



Predicting survival after surgery from miRNAs profiles in Low-Grade-Glioma biopsies

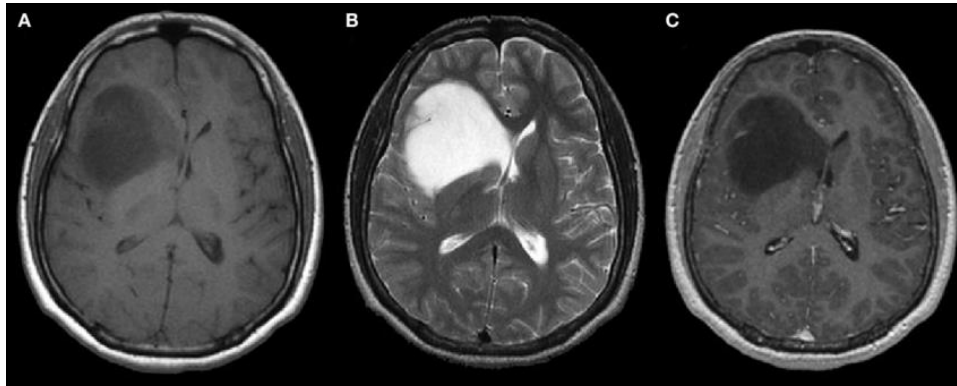
LGG_TCGA case study

Background

- ❖ Low-grade gliomas (LGGs) are a diverse group of primary brain tumors that often arise in young, otherwise healthy patients.
- ❖ Generally, LGGs have an indolent course with longer-term survival in comparison with high-grade gliomas.
- ❖ Predicting the survival time of LGG patients is a difficult task. Known prognostic factors e.g. age, tumor size/location, extent of surgical resection, and histological subtype do not adequately explain the progression and survival differences in low grade glioma patients.
- ❖ This information will aid medical oncologists in understanding disease progression and achieving more personalized care and better management of patients with these aggressive tumors.

Application / Clinical relevance

A reliable test that predicts survival probability of LGG patients could be derived from the analysis of miRNA tumor profiles data.



Typical MRI scan of a low-grade glioma

https://www.researchgate.net/figure/Typical-MRI-scan-of-a-low-grade-glioma-histopathologically-defined-as-a-WHO-grade-II_fig1_5865092



miRNA Microarrays

<https://www.agilent.com/en/product/mirna-microarray-platform/mirna-microarrays/sureprint-human-mirna-microarrays-22851>

The Experiment and The Data

Data from The Cancer Genome Atlas (TCGA) where we want to identify predictors for Low-Grade Gliomas (LGG) survival probability

Samples:

501 primary tumor biopsies

Potential predictors:

616 miRNA expression profile
clinical information

age, gender and primary diagnosis
(type of cell, anaplasia)

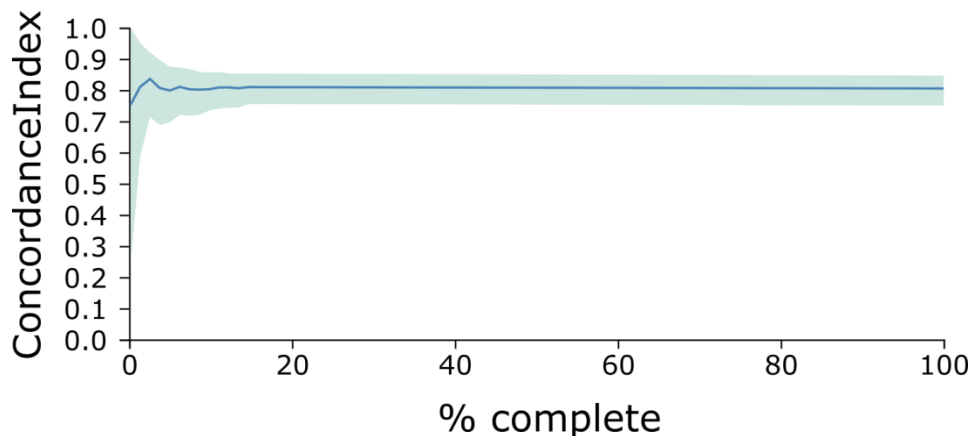
Target:

Vital Status, Time to Event



Data available at: <https://portal.gdc.cancer.gov/>

Running JADBio



- ❖ Analysis type: typical
- ❖ Total time: 03:31:52
- ❖ 176 models tested

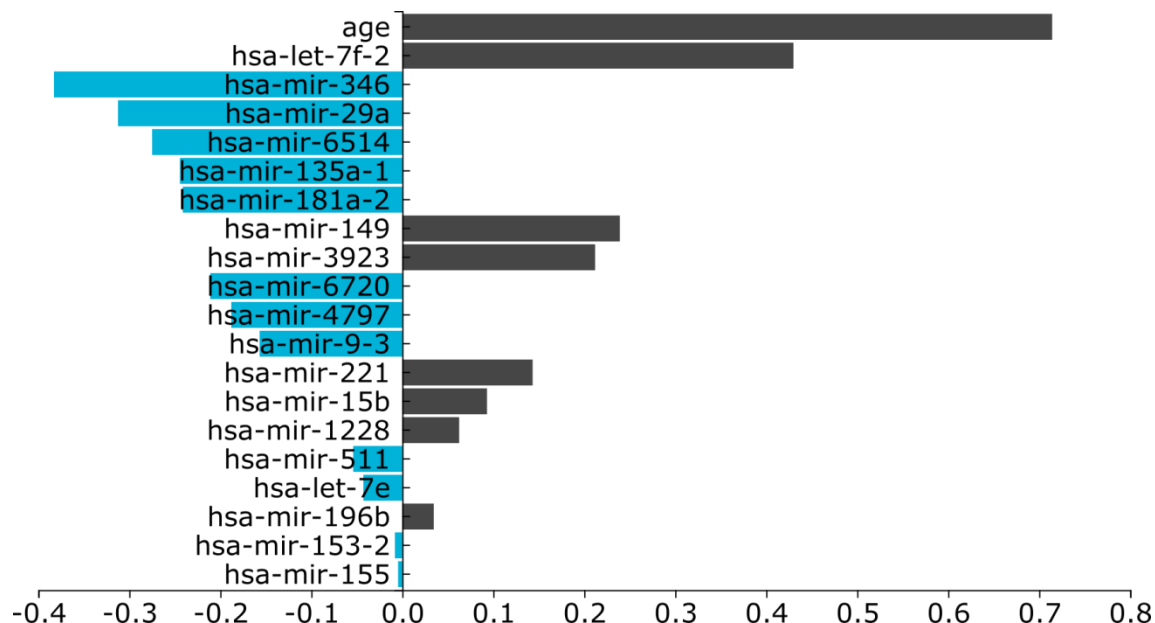
During the Analysis, JADBio

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

What you get:

- ✓ Optimal Model
- ✓ Estimates of Model's performance

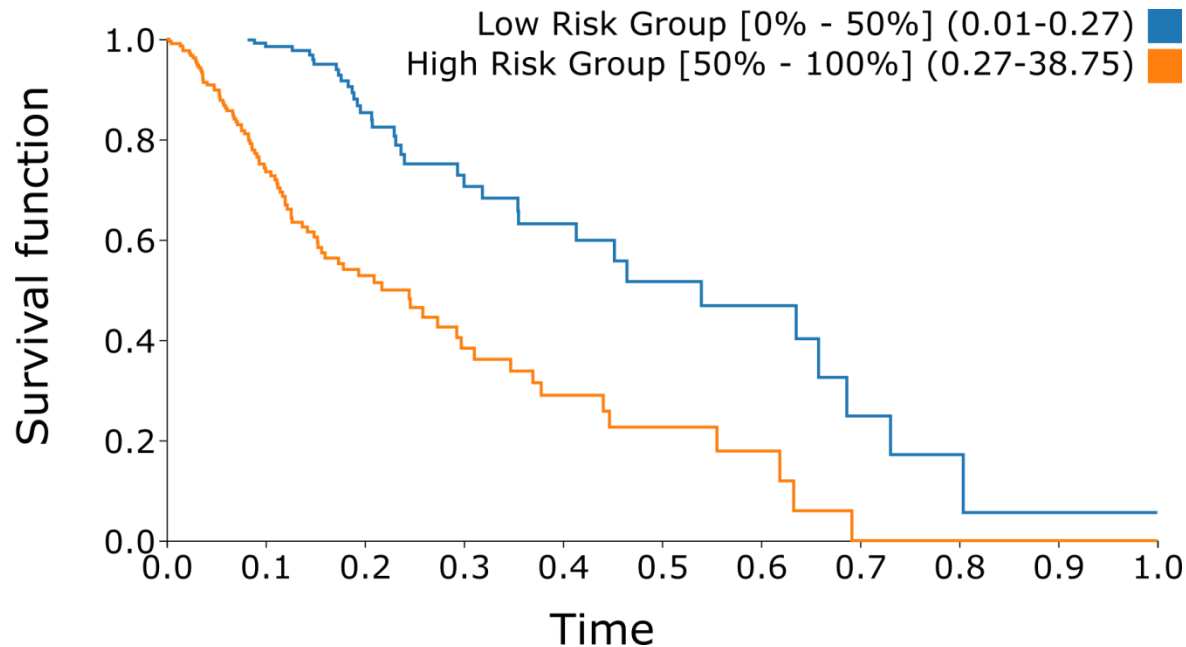
Best performing model: Ridge Cox Regression



- ❖ JADBio displays the 20, out of the total 621 features, that provide the most accurate prediction of survival probability of patients.
- ❖ For this model, ten microRNA's are in a negative relationship to the survival probability, and the age, and another nine microRNA's are in a positive relationship to the survival probability.
- ❖ The values describe the relative strength of the predictors based on the model.

Performance overview

Analysis
visualization



CI index : 0.802 (0.750 – 0.846)

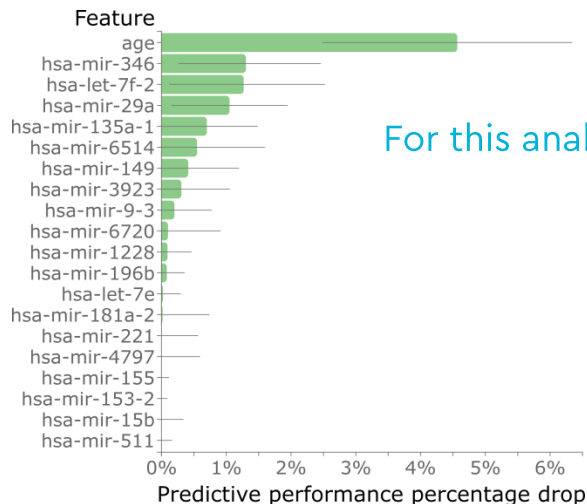
Equivalent signatures

JADBio calculates all relevant biosignatures, that is, minimal-size subsets of variables that are jointly predictive of the outcome of interest.

Apply model

JADBio offers four different methods for model testing:

- External validation, using another dataset
- Prediction, using an unlabeled dataset
- Test, using custom values
- Export the model and execute outside JADBio



Summary

JADBio selected 20 out of 619 features in the original dataset for the reference signature. In total there is only 1 signature.

For this analysis, 1 signature was produced...

Show ICE plots

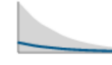
ICE Plots

CORRESPONDING PLOT

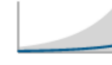
1



2



3



4



5



Signature 1

FEATURE LIST

age

hsa-mir-346

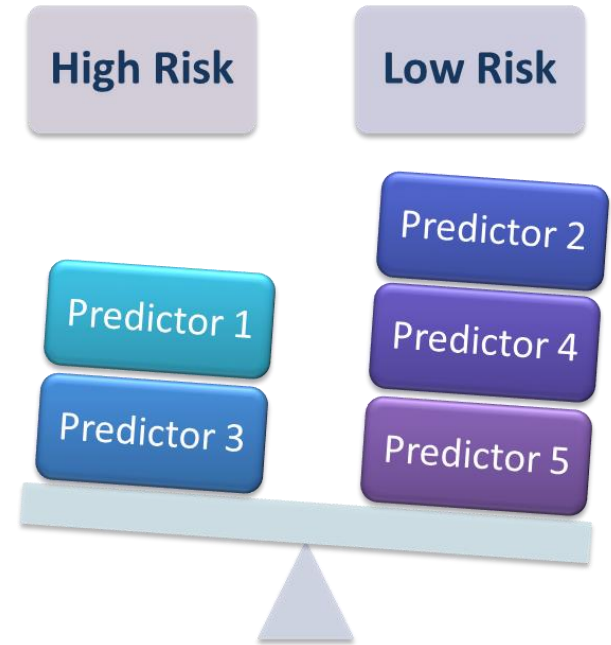
hsa-let-7f-2

hsa-mir-29a

hsa-mir-135a-1

Conclusion

- ❖ JADBio®, applied to miRNA data and clinical information including primary diagnosis, age, gender from The Cancer Genome Atlas, produces accurate and simple prognostic/predictive models that corroborate the findings of an independent publication¹.
- ❖ Furthermore, JADBio requires no expert knowledge on advanced machine learning techniques.
- ❖ These results show JADBio can produce an accurate predictive model for survival probability in LGG in a automated way.



Thank you!



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