ML combining multi-omics data and network algorithms identifies adrenocortical carcinoma prognostic biomarkers

Biomarker ID (multi-omics)

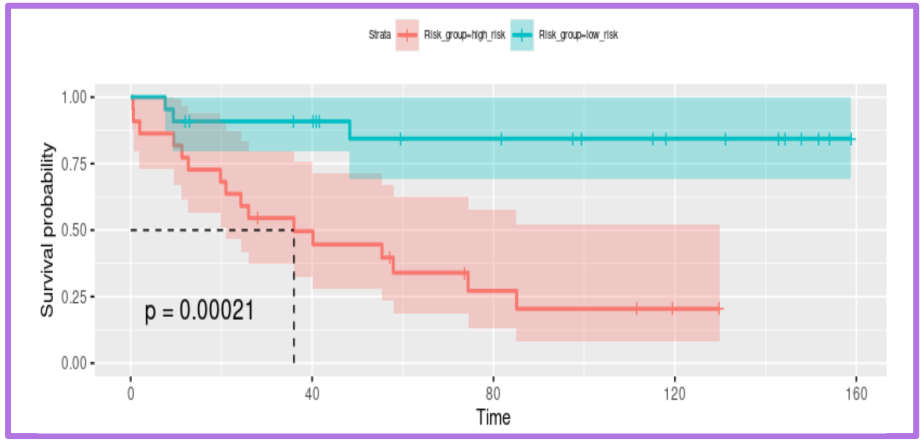
Background and Objectives:

- Multi-omics approaches offer a more comprehensive profiling over single modalities. However, their meaningful integration remains a challenge.
- Demonstrate advantages of network-based integration for biomarker identification in multi-omics datasets

Key Business Questions:

- Can network-based approaches improve the predictive power of multi-omics biomarker identification methods?

Clarivate research paper Published in Front. Mol. Biosci



Solution

- Dataset: GDC TCGA Adrenocortical Cancer (ACC) datasets, and the corresponding phenotypic and clinical data from the UCSC Xena Browser
- Integration of **mRNA**, **micro-RNA** and **methylation** data to identify a **multi-omics** signature using the N-Integration (DIABLO) method.
- Published in ***Front. Mol. Biosci., 06 November 2023. Sec. Molecular Diagnostics and Therapeutics. Volume 10 - 2023 | https://doi.org/10.3389/fmolb.2023.1258902***

Outcomes

- Using multi-omics data integration, combining machine learning and **Clarivate systems biology tools** (MetaBase™, Computational Biology for Drug Discovery), we were able to create the **most complete ACC signature to date with 210 biomarkers**.
- A large fraction of the identified biomarkers using multi-omics integrative analysis are known biomarkers already under investigation, validating the approach .
- Identified multi-omics biomarkers were found to be associated with overall survival using an **external dataset**. These included HAUS8, PLXNA1, SHB,UBE2S, DDX39A, N4BP2L1, TSPYL4 , hsa-miR-376c, hsa-miR-504, hsa-miR-615 and hsa-miR-1258.

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