PNEUMONIA AND LUNG OPACITY CLASSIFICATION

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Pneumonia Opacity Classification

RSNA PNEUMONIA DETECTION CHALLENGE DATASET



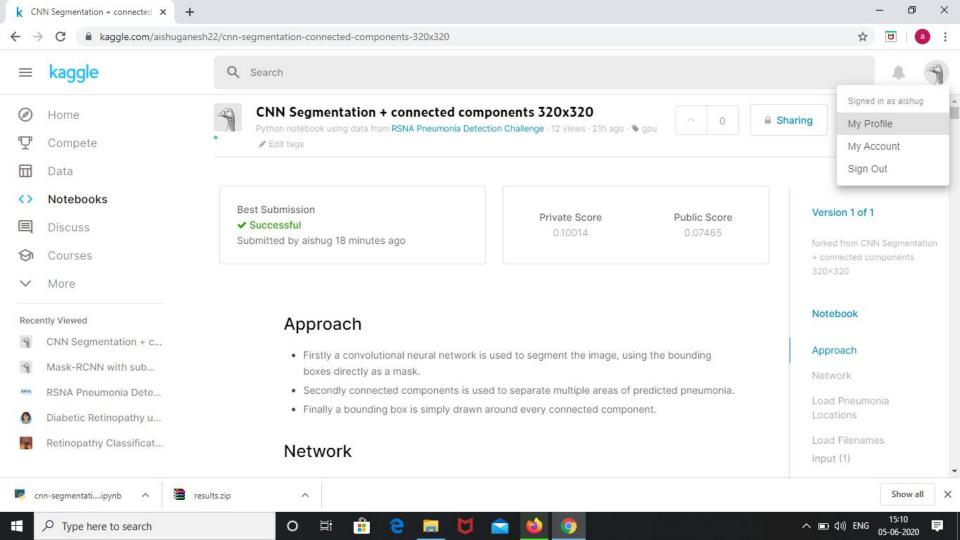
INTRODUCTION

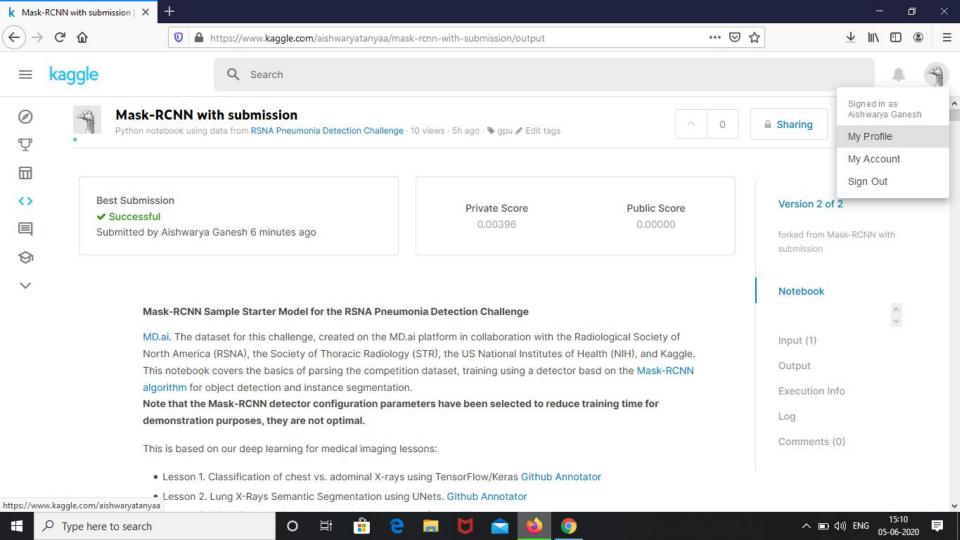
- The main idea of the project is to find the areas affected by pneumonia and classify the patients based on their number of infected regions ie, Lung Opacities.
- We had only the patient datas that had pneumonia, hence we formulated the project to classify the patients based on the lung opacity regions present in their infected lungs.
- This implies that the classification problem is modeled to classes with acute pneumonia and severe pneumonia based on the area of the affected region.

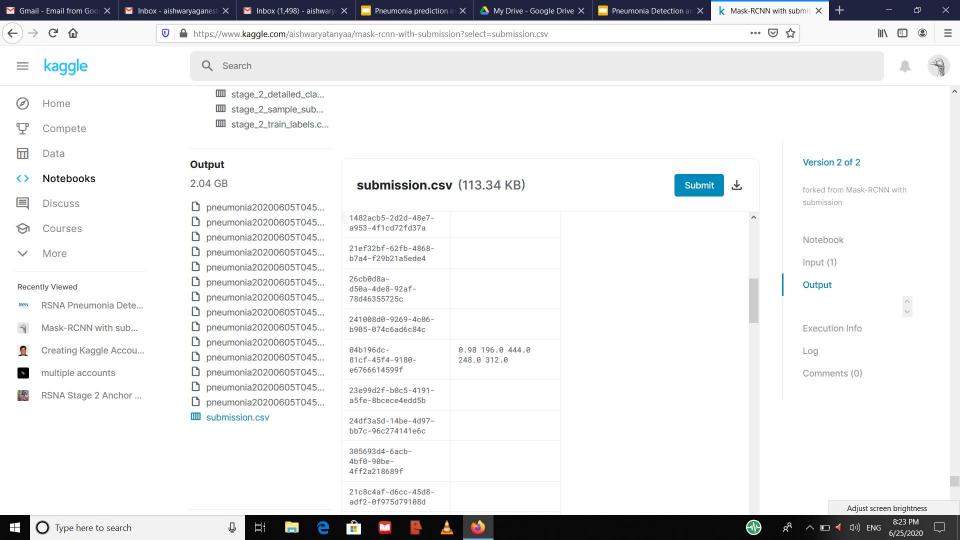
FEATURE EXTRACTION

As suggested by the competition host RSNA and MD.ai, the feature extraction using Mask RCNN was carried out and the results was submitted to kaggle to check accuracy.

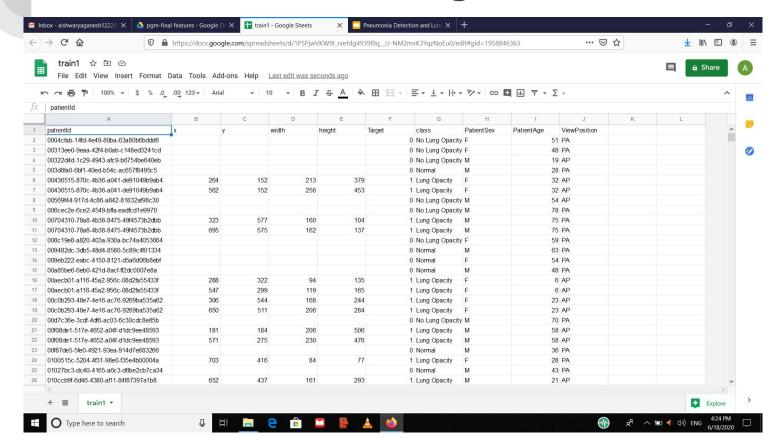
The method that involved general CNN didn't provide great accuracy, while the model that used Mask RCNN along with Gaussian Blur for Image Augmentation provided greater accuracy. That was verified using Kaggle Submissions provided in the screenshots given in next slide







Initial features(Given) + Features from MetaData(Sex, Age, VP included)

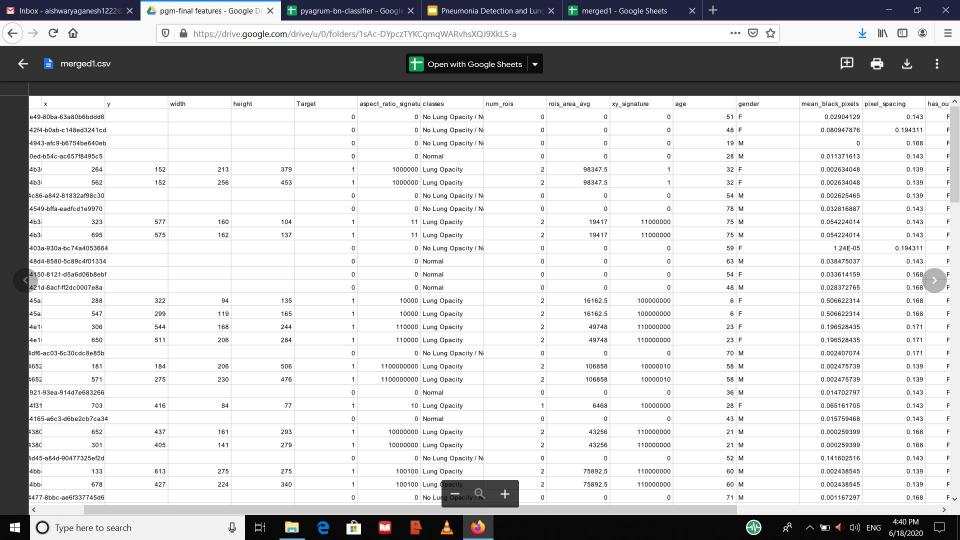


Dataset Observation

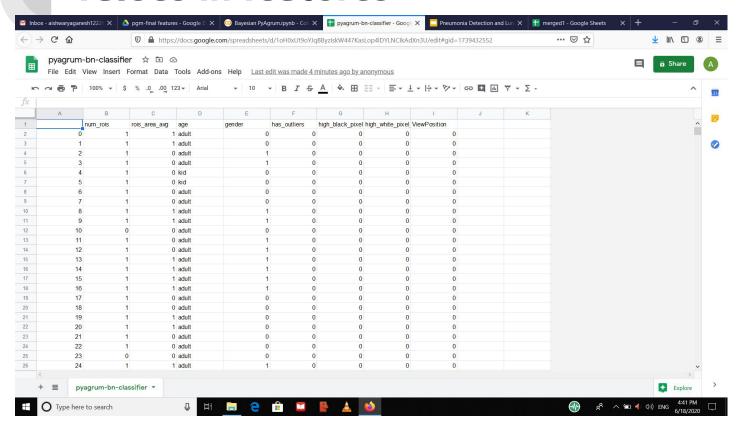
As we can see from the given dataset, the problem is to identify the lung opacity regions and not to classify the data into pneumonia and normal classes.

Hence that part of classification is done using another dataset Chest X-ray from Kaggle(explained later).

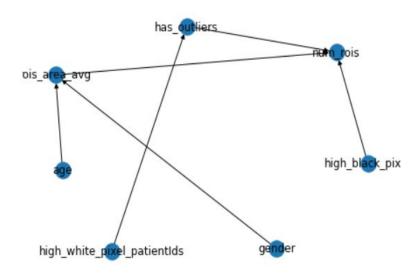
Now for this RSNA dataset, the problem is formulated to find the number of lung opacity regions present in a patient x ray. A bayesian approach is provided for that obtained features by grouping the number of opacity regions as Region of Interest as 0 if less opacity regions and 1 if there are more than 2 opacity region .



After processing and grouping the values in features



BAYESIAN MODELLING USING PYGMPY



from pgmpy.inference import VariableElimination LungDisease infer = VariableElimination(model) q = LungDisease infer.query(variables=['age'], evidence={'num rois': 0}) print (q) Finding Elimination Order: : 100%| | 5/5 [00:00<00:00, 2519.40it/s] Eliminating: has outliers: 100%| | 5/5 [00:00<00:00, 431.28it/s] +----+ | phi(age) | +======+====++======++ | age(adult) 0.8903 | | age(kid) 0.0280 | 0.0125 | | age (old) | age (teen) 0.0649 | | age(toddler) | 0.0042 |

+----+

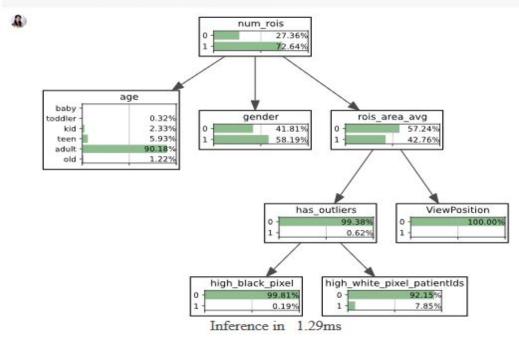
```
File Edit View Insert Runtime Tools Help
     + Code + Text
<>
      [ ] model.fit(LungDisease)
[ ] y_pred = model.predict(predict_data)
      (A) 100%| 48/48 [00:00<00:00, 236.99it/s]</p>
      y_pred.head(10)
             num_rois
                    0
           7
           9
                    0
      [ ] #print('Accuracy is'+ str(counter/LungDisease.shape[0]*100))
     [ ] from sklearn.metrics import accuracy score, confusion matrix
     [ ] print ('Accuracy Score :', accuracy score(actual, y pred)*100)
      Accuracy Score : 62.95655932569699
      [ ] print(confusion_matrix(actual,y_pred))
      [[5270 1671]
           [3471 3469]]
     []
```

BAYESIAN MODELLING USING PYAGRUM - Model Created

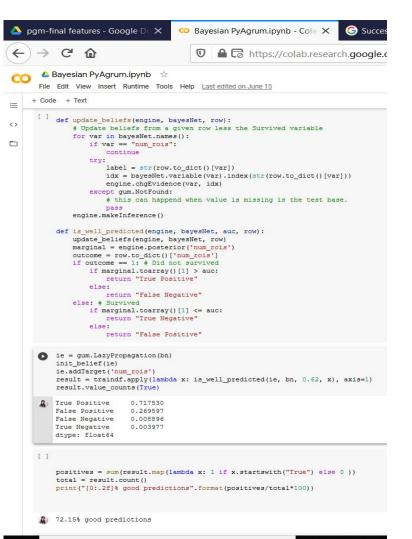
Create Bayesian Network ↑ ↓ © **目 ☆ î** : bn = gum.BayesNet("Pneumonia Detection") bn =qum.fastBN("age[baby|toddler|kid|teen|adult|old]<-num rois[True|False]->qender[0|1]; high black pixel[0|1]<-has outliers[0|1]->high white pixel patientIds[0|1]; has outliers[0|1]<-rois area avg[0|1]; YiewPosition[0|1]<-roi print (bn. variable ("num rois")) print(bn.variable("age")) print (bn. variable ("gender")) print(bn.variable("rois area avq")) print(bn.variable("has outliers")) print(bn.variable("high black pixel")) print(bn.variable("high white pixel patientIds")) print (bn.variable ("ViewPosition")) num rois<True, False> age<baby, toddler, kid, teen, adult, old> gender<0.1> rois area avg<0,1> has outliers<0,1> high black pixel<0,1> high white pixel patientIds<0,1> ViewPosition<0.1> num rois rois_area_avg has outliers ViewPosition high_white_pixel_patientIds high_black_pixel

Markov Blanket of Created Network

Inference when View Position is AP for our designed network



Accuracy: 72.15%

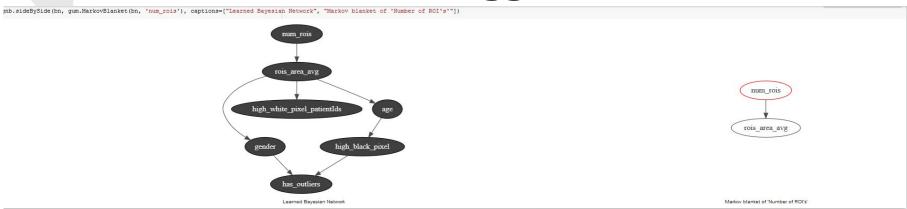


Model the package suggests(Observation: It uses Hill Climbing Algorithm)

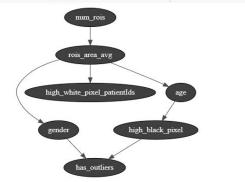
```
traindf.to csv("/content/drive/My Drive/pgm-final features/pyagrum-bn-classifier.csv")
  file = "/content/drive/My Drive/pgm-final features/pyagrum-bn-classifier.csv"
  learner = qum.BNLearner(file, template)
  bn = learner.learnBN()
                    num rois
                  rois area avg
           high white pixel patientIds
                                    high black pixel
            gender
```

has outliers

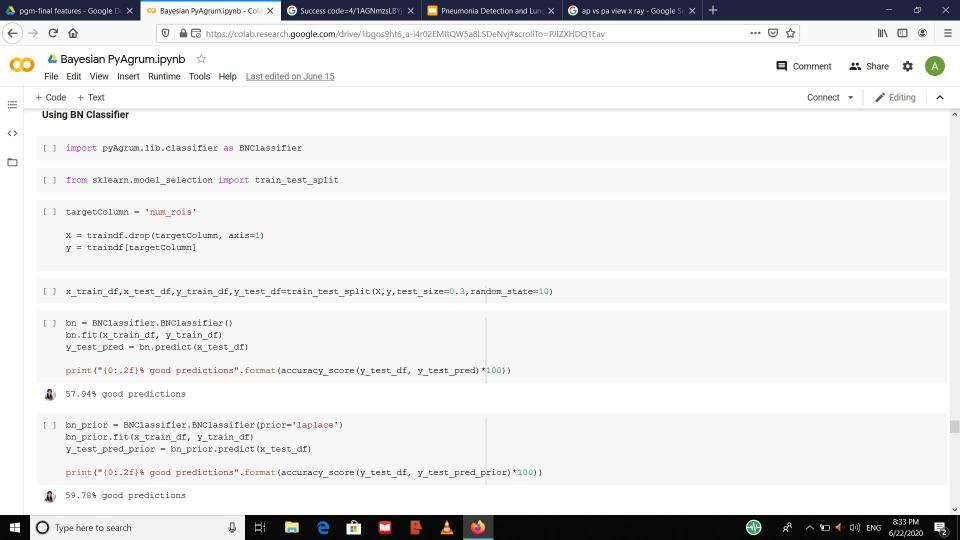
Markov Blanket of Suggested Network



pnb.sideBySide(bn, gum.MarkovBlanket(bn, 'rois_area_avg'), captions=["Learned Bayesian Network", "Markov blanket of 'Average of ROI"])







Pneumonia prediction in Chest X ray images

INTRODUCTION:

- The model proposed is used to classify whether the person has pneumonia or normal lung.
- The steps involved in this work is
 - Principal component analysis
 - o Histogram classifier
 - Bayesian classifier
- PCA is used for dimensionality reduction in the image.
- On the dimension reduced image we perform histogram and bayesian classification.

DATASET DESCRIPTION:

- Dataset that we used is a kaggle challenge dataset.
- It consists of 5216 images.
- Out of that 1341 are normal lung images and 3875 are pneumonia lung images.
- The image format is jpeg.

BAYESIAN CLASSIFIER:

- A Bayesian classifier is based on the idea that the role of a class is to predict the values of features for members of that class.
- In a Bayesian classifier, the learning agent builds a probabilistic model of the features and uses that model to predict the classification of a new example.
- The simplest case is the naive Bayesian classifier, which makes the independence assumption that the input features are conditionally independent of each other given the classification.

PARAMETERS USED IN BAYESIAN MODEL:

- mun -mean vector of normal
- mup -mean vector of pneumonia
- cn-convolution matrix of normal
- cp-convolution matrix of pneumonia
- labeln-unique value i.e zero
- labelp-unique value i.e one(pneumonia)
- Nn-0 existed time
- Np-1 existed time

```
def Bayesian2DClassifier(queries, Nn, Np, mun, mup, cn, cp, labeln, labelp):
    w1 = 1
    w2 = 1
    A = w1 * w2
    N = np.alen(queries)
    [countn, countp] = np.zeros((2, N))
    factorn = Nn * A * (1 / (2 * np.pi * np.sqrt(np.linalg.det(cn))))
    factorp = Np * A * (1 / (2 * np.pi * np.sqrt(np.linalq.det(cp))))
    icn = np.linalg.inv(cn)
    icp = np.linalg.inv(cp)
    for i, q in enumerate (queries):
        countn[i] = factorn*np.exp(-0.5 * np.dot(np.dot(q - mun, icn), q - mun))
        countp[i] = factorp*np.exp(-0.5 * np.dot(np.dot(q - mup, icp), q - mup))
    resultlabel = np.full(N, 999, dtype = int)
    indicesn = countn > countp
    indicesp = countp > countn
    resultlabel[indicesn] = labeln
    resultlabel[indicesp] = labelp
    resultprob = countn/(countn+countp)
    resultprob[indicesp] = 1 - resultprob[indicesp]
    return resultlabel, resultprob
```

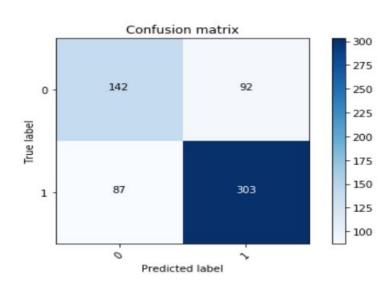
BAYESIAN CLASSIFIER ACCURACY:

• As a result we got 74.29% accuracy rate with the help of bayesian model.

```
[ ] accuracyB = accuracy(T1, Blabels)*100
accuracyB
```



CONFUSION MATRIX:



THANK YOU