



# Discriminating between Alzheimer patients and healthy persons from circulating miRNA biomarkers

Alzheimer's disease miRNAs Use Case

## Background

- ❖ Alzheimer's disease (AD) is the most common form of dementia.
- ❖ Today, final diagnosis of AD can only be achieved by autopsy.
- ❖ Non-invasive, reliable diagnostic tools are of paramount importance, as it appears that identification and early intervention of those patients with mild cognitive impairment may delay the onset of AD substantially.



## Goal

- ❖ Use JADBio's automated machine learning to accurately discriminate a class of Alzheimer's patients from a class of control subjects based on the analysis of molecular biomarkers.



## The data

Data is from the Leidinger et al. study, in which an early diagnosis of AD cases was derived from the analysis of circulating miRNA.

### Samples:

70 subjects

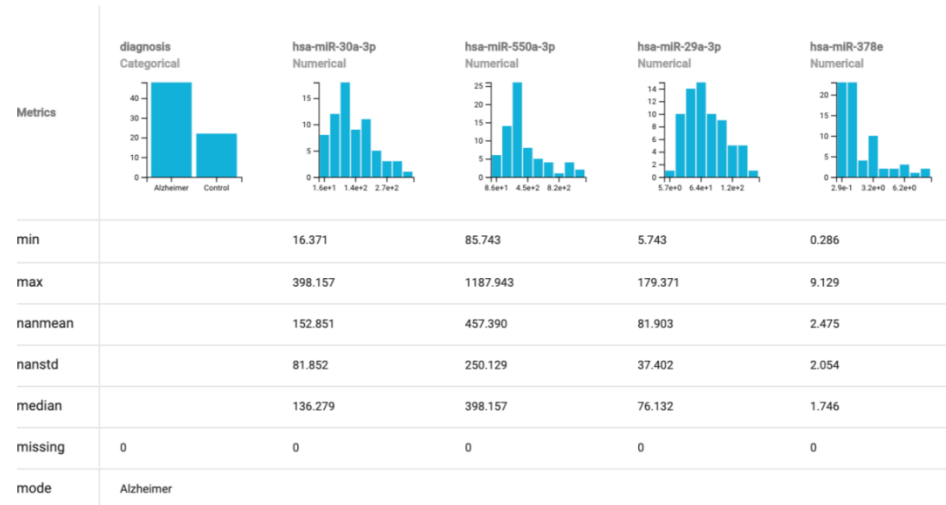
- 48 Alzheimer patients (cases)
- 22 healthy subjects (controls, age-matched)

### Potential predictors:

503 miRNA blood sample measurements

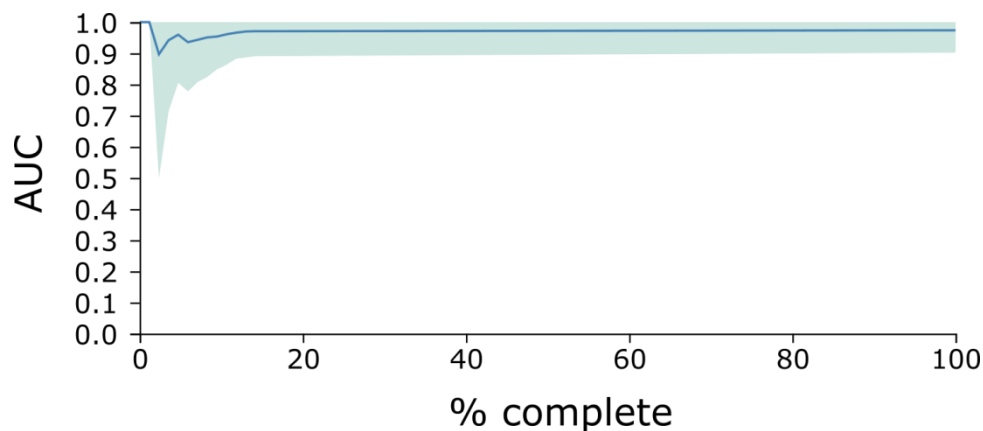
### Target:

Diagnosis [Alzheimer vs Control]



Leidinger, P., Backes, C., Deutscher, S. et al. A blood based 12-miRNA signature of Alzheimer disease patients. *Genome Bio/14*, R78 (2013). Data available at: <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE46579>

## Running JADBio



- ❖ Analysis type: typical
- ❖ Total time: 00:03:36
- ❖ 17880 models tested

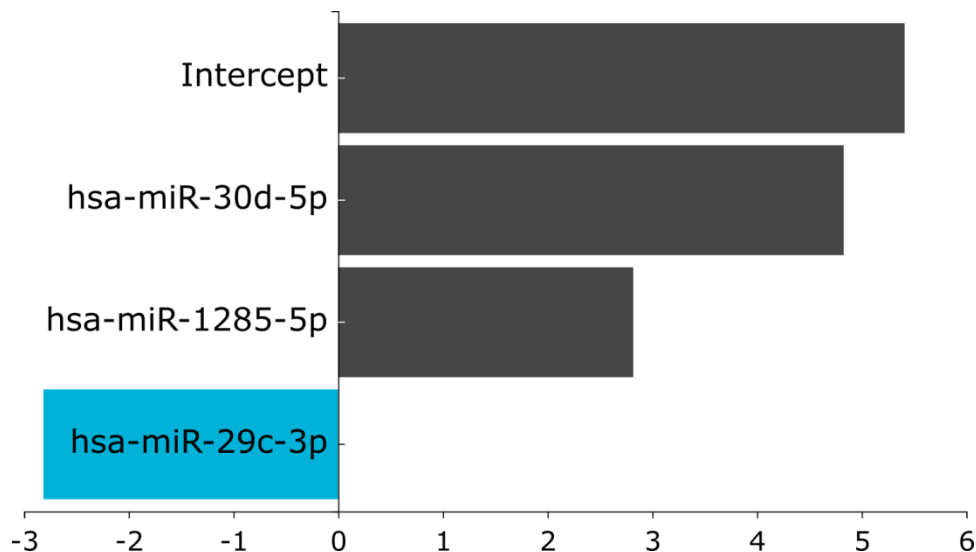
## During the Analysis, JADBio

1. Applies AI rules
2. Selects Features
3. Trains classification models
4. Optimizes model selection
5. Estimates model's performance
6. Creates plots

## What you get:

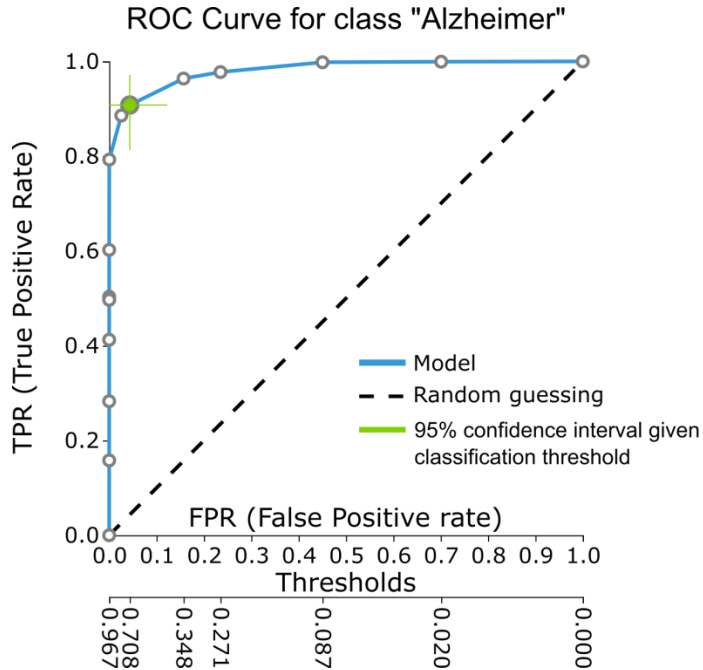
- ✓ Optimal executable model
- ✓ Estimates of model's performance

## Best interpretable model: Ridge Logistic Regression



- ❖ JADBio displays three, out of the 504 measured variables, that provide the most accurate prediction of an Alzheimer's diagnosis.
- ❖ Along with the intercept, these variables include two miRNAs whose expression is in a positive relationship to the diagnosis, and another miRNA whose expression is in a negative relationship to the diagnosis.
- ❖ The values describe the relative strength of the predictors based on the model.

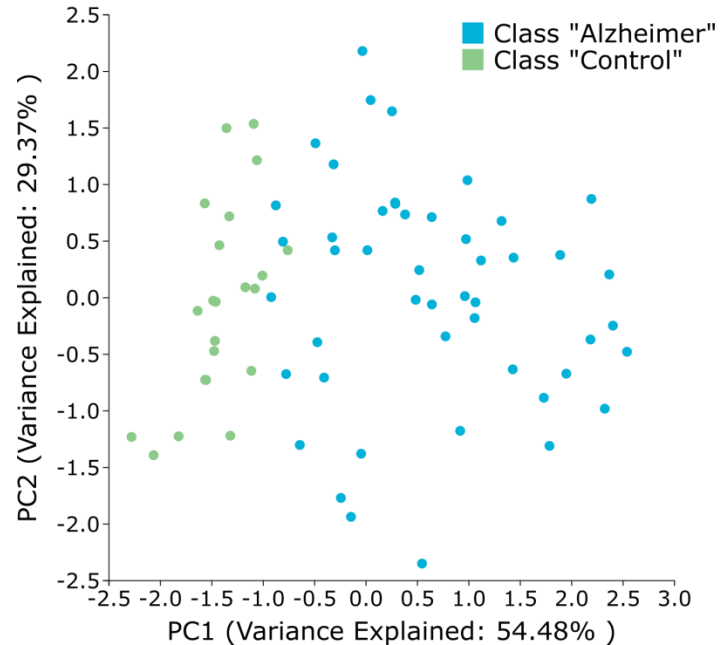
## Performance overview



**AUC : 0.974 (0.902 – 1.000)**

## Analysis visualization

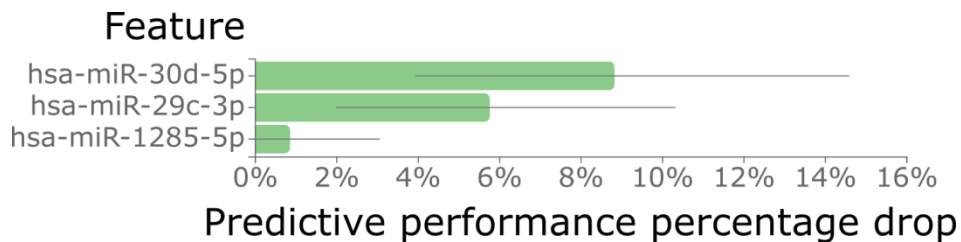
Supervised Principal Component Analysis (PCA)



# Signature

From the complete dataset, JADBio produces **Signatures** each of which includes a minimal-size subset of variables that are jointly predictive of the outcome of interest.

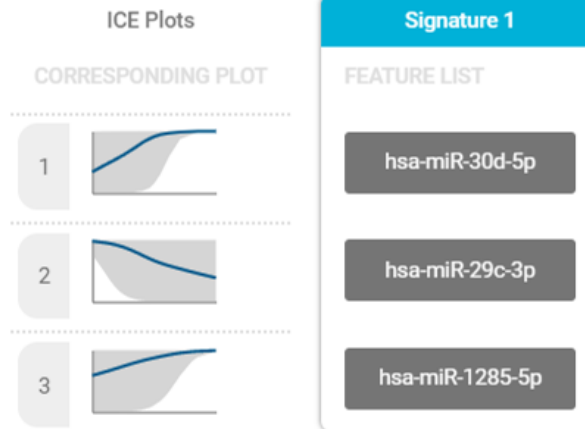
For this analysis, 1 signature was produced...



## Summary

JADBio selected **3** out of **503** features in the original dataset for the reference signature. In total there is only 1 signature.

Show ICE plots





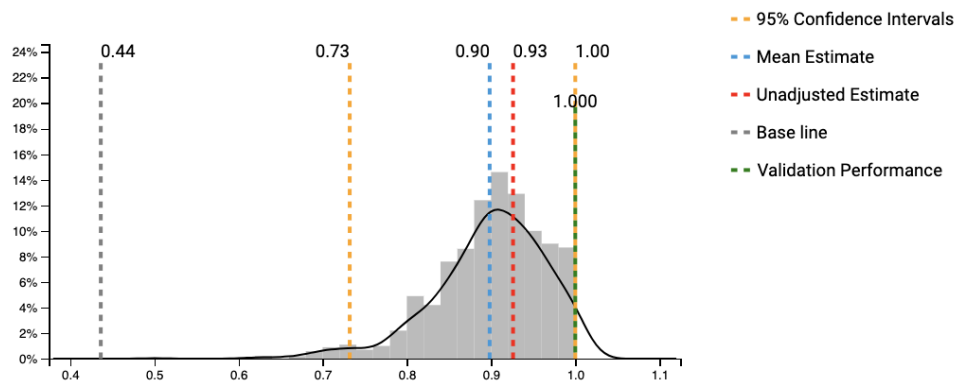
## Apply model

JADBio includes three different methods for model testing:

- External validation, using another dataset
- Prediction, using an unlabeled dataset
- Test, using custom values

And In JADBio Premium...

- Export the model and execute outside JADBio



*External Validation*

## Conclusion

- ❖ JADBio, applied to Leidinger P et al.'s, miRNA data, produces accurate diagnostic models that are on par with the ones presented in the original publication.
- ❖ Furthermore, JADBio requires no expert knowledge of advanced machine learning techniques.
- ❖ These results show JADBio can produce a diagnostic model for early diagnosis of Alzheimer's disease in a automated way.



# Thank you!



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