],],BioCSentence[offset=483,text='a lucent line pro
... r to the glenoid.',infons=[],annotations=[],relations=[],],Bio
CSentence[offset=565,text='this can only be ... kely artifactual.
',infons=[],annotations=[],relations=[],],BioCSentence[offset=626,
text='however, if there ... n may be helpful.',infons=[],annotatio
ns=[],relations=[],],BioCSentence[offset=714,text='in\naddition, t
her ... the lateral view.',infons=[],annotations=[],relations=[],]
,BioCSentence[offset=849,text='this could repres ... cortical def
ect.',infons=[],annotations=[],relations=[],]],annotations=[],rela
tions=[],]],annotations=[],relations=[],],
BioCDocument[id=990,infons=[],passages=[BioCPassage[offset=0,text
='\n \n1.persistent p ... ed up stomach.\n \n',infons=[],sentences
=[BioCSentence[offset=0,text='\n \n1.persistent pulmonary edema.',
infons=[],annotations=[],relations=[],],BioCSentence[offset=35,tex
t='2.unchanged right ... pleural effusion.',infons=[],annotations=
[],relations=[],],BioCSentence[offset=83,text='3.right mid to lo .
.. rsus atelectasis.',infons=[],annotations=[],relations=[],],BioC
Sentence[offset=145,text='attention on follow-up chest x-ray.',inf
ons=[],annotations=[],relations=[],],BioCSentence[offset=183,text=
'4.persistent cont ... ulled up stomach.',infons=[],annotations=[]
,relations=[],]],annotations=[],relations=[],]],annotations=[],rel
ations=[],],
BioCDocument[id=991,infons=[],passages=[BioCPassage[offset=0,text
='\n \n1. no evidenc ... drain.\n \n   \n \n \n',infons=[],senten
ces=[BioCSentence[offset=0,text='\n \n1. no evidenc ... t thoraci
c drain.',infons=[],annotations=[],relations=[],]],annotations=[],
relations=[],]],annotations=[],relations=[],],
BioCDocument[id=992,infons=[],passages=[BioCPassage[offset=0,text
=' \n \n1. there ha ... lower \nlobe. \n \n',infons=[],sentence
s=[BioCSentence[offset=0,text=' \n \n1. there ha ... ar outflow
tract.',infons=[],annotations=[],relations=[],],BioCSentence[offse
t=372,text='2. no pneumothor ... ed on \nthis film.',infons=[],an
notations=[],relations=[],],BioCSentence[offset=455,text='3. inte
rval elev ... ft hemidiaphragm.',infons=[],annotations=[],relation
s=[],],BioCSentence[offset=506,text='interval \ndevelop ... left l
ower \nlobe.',infons=[],annotations=[],relations=[],]],annotations
=[],relations=[],]],annotations=[],relations=[],],
BioCDocument[id=993,infons=[],passages=[BioCPassage[offset=0,text
=' \n \n1.new right i ... ary arteries. \n \n',infons=[],sentences

=[BioCSentence[offset=0,text=' \n \n1.new right i ... elow \nthe c
arina.',infons=[],annotations=[],relations=[],],BioCSentence[offse
t=88,text='no pneumothorax i ... s semierect film.',infons=[],anno
tations=[],relations=[],],BioCSentence[offset=138,text='2.slightly
improv ... ons or effusions.',infons=[],annotations=[],relations=[
],],BioCSentence[offset=226,text='3.stable prominen ... lmonary ar
teries.',infons=[],annotations=[],relations=[],]],annotations=[],r
elations=[],]],annotations=[],relations=[],],
 BioCDocument[id=994,infons=[],passages=[BioCPassage[offset=0,text
=' \n \n1.mild rightw ... cardiomegaly.\n \n',infons=[],sentences
=[BioCSentence[offset=0,text=' \n \n1.mild rightw ... t \non 10_29
_2010.',infons=[],annotations=[],relations=[],],BioCSentence[offse
t=157,text='2.mild pulmonary edema.',infons=[],annotations=[],rela
tions=[],],BioCSentence[offset=182,text='no focal consolidation.',
infons=[],annotations=[],relations=[],],BioCSentence[offset=208,te
xt='3.mild cardiomegaly.',infons=[],annotations=[],relations=[],]]
,annotations=[],relations=[],]],annotations=[],relations=[],],
 BioCDocument[id=995,infons=[],passages=[BioCPassage[offset=0,text
='\n \n1. unchanged ... al pneumothorax.\n',infons=[],sentences=
[BioCSentence[offset=0,text='\n \n1. unchanged ... cal pneumotho
rax.',infons=[],annotations=[],relations=[],]],annotations=[],rela
tions=[],]],annotations=[],relations=[],],
 BioCDocument[id=996,infons=[],passages=[BioCPassage[offset=0,text
='\n \n1.a single por ... , as before.\n \n \n',infons=[],sentence
s=[BioCSentence[offset=0,text='\n \n1.a single por ... est was obt
ained.',infons=[],annotations=[],relations=[],],BioCSentence[offse
t=71,text='the cardiomediast ... in lung volumes.',infons=[],anno
tations=[],relations=[],],BioCSentence[offset=188,text='there is \
nstable ... the aortic arch.',infons=[],annotations=[],relations
=[],],BioCSentence[offset=238,text='2.a tunneled righ ... nged in
position.',infons=[],annotations=[],relations=[],],BioCSentence[of
fset=309,text='median sternotomy ... are again noted.',infons=[],
annotations=[],relations=[],],BioCSentence[offset=402,text='3.inte
rval increa ... ia or aspiration.',infons=[],annotations=[],relati
ons=[],],BioCSentence[offset=519,text='recommend radiogr ... nsure
resolution.',infons=[],annotations=[],relations=[],],BioCSentence[
offset=586,text='4.interval increa ... pleural effusion.',infons=[
],annotations=[],relations=[],],BioCSentence[offset=656,text='5.no
acute osseous abnormality.',infons=[],annotations=[],relations=[],
],BioCSentence[offset=689,text='clips project ove ... egion, as be
fore.',infons=[],annotations=[],relations=[],]],annotations=[],rel
ations=[],]],annotations=[],relations=[],],
 BioCDocument[id=997,infons=[],passages=[BioCPassage[offset=0,text
='\n1. status post p ... al pneumothorax.\n',infons=[],sentences=[
BioCSentence[offset=0,text='\n1. status post p ... ual pneumothora
x.',infons=[],annotations=[],relations=[],]],annotations=[],relati
ons=[],]],annotations=[],relations=[],],
 BioCDocument[id=998,infons=[],passages=[BioCPassage[offset=0,text
='\n1. pulmonary ede ... ally\n indicated.\n',infons=[],sentences=
[BioCSentence[offset=0,text='\n1. pulmonary ede ... leural effusio
ns.',infons=[],annotations=[],relations=[],],BioCSentence[offset=5
9,text='2. cardiomegaly.',infons=[],annotations=[],relations=[],],
BioCSentence[offset=76,text='3. left retrocard ... or consolidatio

```
n.',infons=[],annotations=[],relations=[],],BioCSentence[offset=12
7,text='a pa and\n lateral ... cally\n indicated.',infons=[],annot
ations=[],relations=[],]],annotations=[],relations=[],]],annotatio
ns=[],relations=[],],
 BioCDocument[id=999,infons=[],passages=[BioCPassage[offset=0,text
='\n \n1.stable posit ... ace disease.\n \n \n',infons=[],sentence
s=[BioCSentence[offset=0,text='\n \n1.stable posit ...  venous cat
heter.',infons=[],annotations=[],relations=[],],BioCSentence[offse
t=64,text='2.improvement in lung volumes.',infons=[],annotations=[
],relations=[],],BioCSentence[offset=96,text='mild worsening of ..
. ir space disease.',infons=[],annotations=[],relations=[],]],anno
tations=[],relations=[],]],annotations=[],relations=[],]]
```

Interpreting the Documents

Now your `BioC` collection has been filled with documents, but the output is very hard to read. Let's break it down a little more.

In [6]:
```
len(collection.documents)
```

Out[6]:
```
1000
```

Looks like you have a document for each report impression. But what's stored inside each document? Let's check the first one.

In [7]:
```
collection.documents[0]
```

Out[7]:
```
BioCDocument[id=0,infons=[],passages=[BioCPassage[offset=0,text='\
n \n1.mild pulmona ... lation pads.  \n \n',infons=[],sentences=[B
ioCSentence[offset=0,text='\n \n1.mild pulmona ... and cardiomegal
y.',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=[],],BioCSen
tence[offset=135,text='3.no new focal consolidation.',infons=[],an
notations=[],relations=[],],BioCSentence[offset=168,text='4.interv
al placem ... ibrillation pads.',infons=[],annotations=[],relation
s=[],]],annotations=[],relations=[],]],annotations=[],relations=[]
,]
```

Each document has an attribute called "passages" in which the sentences are stored. Notice that `passages` is a list, but for this case it will only have one element:

In [8]:
```
collection.documents[0].passages[0].sentences
```

Out[8]:
```
[BioCSentence[offset=0,text='\n \n1.mild pulmona ... and cardiomeg
aly.',infons=[],annotations=[],relations=[],],
 BioCSentence[offset=46,text='trace pleural fluid \neffusions.',in
fons=[],annotations=[],relations=[],],
 BioCSentence[offset=80,text='2.low lung volume ... ilar atelectas
is.',infons=[],annotations=[],relations=[],],
 BioCSentence[offset=135,text='3.no new focal consolidation.',info
ns=[],annotations=[],relations=[],],
 BioCSentence[offset=168,text='4.interval placem ... ibrillation p
ads.',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:

In [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.low lung volumes with minimal basilar atelect
asis.

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

sentence number 4: 3.no new focal consolidation.

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

sentence number 5: 4.interval placement of defibrillation pads.

################################
```

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!

In [10]:
```
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
', 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
```

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:

In [11]:
```
CATEGORIES = ["Cardiomegaly", "Lung Lesion", "Airspace Opacity", "E
dema",
              "Consolidation", "Pneumonia", "Atelectasis", "Pneumot
horax",
              "Pleural Effusion", "Pleural Other", "Fracture"]
```

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.

In [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, Lemmatiz
er

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.t
xt'
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
```

In [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|norm
al/}
{} < {} ({} > {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/}) < {depend
ency:/dobj|nsubj/} {lemma:/demonstrate.*|show|present|display/}
{} < {dependency:/nmod:of/} ( {lemma:/appearance/} > {dependency:/
amod/} {lemma:/normal/} & < {dependency:/dobj/} {lemma:/demonstrat
e.*|show|present|display/})

{} < {dependency:/amod/} ({} < {dependency:/dep|nsubj/} {lemma:/no
rmal|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|u
nremarkable/}))

{} < {dependency:/compound/} ({} > {dependency:/neg/} {})
{} < {dependency:/nsubj/} {lemma:/absent/}
{} < {dependency:/amod/} ({} < {dependency:/nmod:of/} ({lemma:/evi
dence/} > {dependency:/case/} {lemma:/without/}))
{} < {dependency:/amod/} ({} < {dependency:/nmod:of/} ({lemma:/evi
dence/} > {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/} & > {dependen
cy:/case/} {lemma:/at|within/}))
{} < {} ({} < {dependency:/nsubj/} ({lemma:/limit.*/} > {dependenc
y:/amod/} {lemma:/normal/} & > {dependency:/case/} {lemma:/at|with
in/}))
({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/} {}
{} <{dependency:/nmod:without/} {}

{} <{dependency:/nmod:without|nmod:of/} {lemma:/clear|clearing/}=k
ey
{} <{dependency:/nmod:out/} {lemma:/rule/}=key

# removal of XXX
{} <{dependency:/nmod:of/} {lemma:/history|free|disappearance|reso
lution|drainage|resolution|removal/}
{} <{dependency:/nmod:for/} {lemma:/negative/}

# exclude XXX
{} <{} {lemma:/exclude/}

{} <{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:/wi
thout/})

# No development of XXX
{} < {dependency:/nmod:of/} ({lemma:/development/} > {} {lemma:/no
/})

# no evidence of|for XXX
{} <{dependency:/nmod:of|nmod:for/} ({lemma:/evidence/} >{dependen
cy:/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/} <{dependency:
/nmod:without/} {}))
{} <{} ({lemma:/developing/} <{} ({lemma:/evidence/} >{} {lemma:/n
o/}))

# 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.*/} > {} {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:/compoun
d/} {lemma:/no/})

# XXX is not enlarged
{} < {dependency:/nsubjpass/} ({lemma:/enlarge/} > {dependency:/ne
g/} {})

# 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/} > {} ({} > {dependenc
y:/neg/} {lemma:/no/}))
{} < {dependency:/nsubjpass/} ({lemma:/see/} > {} {lemma:/no/})

# without evidence seen for XXX
{} < {} ({lemma:/see/} > {} ({} > {} ({lemma:/evidence/} > {} {lem
ma:/without/})))
{} < {} ({lemma:/see/} > {} ({lemma:/evidence/} > {} {lemma:/witho
ut/}))

# 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/}

# XXX has/have cleared
# cleared XXX
{} < {} {lemma:/clear/}
{} > {} {lemma:/clear/}

# no obvious associated XXX
{} < {} ({lemma:/associate.*/} > {} ({lemma:/obvious/} > {dependen
cy:/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.

In [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.

In [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.

In [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 (https://nlp.stanford.edu/IR-book/html/htmledition/stemming-and-lemmatization-1.html).

In [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 (https://github.com/dmcc/PyStanfordDependencies).

The parse tree used here is the Penn Treebank (https://catalog.ldc.upenn.edu/docs/LDC95T7/cl93.html). 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 (https://universaldependencies.org/).

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

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

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

Now you'll instantiate the parser and the loader.

Under the hood, you're using the BLIPP reranking parser (https://github.com/BLLIP/bllip-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 (https://github.com/stanfordmlgroup/chexpert-labeler) is used. This labeler extracts observations from radiology reports specifically, and can provide a vocabulary appropriate to the clinical context.

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

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

In [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.

In [22]:
```
neg_detector = ModifiedDetector(PRE_NEG_PATH, NEG_PATH, POST_NEG_PA
TH)
```

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

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

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:

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

```
100%|██████████| 50/50 [01:01<00:00,  1.23s/it]
```

In [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)
```

In [26]:
```
negbio_pred.head()
```

Out[26]:

	Edema	Lung Lesion	Pleural Effusion	Pneumothorax	Pneumonia	Consolidation	Airspace Opacity	Atelectas
0	True	True	True	True	False	False	False	Fal
1	False	False	False	False	True	False	False	Fal
2	False	False	False	False	True	True	False	Fal
3	False	False	False	True	False	False	True	Fal
4	False	False	False	False	False	True	False	Fal

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!**