RSNA-Intracranial-Hemorrhage-Detection

Repo for RSNA Intracranial Hemorrhage Detection

Intracranial Hemorrhage Detection

This blog post is about the challenge that is hosted on kaggle on RSNA Intracranial Hemorrhage Detection.

This post is divided into following parts

1. Overview
2. Basic EDA Ipython Notebook
3. Data Visualization & Preprocessing
4. Deep Learning Model

1. Overview

What is Intracranial Hemorrhage?

An intracranial hemorrhage is a type of bleeding that occurs inside the skull. Symptoms include sudden tingling, weakness, numbness, paralysis, severe headache, difficulty with swallowing or vision, loss of balance or coordination, difficulty understanding, speaking , reading, or writing, and a change in level of consciousness or alertness, marked by stupor, lethargy, sleepiness, or coma. Any type of bleeding inside the skull or brain is a medical emergency. It is important to get the person to a hospital emergency room immediately to determine the cause of the bleeding and begin medical treatment. It rquires highly trained specialists review medical images of the patient's cranium to look for the presence, location and type of hemorrhage. The process is complicated and often time consuming. So as part of this we will be deep learning techniques to detect acute intracranial hemorrhage and its subtypes.

Hemorrhage Types

1. Epidural
2. Intraparenchymal
3. Intraventricular
4. Subarachnoid
5. Subdural
6. Any

What am i predicting?

In this competition our goal is to predict intracranial hemorrhage and its subtypes. Given an image the we need to predict probablity of each subtype. This indicates its a multilabel classification problem.

2. Basic EDA

Lets look at the data that is provided.

We have a train.csv containing file names and label indicating whether hemorrhage is present or not and train images folder which is set of Dicom files (Medical images are stored in dicom formats) and test images folder containing test dicom files.

```
# load the csv file
train_df = pd.read_csv(input_folder + 'stage_1_train.csv')
train_df.head()
```

	ID	Label
0	ID_63eb1e259_epidural	0
1	ID_63eb1e259_intraparenchymal	0
2	ID_63eb1e259_intraventricular	0
3	ID_63eb1e259_subarachnoid	0
4	ID_63eb1e259_subdural	0

It consists of two columns ID and Label. ID has a format FILE_ID_SUB_TYPE for example ID_63eb1e259_epidural so ID_63eb1e259 is file id and epidural is subtype and Label indicating whether subtype hemorrhage is present or not.

Lets seperate file names and subtypes

```
# extract subtype
train_df['sub_type'] = train_df['ID'].apply(lambda x: x.split('_')[-1])
# extract filename
train_df['file_name'] = train_df['ID'].apply(lambda x: '_'.join(x.split('_')[:2]) + '.dcm')
train_df.head()
```

	ID	Label	sub_type	file_name
0	ID_63eb1e259_epidural	0	epidural	ID_63eb1e259.dcm
1	ID_63eb1e259_intraparenchymal	0	intraparenchymal	ID_63eb1e259.dcm
2	ID_63eb1e259_intraventricular	0	intraventricular	ID_63eb1e259.dcm
3	ID_63eb1e259_subarachnoid	0	subarachnoid	ID_63eb1e259.dcm
4	ID_63eb1e259_subdural	0	subdural	ID_63eb1e259.dcm

```
train_df.shape
```

Output : (4045572, 4)

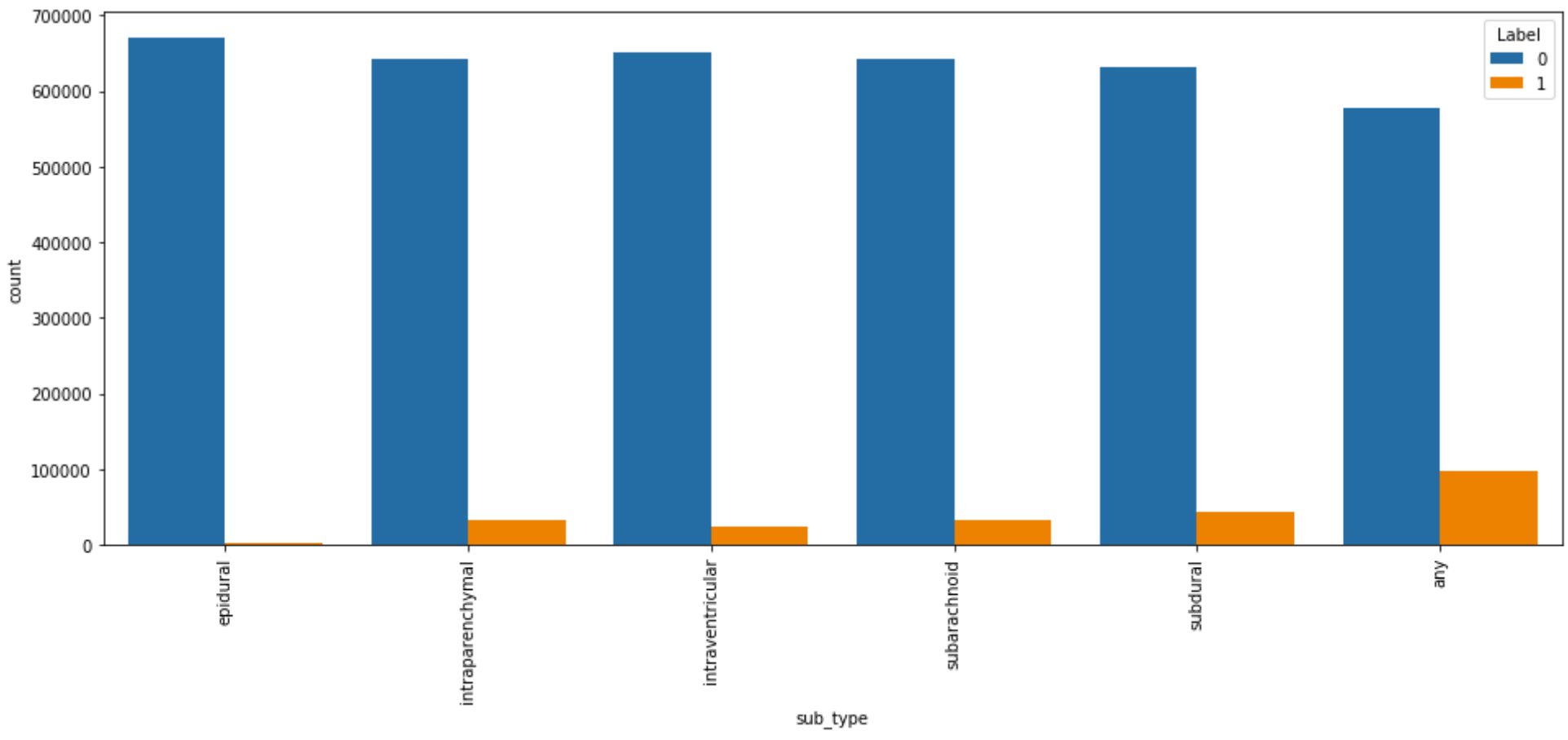
```
print("Number of train images availabe:", len(os.listdir(path_train_img)))
```

Output : Number of train images availabe: 674258

The csv file has a shape of (4045572, 4). For every file(dicom file) present in the train folder has 6 entries in csv indicating possible 6 subtype hemorrhages.

Lets check the files available for each subtype

```
plt.figure(figsize=(16, 6))
graph = sns.countplot(x="sub_type", hue="Label", data=(train_df))
graph.set_xticklabels(graph.get_xticklabels(),rotation=90)
plt.show()
```



Lets check the counts for each subtype

Epidural

```
train_df[train_df['sub_type'] == 'epidural']['Label'].value_counts()
```

Output:

0 671501

1 2761

Name: Label, dtype: int64

For epidural sub type we have 6,71,501 images labeled as 0 and 2,761 labelled as 1.

Intraparenchymal

```
train_df[train_df['sub_type'] == 'intraparenchymal']['Label'].value_counts()
```

Output:
0 641698
1 32564
Name: Label, dtype: int64

For intraparenchymal sub type we have 6,41,698 images labeled as 0 and 32,564 labelled as 1.

Intraparenchymal

```
train_df[train_df['sub_type'] == 'intraparenchymal']['Label'].value_counts()
```

Output:
0 650496
1 23766
Name: Label, dtype: int64

For intraparenchymal sub type we have 6,50,496 images labeled as 0 and 23,766 labelled as 1.

Subarachnoid

```
train_df[train_df['sub_type'] == 'subarachnoid']['Label'].value_counts()
```

Output:
0 642140
1 32122
Name: Label, dtype: int64

For subarachnoid sub type we have 6,42,140 images labeled as 0 and 32,122 labelled as 1.

Subdural

```
train_df[train_df['sub_type'] == 'subdural']['Label'].value_counts()
```

Output:
0 631766
1 42496
Name: Label, dtype: int64

For Subdural sub type we have 6,31,766 images labeled as 0 and 42,496 labelled as 1.

Any

```
train_df[train_df['sub_type'] == 'any']['Label'].value_counts()
```

Output:
0 577159
1 97103
Name: Label, dtype: int64

For any sub type we have 5,77,159 images labeled as 0 and 97,103 labelled as 1.

3. Data Visualization & Preprocessing

Lets look at the dicom files in the dataset

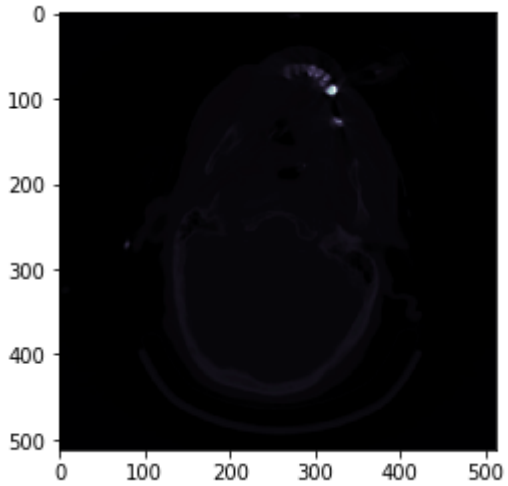
```
dicom = pydicom.read_file(path_train_img + 'ID_ffff922b9.dcm')
print(dicom)
```

```
(0008, 0018) SOP Instance UID                    UI: ID_ffff922b9
(0008, 0060) Modality                            CS: 'CT'
(0010, 0020) Patient ID                          LO: 'ID_5964c5e5'
(0020, 000d) Study Instance UID                  UI: ID_b47ca0ad05
(0020, 000e) Series Instance UID                 UI: ID_6d2a9b2810
(0020, 0010) Study ID                            SH: ''
(0020, 0032) Image Position (Patient)            DS: ['-126.408875', '-126.40887
5', '-235.611511']
(0020, 0037) Image Orientation (Patient)         DS: ['1.000000', '0.000000', '0.
000000', '0.000000', '1.000000', '0.000000']
(0028, 0002) Samples per Pixel                   US: 1
(0028, 0004) Photometric Interpretation          CS: 'MONOCHROME2'
(0028, 0010) Rows                                US: 512
(0028, 0011) Columns                             US: 512
(0028, 0030) Pixel Spacing                       DS: ['0.494750976563', '0.494750
976563']
(0028, 0100) Bits Allocated                      US: 16
(0028, 0101) Bits Stored                         US: 16
(0028, 0102) High Bit                            US: 15
(0028, 0103) Pixel Representation                US: 1
(0028, 1050) Window Center                       DS: "35.000000"
(0028, 1051) Window Width                        DS: "135.000000"
(0028, 1052) Rescale Intercept                   DS: "-1024.000000"
(0028, 1053) Rescale Slope                       DS: "1.000000"
(7fe0, 0010) Pixel Data                          OW: Array of 524288 elements
```

Dicom data format files contain pixel data of image and other meta data like patient name, instance id, window width etc...

Original image

```
plt.imshow(dicom.pixel_array, cmap=plt.cm.bone)
plt.show()
```

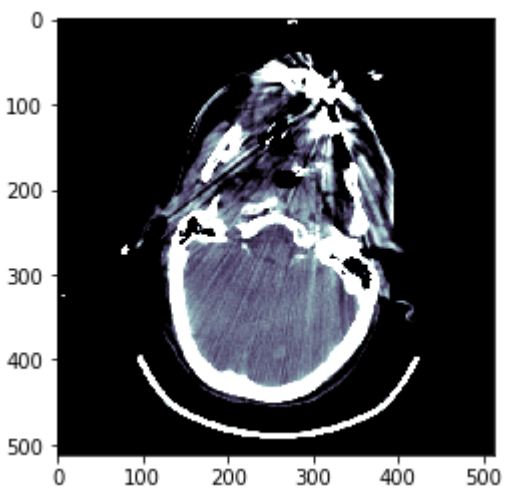


The orginal image seems to have difficult to understand, lets check meta deta features like Window Center, Window Width, Rescale Intercept, Rescale Slope

```
(0028, 1050) Window Center                       DS: "35.000000"
(0028, 1051) Window Width                        DS: "135.000000"
(0028, 1052) Rescale Intercept                   DS: "-1024.000000"
(0028, 1053) Rescale Slope                       DS: "1.000000"
```

We can use these features to construct the new image.

```
def get_dicom_field_value(key, dicom):
    """
    @param key: key is tuple
    @param dicom: dicom file
    """
    return dicom[key].value

window_center = int(get_dicom_field_value(('0028', '1050'), dicom))
window_width = int(get_dicom_field_value(('0028', '1051'), dicom))
window_intercept = int(get_dicom_field_value(('0028', '1052'), dicom))
window_slope = int(get_dicom_field_value(('0028', '1053'), dicom))
window_center, window_width, window_intercept, window_slope

def get_windowed_image(image, wc,ww, intercept, slope):
    img = (image*slope +intercept)
    img_min = wc - ww//2
    img_max = wc + ww//2
    img[img<img_min] = img_min
    img[img>img_max] = img_max
    return img

windowed_image = get_windowed_image(dicom.pixel_array, window_center, window_width, \
                                    window_intercept, window_slope)

plt.imshow(windowed_image, cmap=plt.cm.bone)
plt.show()
```

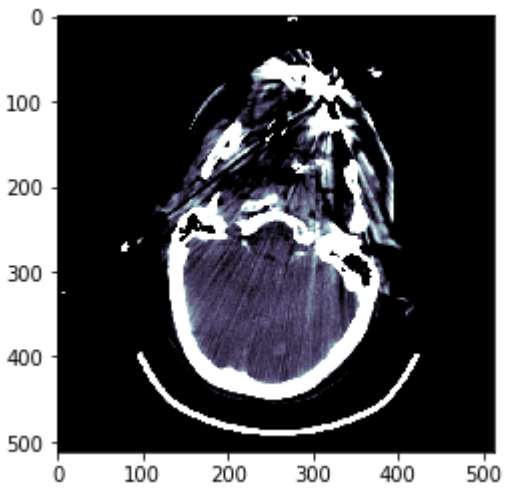


The windowed image using meta data is much better than the orginal image this is because the dicom pixel array which contain pixel data contain raw data in Hounsfield units (HU).

Scaling the image:

Rescale the image to range 0-255.

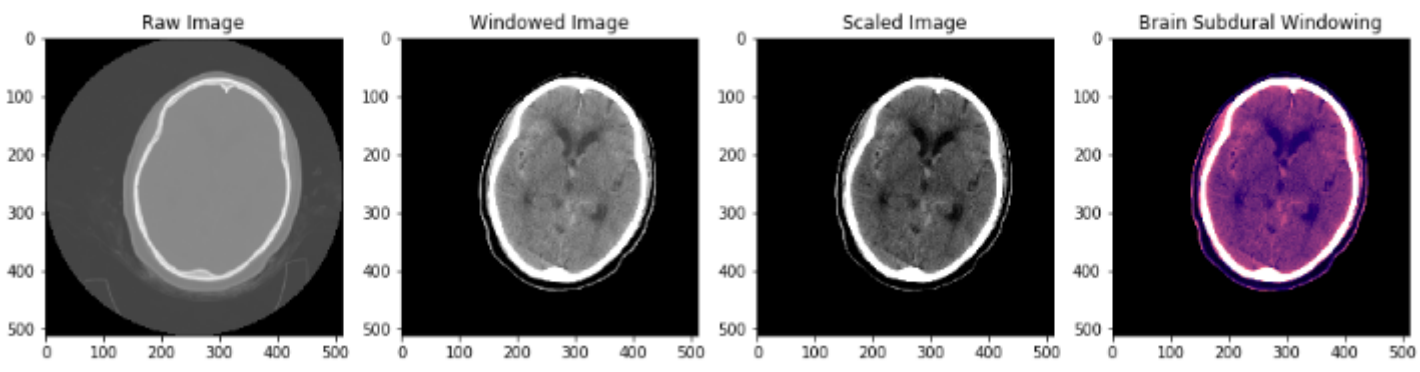
```
def get_scaled_windowed_image(img):
    """
    Get scaled image
    1. Convert to float
    2. Rescale to 0-255
    3. Convert to unit8
    """
    img_2d = img.astype(float)
    img_2d_scaled = (np.maximum(img_2d,0) / img_2d.max()) * 255.0
    img_2d_scaled = np.uint8(img_2d_scaled)
    return img_2d_scaled

scaled_image = get_scaled_windowed_image(windowed_image)
plt.imshow(scaled_image, cmap=plt.cm.bone, vmin=0, vmax=255)
plt.show()
```



Hounsfield Units (HU) are the best source for constructing CT images. Here is detailed table showing the substance and HU range.

A detailed explanation of all the possible windowing techniques can be found in this great kernel (Gradient Sigmoid Windowing)

```
def correct_dcm(dcm):
    # Refer Jeremy Howard's Kernel https://www.kaggle.com/jhoward/from-prototyping-to-submission-fastai
    x = dcm.pixel_array + 1000
    px_mode = 4096
    x[x>=px_mode] = x[x>=px_mode] - px_mode
    dcm.PixelData = x.tobytes()
    dcm.RescaleIntercept = -1000

def window_image(dcm, window_center, window_width):

    if (dcm.BitsStored == 12) and (dcm.PixelRepresentation == 0) and (int(dcm.RescaleIntercept) > -100):
        correct_dcm(dcm)

    img = dcm.pixel_array * dcm.RescaleSlope + dcm.RescaleIntercept
    img_min = window_center - window_width // 2
    img_max = window_center + window_width // 2
    img = np.clip(img, img_min, img_max)

    return img

def bsb_window(dcm):
    brain_img = window_image(dcm, 40, 80)
    subdural_img = window_image(dcm, 80, 200)
    soft_img = window_image(dcm, 40, 380)

    brain_img = (brain_img - 0) / 80
    subdural_img = (subdural_img - (-20)) / 200
    soft_img = (soft_img - (-150)) / 380
    bsb_img = np.array([brain_img, subdural_img, soft_img]).transpose(1,2,0)

    return bsb_img

display_dicom_image('ID_0005d340e.dcm')
```



It looks like Brain + Subdural is a good start for our models it has three chaneels and cab be easily fed to any pretrained models.

4. Deep Learning Model

The whole code for the training of the model can be found here

We will using normal windowed images for training the model with augmentations like flip left right and random cropping.

Here are steps for training the model

1. Prepare train and validation data generators we will be splitting the data by stratifying the labels here id the link to multilabel stratification. We will make two splits and onlt work on the first split and check the results.
2. Load pretrained Efficient Net B0 model.
3. For the first epoch use all the train images for training the model with the first head layers using as it as is by setting trainable as False but train all the later images and save the model.
4. Load the saved model and for the further epochs we train whole model except the last layer thus our model will learn most compliated features.
5. Make predictions.

Sample code:

```
# 1. ---------prepare data generators------------#
# https://github.com/trent-b/iterative-stratification
# Mutlilabel stratification
splits = MultilabelStratifiedShuffleSplit(n_splits = 2, test_size = TEST_SIZE, random_state = SEED)
file_names = train_final_df.index
labels = train_final_df.values
# Lets take only the first split
split = next(splits.split(file_names, labels))
train_idx = split[0]
valid_idx = split[1]
submission_predictions = []
len(train_idx), len(valid_idx)
# train data generator
data_generator_train = TrainDataGenerator(train_final_df.iloc[train_idx],
                                          train_final_df.iloc[train_idx],
                                          TRAIN_BATCH_SIZE,
                                          (WIDTH, HEIGHT),
                                          augment = True)

# validation data generator
data_generator_val = TrainDataGenerator(train_final_df.iloc[valid_idx],
                                        train_final_df.iloc[valid_idx],
                                        VALID_BATCH_SIZE,
                                        (WIDTH, HEIGHT),
                                        augment = False)
# 2. ---------load efficient net B0 model-----------#
base_model =  efn.EfficientNetB0(weights = 'imagenet', include_top = False, \
                                 pooling = 'avg', input_shape = (HEIGHT, WIDTH, 3))
x = base_model.output
x = Dropout(0.125)(x)
output_layer = Dense(6, activation = 'sigmoid')(x)
model = Model(inputs=base_model.input, outputs=output_layer)
model.compile(optimizer = Adam(learning_rate = 0.0001),
                  loss = 'binary_crossentropy',
                  metrics = ['acc', tf.keras.metrics.AUC()])
model.summary()

# 3. ---------for 1 st epoch train on whole dataset ------------#
for layer in model.layers[:-5]:
    layer.trainable = False

model.compile(optimizer = Adam(learning_rate = 0.0001),
                  loss = 'binary_crossentropy',
                  metrics = ['acc'])

model.fit_generator(generator = data_generator_train,
                        validation_data = data_generator_val,
                        epochs = 1,
                        callbacks = callbacks_list,
                        verbose = 1)

# 4. ---------for rest of epochs train on sample data----------#
model.load_weights('model.h5')
model.compile(optimizer = Adam(learning_rate = 0.0004),
                  loss = 'binary_crossentropy',
                  metrics = ['acc'])
model.fit_generator(generator = data_generator_train,
                        validation_data = data_generator_val,
                        steps_per_epoch=len(data_generator_train)/6,
                        epochs = 10,
```

```
                        callbacks = callbacks_list,
                        verbose = 1)
# 5. --------Make Predictions ------- -------------------------#
model.load_weights('model.h5')

preds = model.predict_generator(TestDataGenerator(test_df.index, None, VALID_BATCH_SIZE, \
                                                   (WIDTH, HEIGHT), path_test_img),
                                verbose=1)
```

All notebooks can be found here

References

https://my.clevelandclinic.org/health/diseases/14480-intracranial-hemorrhage-cerebral-hemorrhage-and-hemorrhagic-stroke
https://github.com/MGH-LMIC/windows_optimization
https://arxiv.org/abs/1812.00572(Must read) https://www.kaggle.com/c/rsna-intracranial-hemorrhage-detection/discussion/111325#latest-650043 https://www.kaggle.com/c/rsna-intracranial-hemorrhage-detection/discussion/109261#latest-651855

Kaggle Kernels

https://www.kaggle.com/jhoward/some-dicom-gotchas-to-be-aware-of-fastai https://www.kaggle.com/reppic/gradient-sigmoid-windowing
https://www.kaggle.com/jhoward/from-prototyping-to-submission-fastai https://www.kaggle.com/suryaparsa/rsna-basic-eda-part-1
https://www.kaggle.com/suryaparsa/rsna-basic-eda-part-2
