Detecting abnormalities on chest X-rays using deep neural networks

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Abstract

Diseases like pneumonia and tuberculosis are leading causes of death world-wide, Although conclusive diagnosis requires other tests such as a sputum culture, chest radiography can be an important diagnostic aid and is routinely recommended since it is fast, affordable and highly sensitive. Moreover, automated detection of abnormalities on the chest X-ray can help in screening and severity-based prioritization. There has been increasing interest in using deep learning for computer-aided diagnosis in both the machine learning and radiology communities. There has also been recent work in model explainability and unsupervised localization, and methods for dealing with label noise in a weakly supervised setting

Inspired by previous work, we develop algorithms that can detect abnormalities on the X-ray and explain these detections using unsupervised localization. We establish baselines, benchmark against previous work and evaluate the effects of recent techniques such as mixup on performance and generalizability to other datasets. In terms of AUROC, we acheive performance competitive with previous work in a) detecting pneumonia-like and other abnormalities on the NIH chestX-ray14 dataset and b) in detecting tuberculosis on the Shenzhen hospital dataset, and we achieve state-of-theart performance on the Montgomery county tuberculosis dataset. We also test our algorithms for bias with respect to gender, age and view position.

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Introduction

- 1.1 Problem definition
- 1.2 Motivation
- 1.3 Previous work
- 1.4 Our work
- 1.5 Report layout

Literature survey

- 2.1 CheXNet and CheXNext
- 2.2 Explainability
- 2.3 Fairness
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Data

- 3.1 NIH CXR-14
- 3.1.1 Challenges and issues
- 3.2 Mendeley
- 3.3 Shenzhen and Montgomery

Baselines

- 4.1 Model architecture
- 4.2 Training procedure
- 4.3 Unsupervised localization
- 4.3.1 LIME as an alternative

Experiments

- 5.1 Data augmentation
- 5.2 Test-time augmentation
- 5.3 Higher resolution
- 5.4 Progressive resizing
- 5.5 Ensembling for scale-invariance
- 5.6 Location-sensitive ensembling
- 5.7 Mixup
- 5.8 Label drift

Choose a better name

- 5.9 Transfer learning for tuberculosis
- 5.10 Generalizability

Results

- 6.1 Comparison metrics
- 6.2 Comparison to previous work
- 6.3 Comparison to human radiologists
- 6.3.1 Caveats with comparison to human radiologists
- 6.4 Other important factors

Such as how well predicted probabilities correspond to actual severity, localization, and time

6.5 Examples

Bias

- 7.1 Gender
- 7.2 Age
- 7.3 View position

Conclusion

Future work

- 9.1 Limitations of proposed work
- 9.2 Avenues for further research
- ${\bf 9.3 \quad Practical\ implementation\ and\ clinical\ relevance}$ ${\bf Scalability}$
- 9.4 More recent datasets