ProjectX: Classification, Localization and Progression tracking of Thoracic Diseases

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I. Introduction

A. Related Work

B. Dataset

This includes the data set.

We did analysis of data set for age,gender and disease distribution to check if there exists a statistical relationship which we could use for prediction. [1] The figure 1 shows the distribution of male and female patients for each pathology.

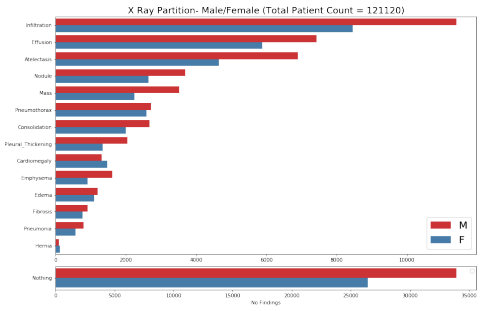

Fig. 1. Data Set with Disease Labels and Gender Partitions

The figure 2 shows the distribution of multiple pathology in the data.

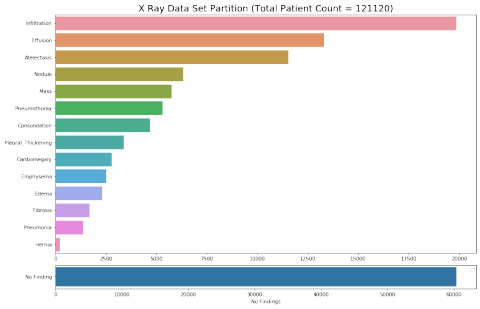

Fig. 2. Data Set with Disease labels

We can infer from figure 1 and figure 2 that the ratio of male and female patents for all the pathology's is quite balanced so there is no apparent relationship between these diseases and gender.

The figure 4 and 3 shows the relationship between age and the different diseases.

We plot the the distribution of data in figure 5 for patients along with follow ups as we are interested in the progression tracking of diseases.

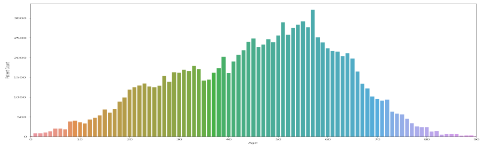

Fig. 3. Overall Distribution of Data with age

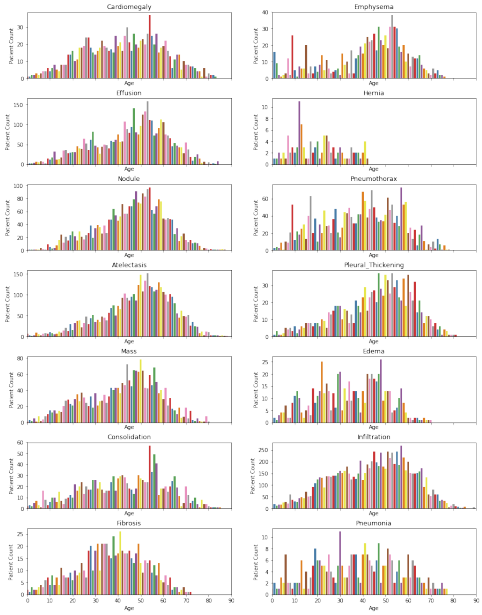

Fig. 4. Disease Distribution with Age

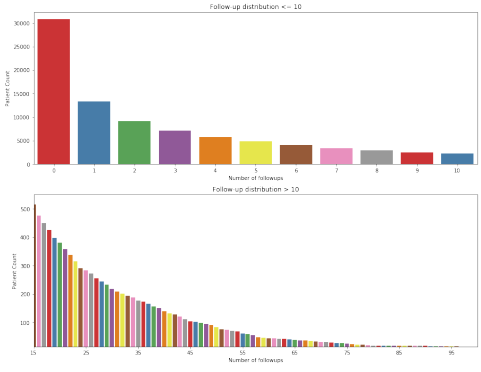

Fig. 5. Follow Up Distribution of Data

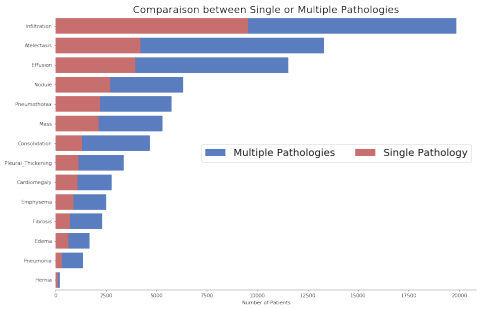

Fig. 6. Follow Up Distribution of Data

We plot the distribution in figure 6between patients with multiple pathology's vs those with single pathology. This gives us insights for out multi-class classification.

C. Architecture

We have developed this solution using Pytorch and it's pre trained version of Resnet50. While deeper nets are likely to give better performance, the training time and resource requirements deterred us from pursuing them. The last fully connected layer is modified to output 15 logits, for each of our categories. The objective function is Multi label soft margin loss which allows us to minimize the binary cross entropy for each category, as they may not necessarily share probability mass.

TODO: Section about resnet50 and its architecture TODO:

1) Disease Localization: The X-Ray image to be analyzed is passed through the Resnet network, and information of the output of the final convolutional layer and the predicted disease probabilities are extracted. Using the fully connected layer weights associated with the most probable disease (in cases where actual disease is not known) or the weights associated with the known disease, a weighted average of the output of the final convolutional layer of Resnet is derived. The resultant 8x8 grayscale image is resized to match the size of the display image. Contours are generated around areas in the image with intensities greater than a threshold value, and the corner points of the box bounding the contours are identified. The grayscale image is converted into a colored heat-map to better represent the variations in image intensities, and then blended with the original image. Bounding boxes are drawn to highlight the most probable affected area using corner-points identified in the previous step. Image X shows an overview of the disease localization process.

2) X-Ray Image Differencing: We developed two techniques to identify the changes that occur over a period of time. The first technique involves identifying structural differences and the second involves identifying differences in heat maps.

Structural differences: In this approach, we differentiate between the X-Ray images based on the observed structural differences. At a broad level this involves three steps:
Pre-processing: The X-Ray images could differ because of differences in orientation and image brightness. This would impact the precision of the differences identified. To address this, the images are first normalized to have similar brightness. To address the issues related to orientation differences, we use affine transformation to align the second image to the first one. The affine matrix required for this transformation is computed using the ECC algorithm.
Analysis: Once the two images are aligned and normalized, the structural similarity around each point is computed using the structural similarity index (SSIM). The point-wise difference information is derived from this score. Points with considerable difference are determined by comparing with a threshold value. The resultant binary threshold image would have many minor difference areas which may have occurred due to medically inconsequential factors like orientation differences. To remove such minor areas, morphological opening technique is used. This gives a binary image with areas with considerable difference highlighted. Contours are generated around areas of difference and the two images are displayed with bounding boxes around the contours. Image X gives an overview of the process.

Heat-map based differences: We first generate the heat-maps for the two images to be compared using process mentioned in section X. We also extract the gray-scale image which was originally used for generating the heat-maps. The points in the gray-scale which are brighter than a given threshold are identified and a binary image representing the most affected areas are generated. The binary image of the second X-ray is transformed using the affine matrix generated for aligning image 2 to image 1 [section reference]. We then compare the two binary images and identify points which are present in one image but absent in the other. We find the co-ordinates of the bounding boxes and use these to draw on the blended image of the original X-Ray and heat maps.

D. Experiments

1) Pipeline:

II. Limitations

- The training of a networks can be really slow, especially when hyperparameters are being tuned.

III. Results

A. Disease Localization

Image X shows the results of disease localization prediction on X-rays of patients suffering from Cardiomegaly and Atelectasis. The blue box indicates the predicted affected area, and the red box indicates the area manually identified by radiologists.

B. X-Ray Image Differencing

To give a quick snapshot of the various differences in the X-Ray images, we created a dashboard that displays the input images, probabilities of diseases, most likely affected areas, image differences computed based on heat-map and structural differences.

Image compares the X-Rays of a patient who initially suffered from effusion and who later also developed Atelectasis. The heat-map difference images clearly highlight how the affected areas have changed over a period of time. The black box indicates the affected area present only in the particular image, and the red box indicates the affected area in the other image which was not an affected area in the particular image.

1) Comparison of the Structural differencing and Heat-map differencing techniques: We observed that the heat-map based differencing technique identifies differences which are more medically relevant. It can better tolerate variations due to subject-orientation, brightness and presence of equipment like heart pace makers.

IV. Conclusion

References

[1] S. Bernadac, Chest x ray data analysis.
URL https://goo.gl/wECm8B