

Utility of the concept bottleneck model in a CT scans analysis

Jakub Binda

University of Warsaw, Faculty of Mathematics, Informatics and Mechanics.

April 2024



Table of contents

- 1 LIDC-IDRI dataset
- 2 ConRad model



LIDC-IDRI dataset

- Lung Image Database Consortium and Image Database Resource Initiative (LIDC-IDRI)
- Publicly available database.
- Contains 1018 chest CT scans from 1010 patients.



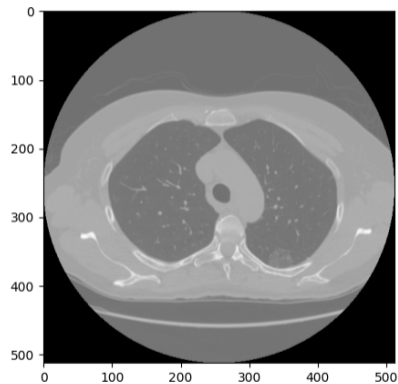


Figure: Slice of an exemplary CT scan.

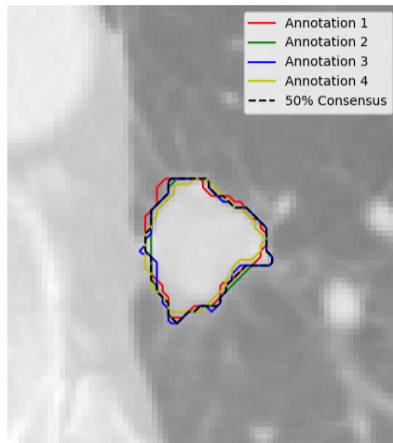


Figure: Slice of an exemplary CT scan with an annotations.

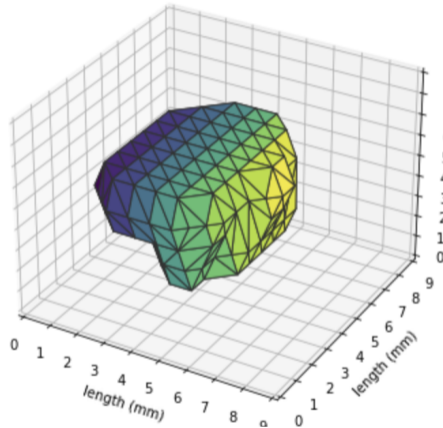


Figure: 3D visualisation of a nodule.

Dataset preparation

- 1 Clustering nodule's annotations with the PyIidc package.
- 2 Extracting small volumes around nodules.
- 3 Extracting nodule's features.
- 4 Assigning benign or malignant label.
- 5 In summary 854 nodules (442 benign) after preprocessing.



Dataset preparation

- 1 Clustering nodule's annotations with the PyIidc package.
- 2 Extracting small volumes around nodules.
- 3 Extracting nodule's features.
- 4 Assigning benign or malignant label.
- 5 In summary 854 nodules (442 benign) after preprocessing.



Dataset preparation

Examples of the original images

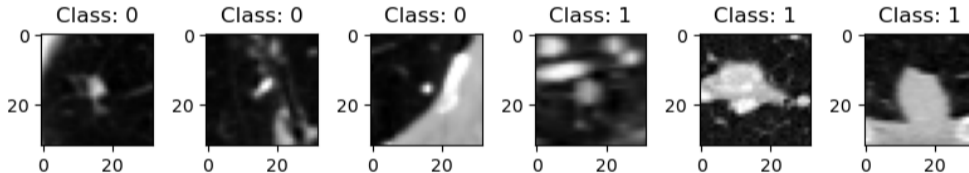


Figure: Slices of examples from prepared dataset.



Explainable models

- Why model is predicting that nodule is malignant?
- Explainability is especially important in medicine.
- Concept Bottleneck Model

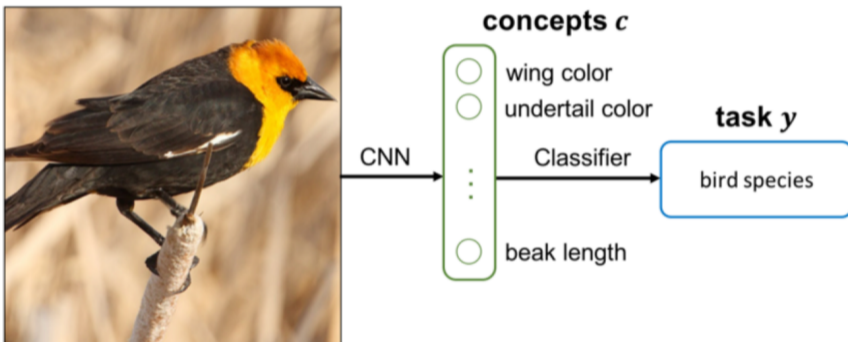


Explainable models

- Why model is predicting that nodule is malignant?
- Explainability is especially important in medicine.
- **Concept Bottleneck Model**



Concept Bottleneck Model



Koh et al, (2020) [2]

Concept Bottleneck Model (CBM)

Let's take a regression task as an example, then formally:

$$x \in \mathbb{R}^d$$

$$c \in \mathbb{R}^k$$

$$y \in \mathbb{R}$$

training points:

$$(x^{(i)}, y^{(i)}, c^{(i)})_{i=1}^n$$

$CBM = f(g(x))$, where

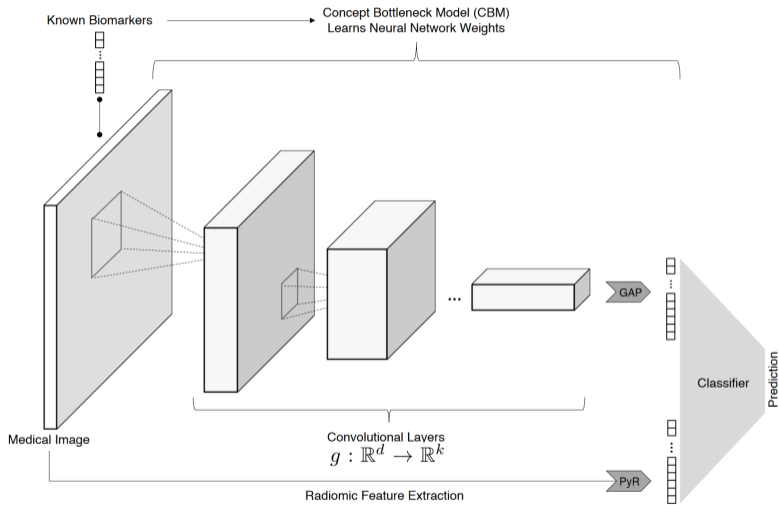
$$g : \mathbb{R}^d \rightarrow \mathbb{R}^k$$

$$f : \mathbb{R}^k \rightarrow \mathbb{R}$$



- ConRad model is based on the Concept Bottleneck Model.
- CNN predicts biomarkers from a nodule slice. (8 biomarkers)
- Radiomics features are computed from an segmented image with PyRadiomics package. (107 features)

ConRad - general architecture



Brocki and Chung, (2023) [1]

ConRad - concept space

- ConRad model is based on Concept Bottleneck Model.
- CNN predicts biomarkers from a nodule slice. (8 biomarkers)
- Radiomics features are computed from an segmented image with PyRadiomics package. (107 features)



Biomarkers which are predicted with CNN:

- subtlety
- calcification
- sphericity
- margin
- lobulation
- spiculation
- texture
- diameter

All biomarkers are numeric.

ConRad - concept space

- ConRad model is based on Concept Bottleneck Model.
- CNN predicts biomarkers from a nodule slice. (8 biomarkers)
- Radiomics features are computed from an segmented image with PyRadiomics package. (107 features)



Utilized classifiers:

- Non-linear/linear SVM
- Random Forest
- Logistic Regression
- Logistic Regression with the Lasso

Biomarkers and radiomics in the concept's space.

Final Layer Classifier	Recall	Precision	Accuracy
Non-linear SVM	0.886	0.899	0.897
Linear SVM	0.886	0.893	0.893
Random Forest	0.879	0.883	0.881
Logistic Regression	0.884	0.893	0.892
Logistic Regression with the Lasso	0.896	0.893	0.896

Baseline results for End2End CNN classifier.

Classifier	Accuracy
End-to-end CNN	0.891

- ConRad model performs as good as End2End CNN model.
- However, thanks to concept's space ConRad is much more interpretable.

- ConRad model performs as good as End2End CNN model.
- However, thanks to concept's space ConRad is much more interpretable.

Features selection with Lasso

- Adding L1 penalty (Lasso) to Logistic regression drastically reduced number of features.
- From 107 **PyRadiomics** features only 13 have non-zero weights.
- However, **all** biomarkers were preserved.



Features selection with Lasso

- Adding L1 penalty (Lasso) to Logistic regression drastically reduced number of features.
- From 107 **PyRadiomics** features only 13 have non-zero weights.
- However, **all** biomarkers were preserved.

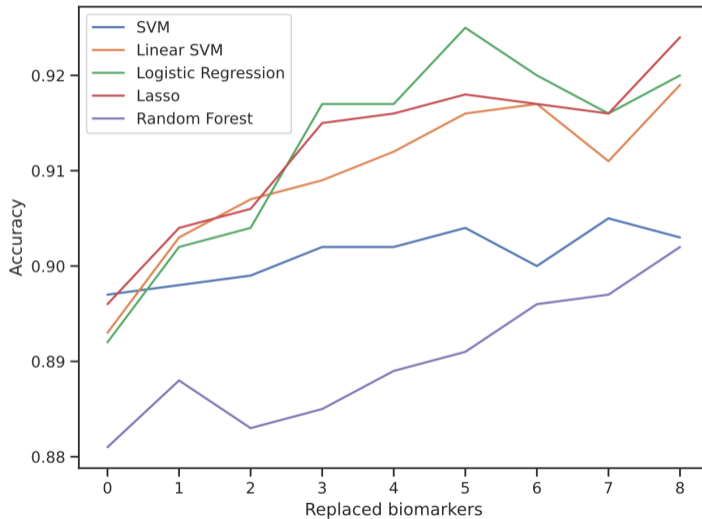


Features selection with Lasso

- Adding L1 penalty (Lasso) to Logistic regression drastically reduced number of features.
- From 107 **PyRadiomics** features only 13 have non-zero weights.
- However, **all** biomarkers were preserved.



Simulation of human in the loop



 Lennart Brocki and Neo Christopher Chung.
Integration of Radiomics and Tumor Biomarkers in Interpretable Machine Learning Models.
Cancers, 15(9):2459, January 2023.
Number: 9 Publisher: Multidisciplinary Digital Publishing Institute.

 Pang Wei Koh, Thao Nguyen, Yew Siang Tang, Stephen Mussmann, Emma Pierson, Been Kim,
and Percy Liang.
Concept Bottleneck Models.
In *Proceedings of the 37th International Conference on Machine Learning*, pages 5338–5348.
PMLR, November 2020.
ISSN: 2640-3498.

Thank you!

