# Research

September 27, 2018

# 1 Competition research

```
In [1]: import pandas as pd
        import numpy as np
        import matplotlib.pyplot as plot
        import pylab
        /matplotlib inline
```

## 1.1 Background

#### 1.1.1 Goal

- Detect visual signals of pneumonia.
- Need to automatically locate lung opacities on chest radiographs.

#### 1.1.2 Evaluation metric

Mean average precision at different intersection over union thresholds. The metric sweeps over a range of *IoU* thresholds (namely 0.4 to 0.75 in increments of 0.05), at each point calculating an average precision value.

To understand this, we need to know these things:

- What is Intersection over Union?
- What is precision?
- What is the average precision value?

What is intersection over union? *IoU* is defined as:

$$IoU(A,B) = \frac{A \cap B}{A \cup B}$$

This mearsures the extent of overlap between the ground-truth bounding box and the predicted bounding box as a proportion of the total area covered by the two bounding boxes.

**An example** Here, the ground-truth bounding box is created manually by a human. The predicted bounding box is the algorithm's prediction of where the object is.

**What is precision?** Precision is the percentage of your positive predictions that are correct. It is defined as:

$$Precision = \frac{TP}{TP + FP}$$

Related to precision is recall, which is a measure of how well your model classifies positive values given all positive values:

$$Recall = \frac{TP}{TP + FN}$$

**What is precision in the context of this competition?** At each threshold value *t*, a precision value is calculated based on the number of true positives, false positives and false negatives:

$$\frac{TP(t)}{TP(t) + FP(t) + FN(t)}$$

When is a true positive counted in the above precision value?

TP(t) = single predicted bounding box matches ground truth bounding box with an IoU above threshold, t When is a false positive counted in the above precision value?

FP(t) =single predicted bounding box has no associated ground truth bounding box

When is a false negative counted in the above precision value?

FN(t) = no predicted bounding box when there is a ground truth bounding box

What happens if there are no ground truth objects for an image, but we predict that there is a bounding box? The image will receive a score of zero.

What is mean precision?

**Per image** Mean precision for a single image is calculated as the mean of the precision values at each *IoU* threshold:

$$\frac{1}{|\textit{thresholds}|} \sum_{t} \frac{TP(t)}{TP(t) + FP(t) + FN(t)}$$

Across all images

The final score is the mean of the per image mean precision values.

#### 1.2 Submission file

Space delimited set of bounding boxes, in the format:

<image\_name>, <confidence>, <x>, <y>, <width>, <height>
where:

- confidence = some confidence level of the bounding box. Apparently it's used to break ties to determine the order in which bounding boxes are evaluated by the evaluation metric. We can hardcode with 1.0 for all to make our lives easier because it is rarely used.
- x = x coordinate of the upper left hand corner
- y = y coordinate of the upper left hand corner

- width = width in pixels from the coordinate (x, y)
- height = height in pixels from the coordinate (x, y)

Each row should contain all bounding boxes for a given image. E.g.

```
00322d4d-1c29-4943-afc9-b6754be640eb,0.8 10 10 50 50 0.75 100 100 5 5
```

contains 2 bounding boxes - one with a confidence of 0.8, and another with a confidence of 0.75.

### 1.2.1 Competition data

- DICOM images
- stage\_1\_train\_labels.csv
- stage\_1\_detailed\_class\_info.csv

**DICOM images** DICOM is a format used to store medical images. They contain metadata (e.g. patient information, date taken) and pixel arrays.

**stage\_1\_train\_labels.csv** This file contains the ground-truth bounding boxes.

**stage\_1\_detailed\_class\_info.csv** Contains further detail on patient images, split into three categories:

- Normal
- Lung Opacity
- No Lung Opacity / Not Normal

### **DICOM** images

**pydicom - working with DICOM files** We can use the pydicom package to read DICOM metadata and pixel arrays. We can use matplotlib to render the images themselves.

```
In [2]: import pydicom
```

A pneumonia example

To read in the penumonia DICOM file, we can use read\_file().

```
In [3]: dcm_pneumonia = pydicom.read_file('pneumonia.dcm')
```

Let's take a look at the metadata.

```
In [4]: print(dcm_pneumonia, 2)
```

```
(0008, 0005) Specific Character Set
(0008, 0016) SOP Class UID
UI: Secondary Capture Image Storage
(0008, 0018) SOP Instance UID
UI: 1.2.276.0.7230010.3.1.4.8323329.6379.15179
(0008, 0020) Study Date
DA: '19010101'
(0008, 0030) Study Time
TM: '000000.00'
```

```
(0008, 0050) Accession Number
                                                  SH: ''
(0008, 0060) Modality
                                                  CS: 'CR'
(0008, 0064) Conversion Type
                                                  CS: 'WSD'
(0008, 0090) Referring Physician's Name
                                                  PN: ''
(0008, 103e) Series Description
                                                  LO: 'view: AP'
(0010, 0010) Patient's Name
                                                  PN: '00436515-870c-4b36-a041-de91049b9ab4'
(0010, 0020) Patient ID
                                                  LO: '00436515-870c-4b36-a041-de91049b9ab4'
(0010, 0030) Patient's Birth Date
                                                  DA: ''
(0010, 0040) Patient's Sex
                                                  CS: 'F'
(0010, 1010) Patient's Age
                                                  AS: '32'
                                                  CS: 'CHEST'
(0018, 0015) Body Part Examined
(0018, 5101) View Position
                                                  CS: 'AP'
(0020, 000d) Study Instance UID
                                                  UI: 1.2.276.0.7230010.3.1.2.8323329.6379.1517
(0020, 000e) Series Instance UID
                                                  UI: 1.2.276.0.7230010.3.1.3.8323329.6379.1517
(0020, 0010) Study ID
                                                  SH: ''
(0020, 0011) Series Number
                                                  IS: '1'
(0020, 0013) Instance Number
                                                  IS: '1'
                                                  CS: ''
(0020, 0020) Patient Orientation
(0028, 0002) Samples per Pixel
                                                  US: 1
(0028, 0004) Photometric Interpretation
                                                  CS: 'MONOCHROME2'
(0028, 0010) Rows
                                                  US: 1024
(0028, 0011) Columns
                                                  US: 1024
(0028, 0030) Pixel Spacing
                                                  DS: ['0.139', '0.139']
(0028, 0100) Bits Allocated
                                                  US: 8
(0028, 0101) Bits Stored
                                                  US: 8
(0028, 0102) High Bit
                                                  US: 7
(0028, 0103) Pixel Representation
                                                  US: 0
(0028, 2110) Lossy Image Compression
                                                  CS: '01'
                                                  CS: 'ISO_10918_1'
(0028, 2114) Lossy Image Compression Method
(7fe0, 0010) Pixel Data
                                                  OB: Array of 119382 bytes 2
In [5]: dir(dcm_pneumonia)
Out[5]: ['AccessionNumber',
         'BitsAllocated',
         'BitsStored',
         'BodyPartExamined',
         'Columns',
         'ConversionType',
         'HighBit',
         'InstanceNumber',
         'LossyImageCompression',
         'LossyImageCompressionMethod',
         'Modality',
         'PatientAge',
         'PatientBirthDate',
```

'PatientID',

```
'PatientName',
'PatientOrientation',
'PatientSex',
'PhotometricInterpretation',
'PixelData',
'PixelRepresentation',
'PixelSpacing',
'ReferringPhysicianName',
'Rows',
'SOPClassUID',
'SOPInstanceUID',
'SamplesPerPixel',
'SeriesDescription',
'SeriesInstanceUID',
'SeriesNumber',
'SpecificCharacterSet',
'StudyDate',
'StudyID',
'StudyInstanceUID',
'StudyTime',
'ViewPosition',
'__contains__',
'__delattr__',
'__delitem__',
'__dir__',
'__enter__',
'__eq__',
'__exit__',
'__format__',
'__ge__',
'__getattr__',
'__getattribute__',
'__getitem__',
'__gt__',
'__init__',
'__init_subclass__',
'__iter__',
'__le__',
'__len__',
__
'__lt__',
'__ne__',
'__new__',
__reduce__',
'__reduce_ex__',
'__repr__',
'__setattr__',
'__setitem__',
'__sizeof__',
```

```
'__str__',
'__subclasshook__',
'__weakref__',
'_character_set',
'_convert_YBR_to_RGB',
'_dataset_slice',
'_get_pixel_array',
'_is_uncompressed_transfer_syntax',
'_pretty_str',
'_reshape_pixel_array',
'_slice_dataset',
'add',
'add_new',
'clear',
'convert_pixel_data',
'copy',
'data_element',
'decode',
'decompress',
'dir',
'elements',
'formatted_lines',
'fromkeys',
'get',
'get_item',
'group_dataset',
'is_original_encoding',
'items',
'iterall',
'keys',
'pixel_array',
'pop',
'popitem',
'remove_private_tags',
'save_as',
'setdefault',
'top',
'trait_names',
'update',
'values',
'walk']
```

Here we extract the pixel arrays by referring to the pixel\_array property of the object.

```
[0 1 2 ..., 3 3 3]
...,
[1 3 4 ..., 7 7 7]
[0 2 3 ..., 5 5 5]
[0 0 1 ..., 0 0 0]]
```

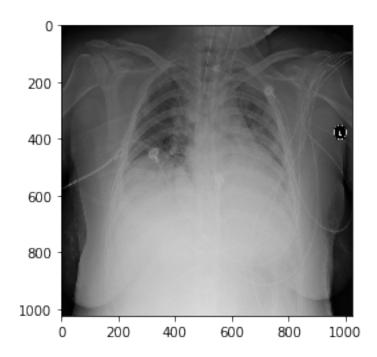
We can get the dimensions of the image by using the shape method.

```
In [7]: print(pneumonia_image.shape)
(1024, 1024)
```

To plot the image, we use matplotlib.pyplot.imshow().

In [8]: plot.imshow(pneumonia\_image, cmap = pylab.cm.gist\_gray)

Out[8]: <matplotlib.image.AxesImage at 0x195649c3160>



## A non-pneumonia example

Out[9]: <matplotlib.image.AxesImage at 0x19564ba4cc0>



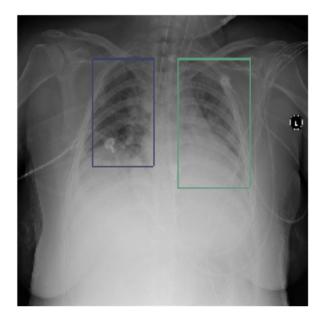
Visualising bounding boxes We will read the labelled training data csv into a pandas dataframe.

```
In [11]: train_labels = pd.read_csv('../input/stage_1_train_labels.csv')
In [12]: print(train_labels.columns)
Index(['patientId', 'x', 'y', 'width', 'height', 'Target'], dtype='object')
```

Let's use the parse\_data() from the starter kernel to parse the csv file of labels into a nested dictionary.

```
'label': either 0 or 1 for normal or pnuemonia,
                      'boxes': list of box(es)
                 }, ...
               }
             # --- Define lambda to extract coords in list [y,\ x,\ height,\ width]
             extract_box = lambda row: [row['y'], row['x'], row['height'], row['width']]
             parsed = {}
             for n, row in df.iterrows():
                 # --- Initialize patient entry into parsed
                 pid = row['patientId']
                 if pid not in parsed:
                     parsed[pid] = {
                          'dicom': '../input/stage_1_train_images/%s.dcm' % pid,
                          'label': row['Target'],
                          'boxes': []}
                 # --- Add box if opacity is present
                 if parsed[pid]['label'] == 1:
                     parsed[pid]['boxes'].append(extract_box(row))
             return parsed
In [14]: train_labels_dict = parse_data(train_labels)
   Here, we find a patient who has pneumonia. Note the two bounding boxes.
In [15]: print(train_labels_dict['00436515-870c-4b36-a041-de91049b9ab4'])
{'dicom': '../input/stage_1_train_images/00436515-870c-4b36-a041-de91049b9ab4.dcm', 'label': 1
   To draw the bounding boxes for this patient, we will use the functions provided in the starter
kernel.
In [16]: def draw(data):
             Method to draw single patient with bounding box(es) if present
             11 11 11
             # --- Open DICOM file
             d = pydicom.read_file(data['dicom'])
             im = d.pixel_array
             # --- Convert from single-channel grayscale to 3-channel RGB
             im = np.stack([im] * 3, axis=2)
```

```
# --- Add boxes with random color if present
             for box in data['boxes']:
                 rgb = np.floor(np.random.rand(3) * 256).astype('int')
                 im = overlay_box(im=im, box=box, rgb=rgb, stroke=6)
             pylab.imshow(im, cmap=pylab.cm.gist_gray)
             pylab.axis('off')
         def overlay_box(im, box, rgb, stroke=1):
             Method to overlay single box on image
             # --- Convert coordinates to integers
             box = [int(b) for b in box]
             # --- Extract coordinates
             y1, x1, height, width = box
             y2 = y1 + height
             x2 = x1 + width
             im[y1:y1 + stroke, x1:x2] = rgb
             im[y2:y2 + stroke, x1:x2] = rgb
             im[y1:y2, x1:x1 + stroke] = rgb
             im[y1:y2, x2:x2 + stroke] = rgb
             return im
In [17]: draw(train_labels_dict['00436515-870c-4b36-a041-de91049b9ab4'])
```



**stage\_1\_detailed\_class\_info.csv** This file contains further information on the images. 3 classes are provided:

- Normal
- Lung Opacity
- No Lung Opacity / Not Normal

The third class (No Lung Opacity / Not Normal) indicates that pneumonia wasn't present, but some image abnormality was detected. These abnormalities may mimic the appearance of pneumonia. This information can be used to help improve the accuracy of our algorithms.

Let's take a look at an example of this third class.

In [18]: draw(train\_labels\_dict['0004cfab-14fd-4e49-80ba-63a80b6bddd6'])



1.3 Conclusion

Let's do it!