



miRNA Biomarker for Lung Cancer Diagnostics

Selecting a test panel for
patient classification

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miRNA

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Project Goals & Objectives

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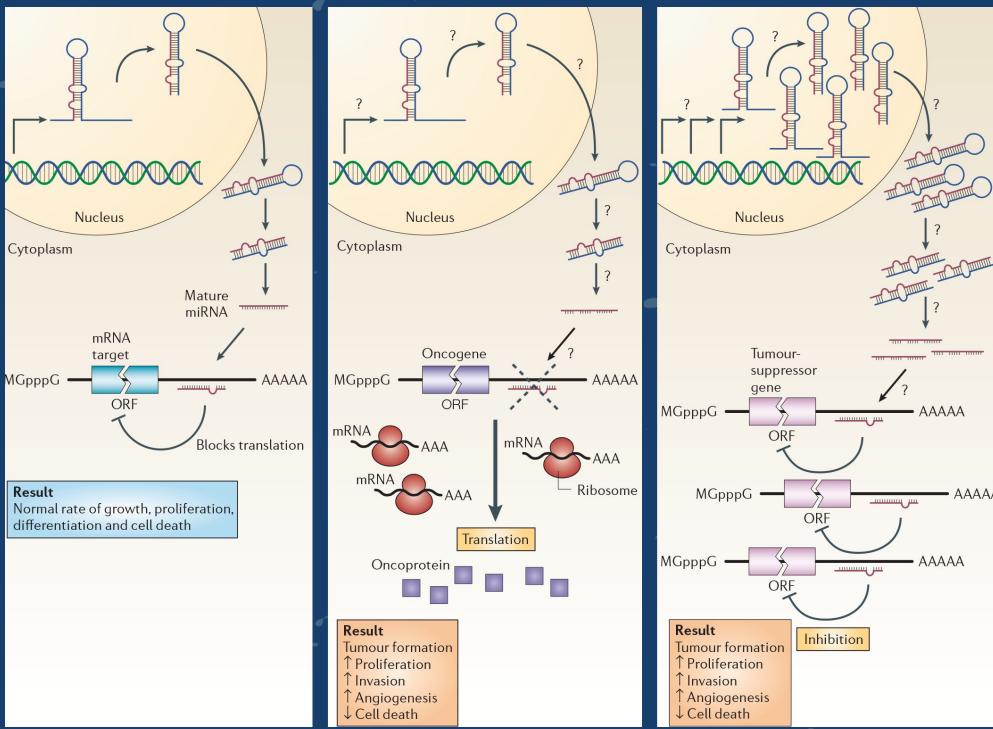
Feature Selection, Model Selection, Model
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CONCLUSION & FUTURE WORK

Conclusion & Future Work

miRNA



Esquela-Kerscher & Slack, 2006

- Small non-protein coding RNA (~22 nucleotides)
- Post-transcriptional negative gene regulators
- Multi target genes
- Oncomirs (tumor-suppressive or oncogenic)

LUNG CANCER - KEY NUMBERS

2,090,000

Worldwide new cases of lung cancer
(Ferlay et al., 2018)

1,760,000

Worldwide deaths from lung cancer
(Ferlay et al., 2018)

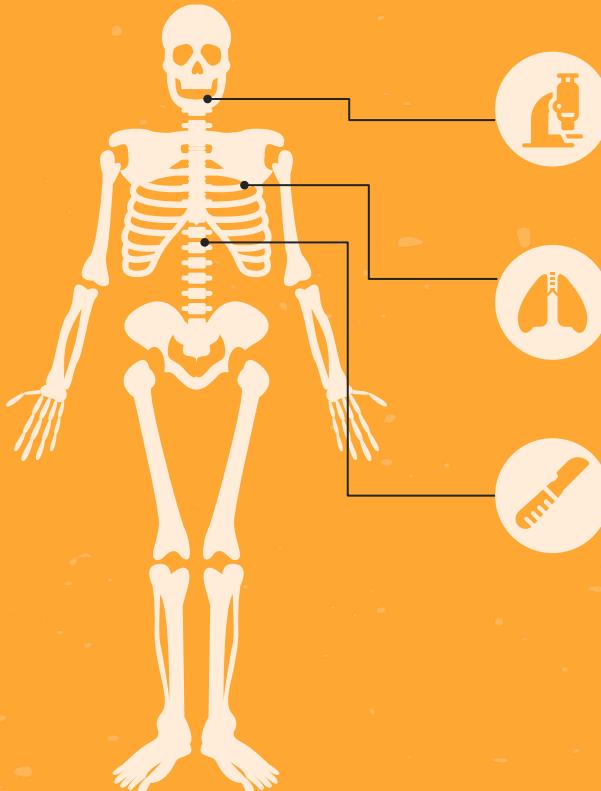
70%

5-year overall survival if detected at
earlier stages (Robinson et al., 2011)

5%

5-year overall survival if detected at
advanced stage (Siegel et al., 2012)

LUNG CANCER - CURRENT DIAGNOSTICS



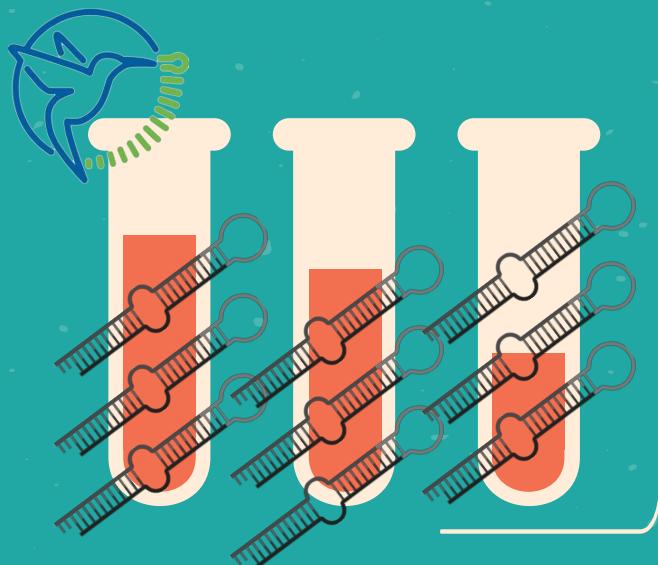
Sputum cytology

X-ray imaging

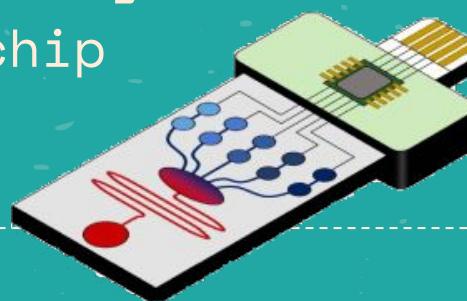
Tissue sample
(Biopsy)

- No early detection screening methods
- High false positive rates & radiation exposure

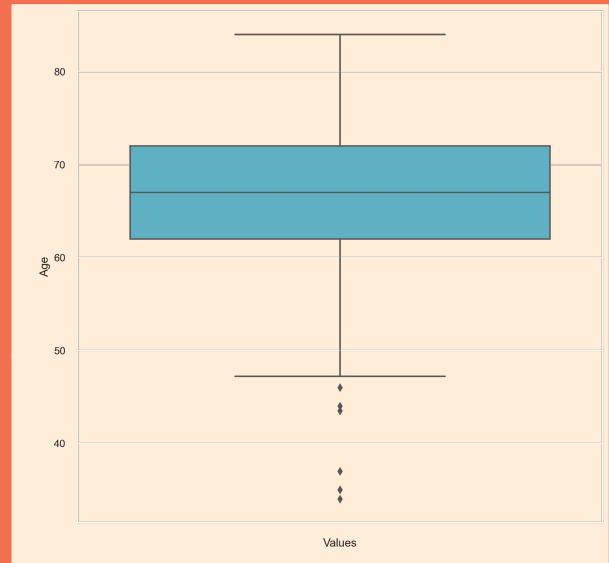
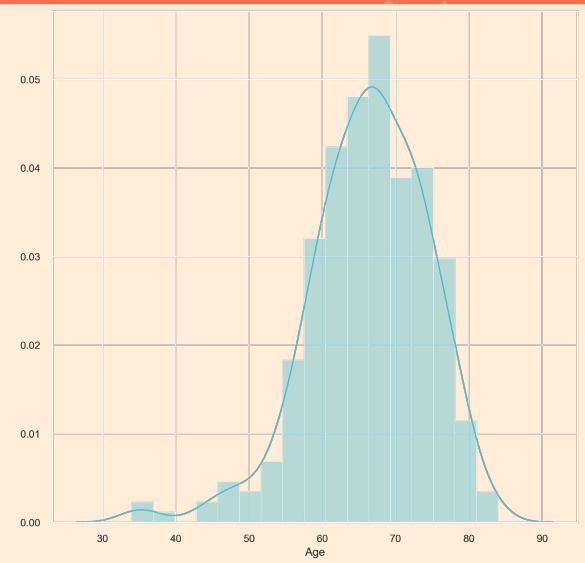
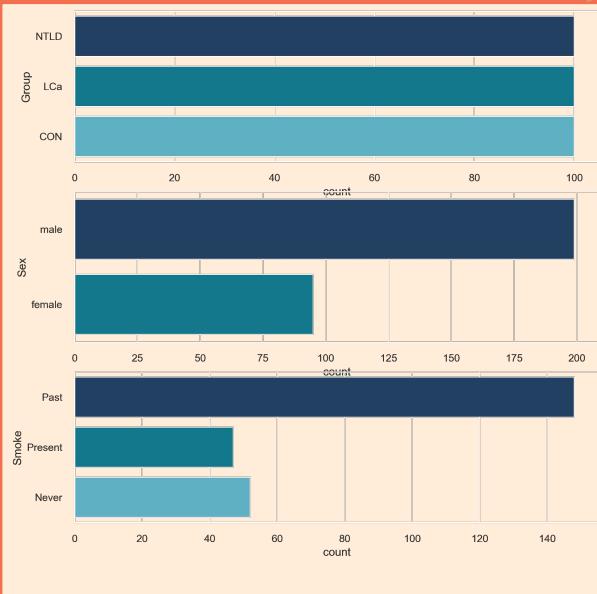
PROJECT GOALS AND OBJECTIVES



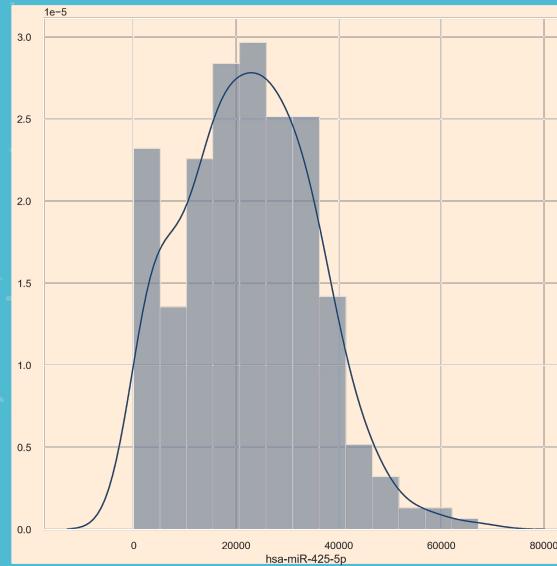
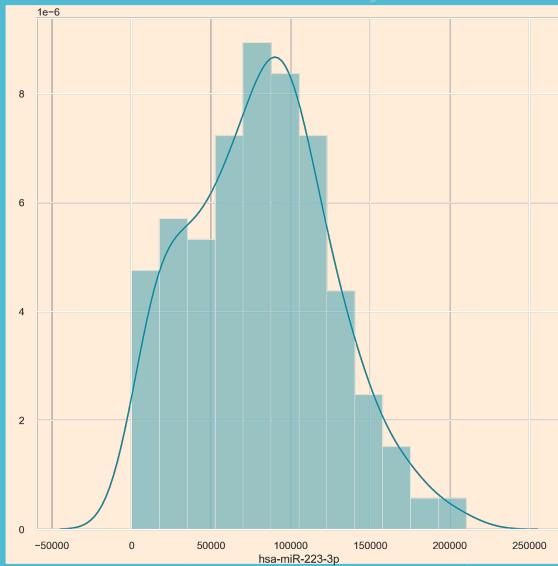
- miRNA Expression Levels of 300 blood samples
- Annotation Data with 3 classes (LCa, NTLD, CON)
- Identify 10-20 miRNA for biochip



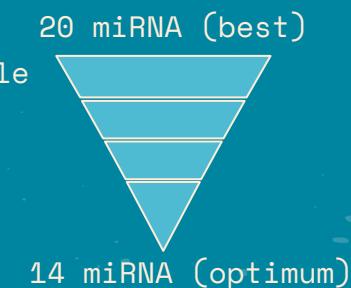
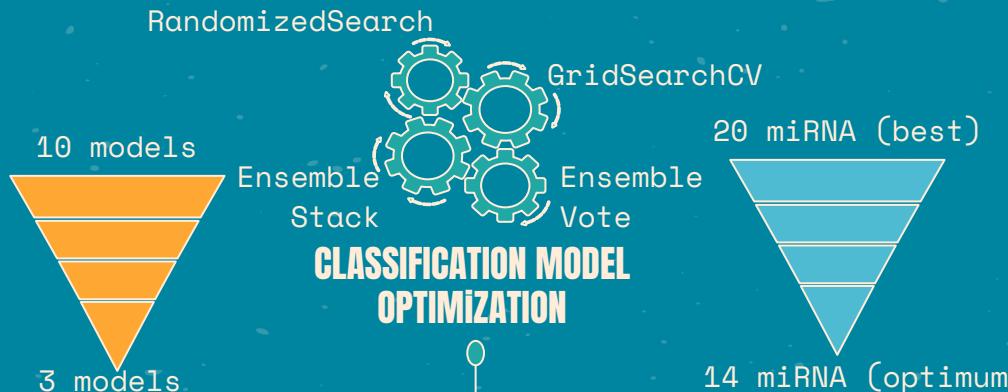
DATA EXPLORATION - ANNOTATION



DATA EXPLORATION - miRNA



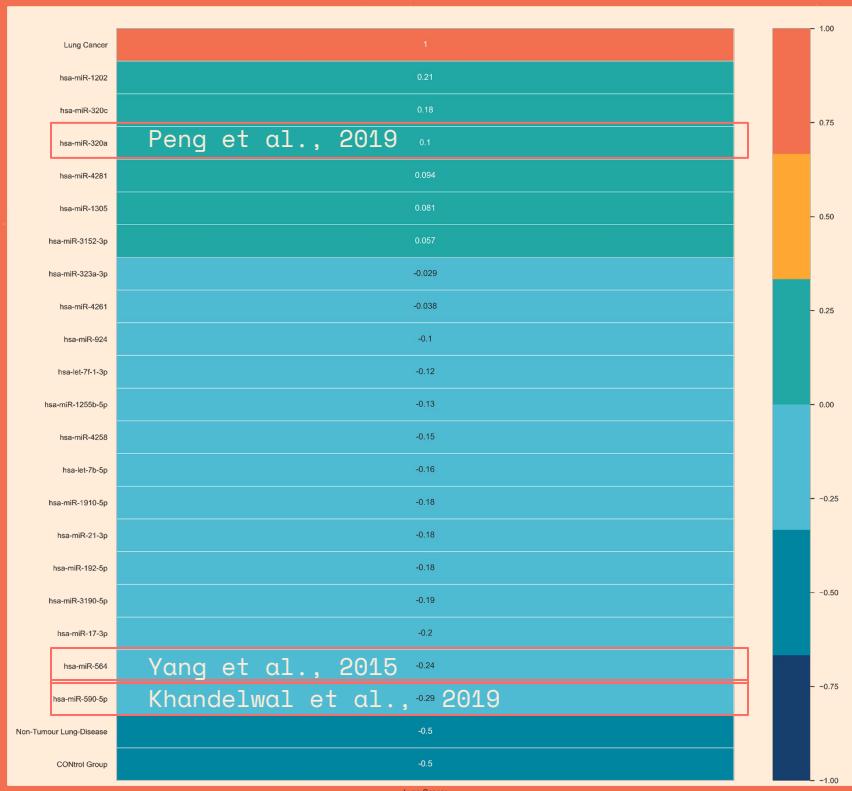
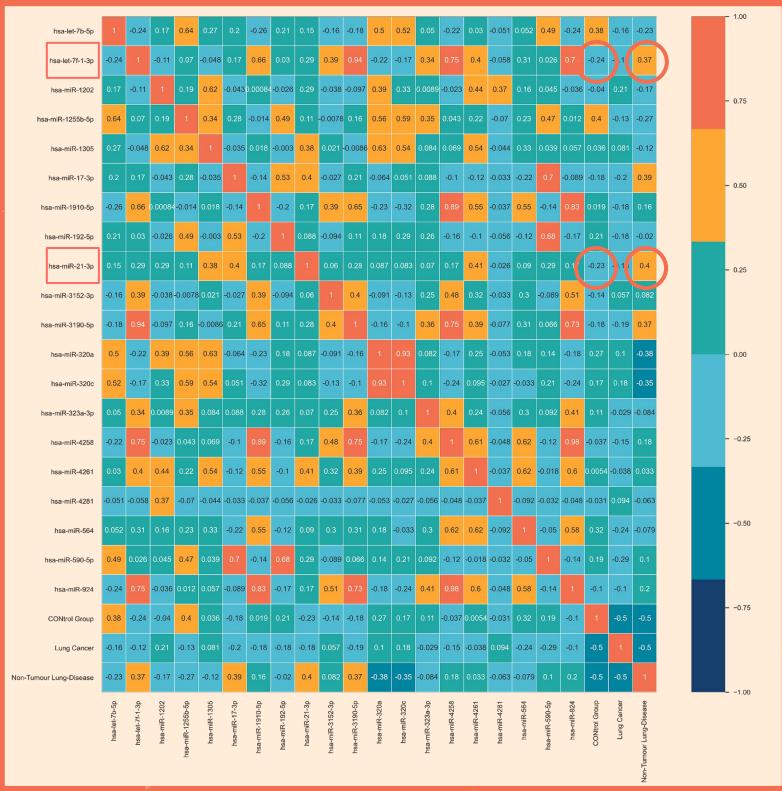
WORK-FLOW



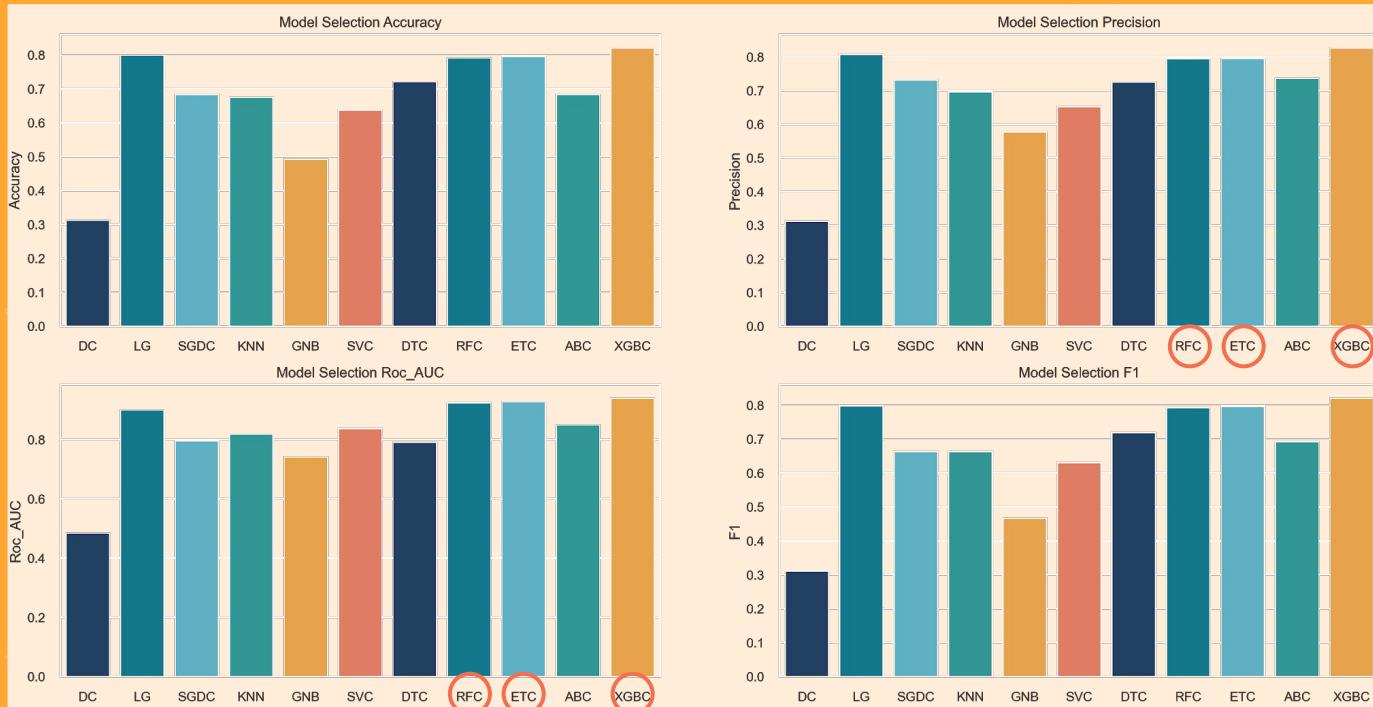
MODEL EVALUATION



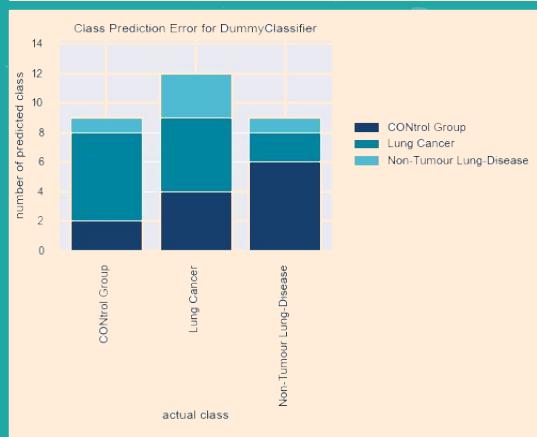
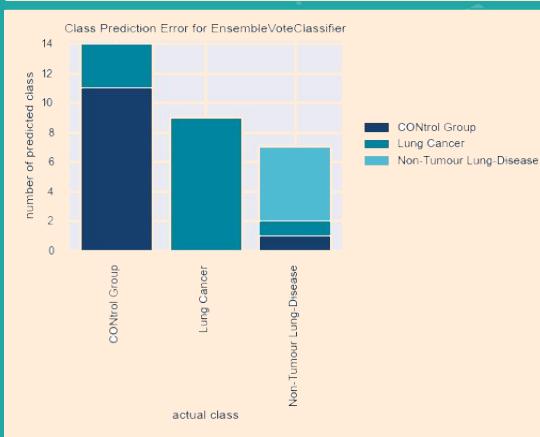
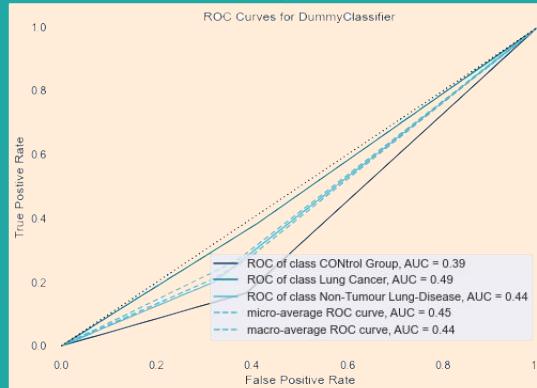
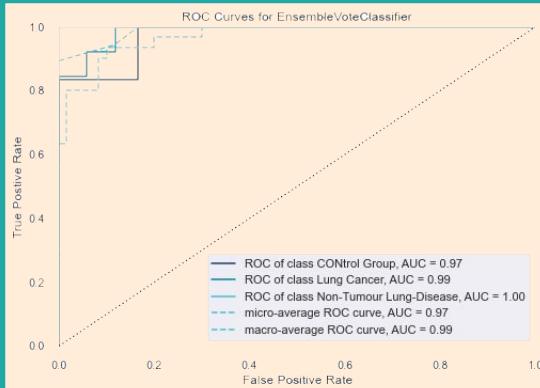
RESULTS - FEATURE SELECTION



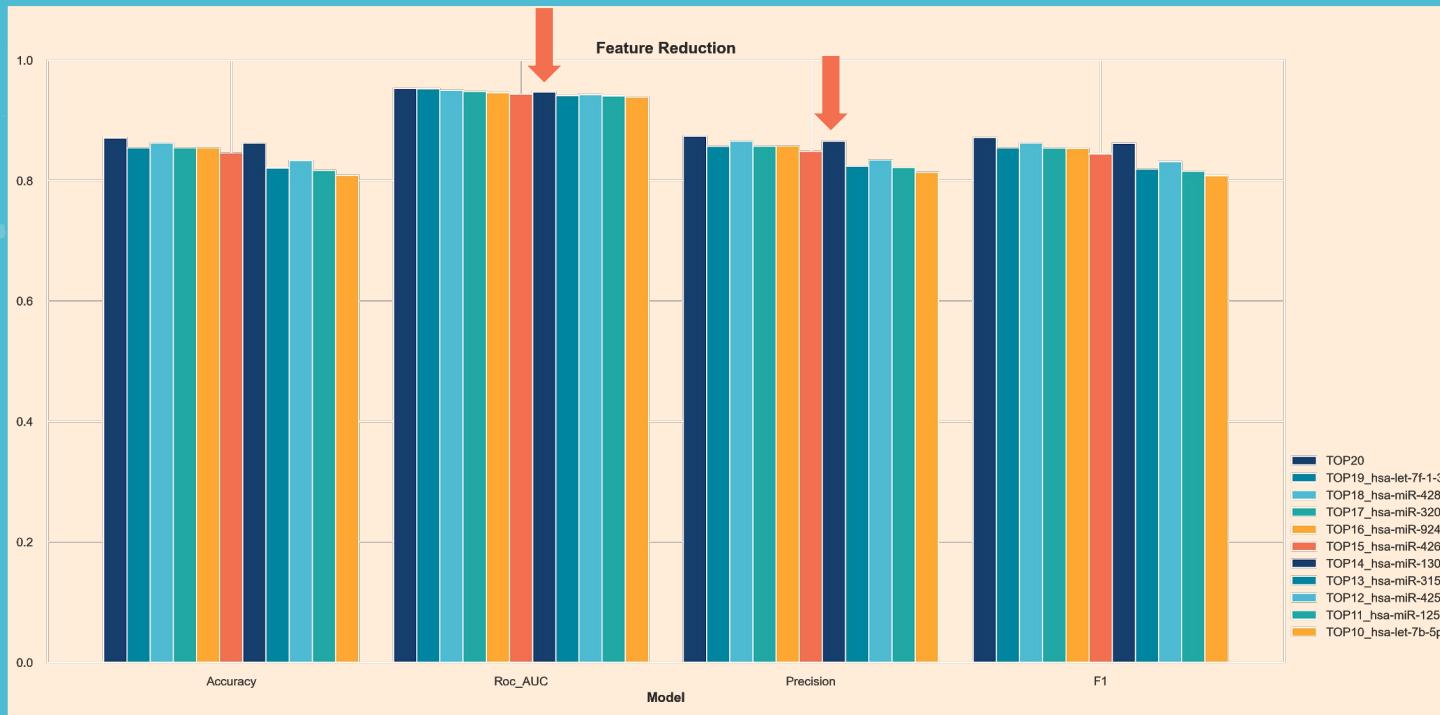
RESULTS - MODEL SELECTION



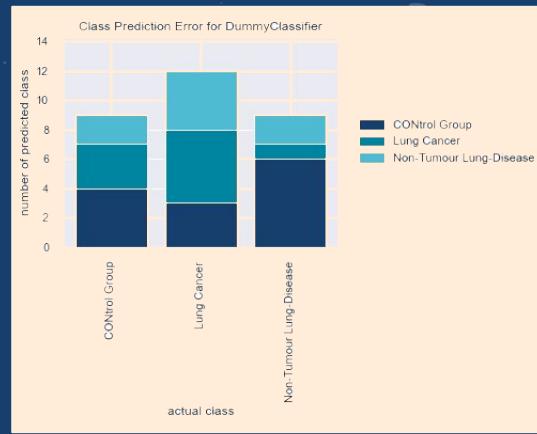
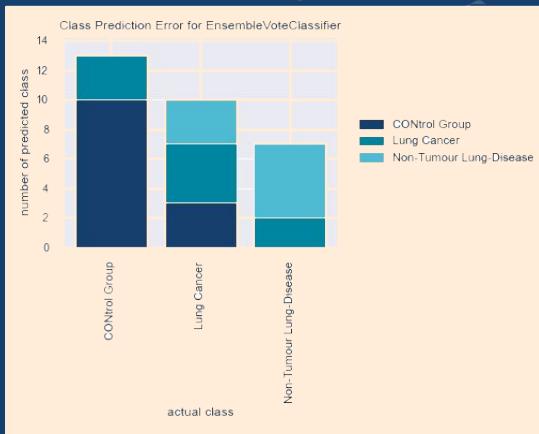
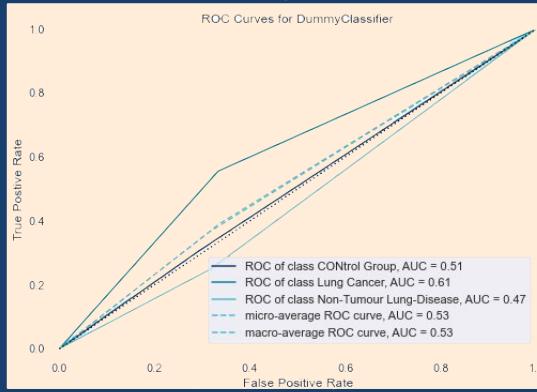
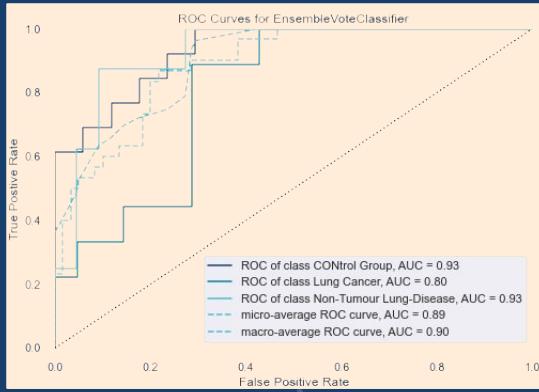
RESULTS - MODEL OPTIMIZATION



RESULTS - FEATURE REDUCTION



RESULTS - MODEL EVALUATION



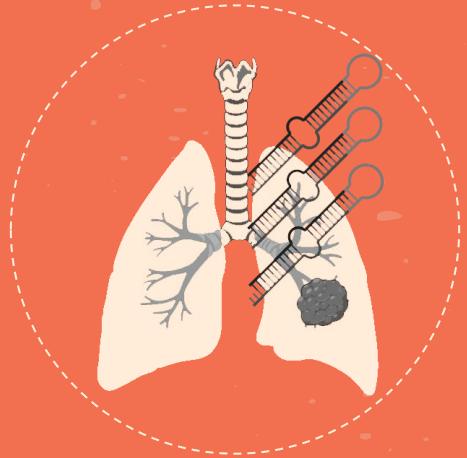
CONCLUSION & FUTURE WORK



- Defined a TOP20 (best) and TOP14 (optimum) panel of miRNA applicable in a biochip test system for lung cancer
- 3 of high-correlating-LCa miRNAs were already described in literature for their implication in Lung Tumors
- Built a classification model with medium performance to predict LCa, NTLD and CON classes



- Reduce classification to binary problem
- Use different models for prediction of each class
- Implement more regularization penalizing overfitting and other preprocessing methods
- Collect more samples to improve modeling (e.g. deep learning)



THANKS!

Do you have any questions?



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https://github.com/Patrick-Neubert/miRNA_LCa_Diagnostics

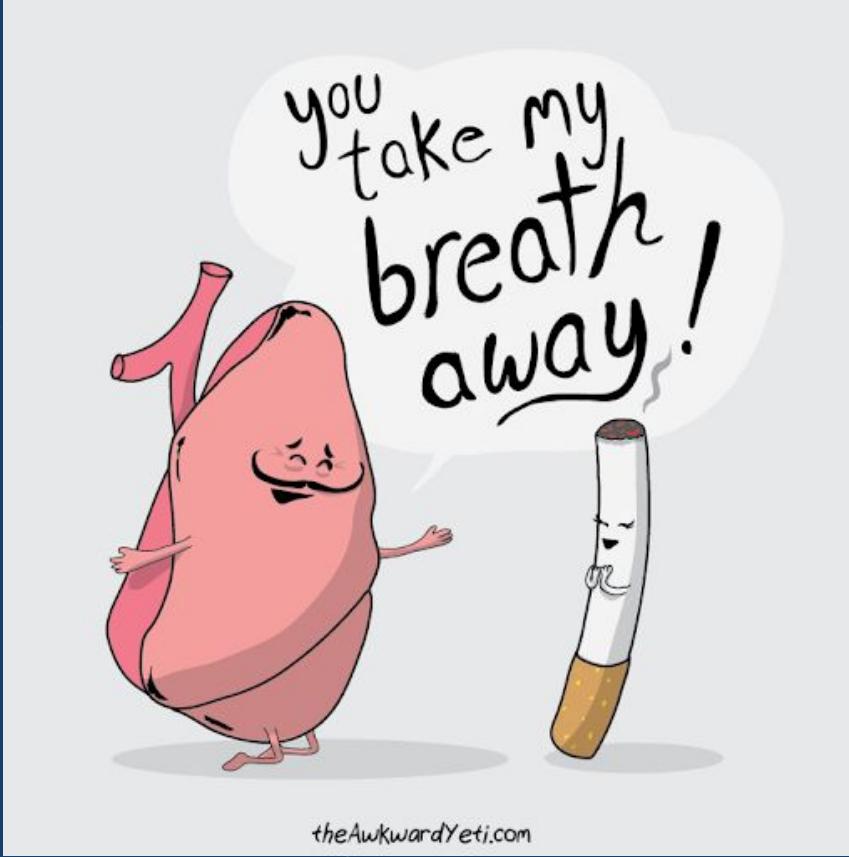


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