

A computational pipeline for translating spatial proteomics into prognostic biomarkers for GEP-NETs

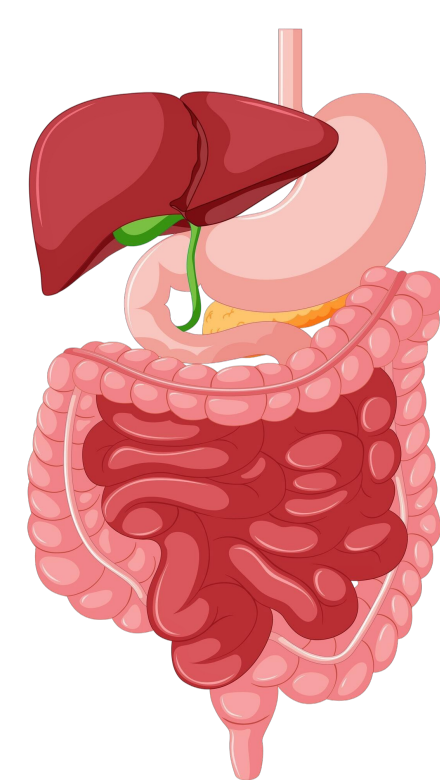
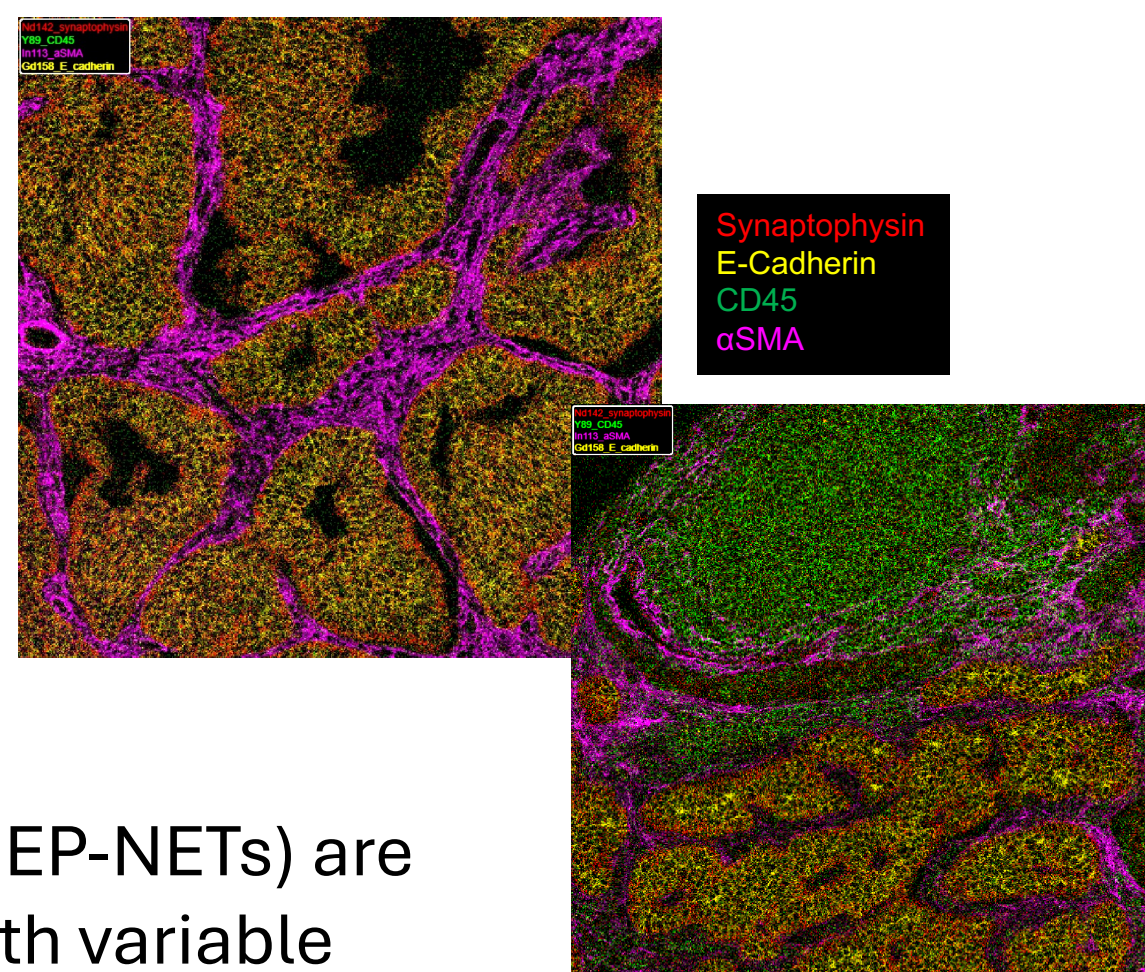
Anushka Poddar¹, Tianfeng Miao¹, Alexander Xu¹

¹Fischell Department of Bioengineering, University of Maryland, College Park, MD



Background

- Spatial proteomics enables high-resolution characterization of tumor microenvironments by capturing protein expression within tissue's spatial context
- Gastroenteropancreatic neuroendocrine tumors (GEP-NETs) are heterogeneous cancers with variable clinical outcomes, requiring improved prognostic strategies
- Single-cell imaging data is expensive, complex, and difficult to translate into clinically useful prognostic tools
- Computational approaches can convert high-dimensional spatial data into practical composite biomarkers for patient risk assessment in clinical settings¹



Objective

Apply machine learning methods to translate spatial proteomics data into composite biomarkers for predicting patient survival in gastroenteropancreatic neuroendocrine tumors (GEP-NETs)

Results

Target Variable: Progression-Free Survival (PFS); **Cohort:** Pancreatic Cancer – Primary Tissue Samples

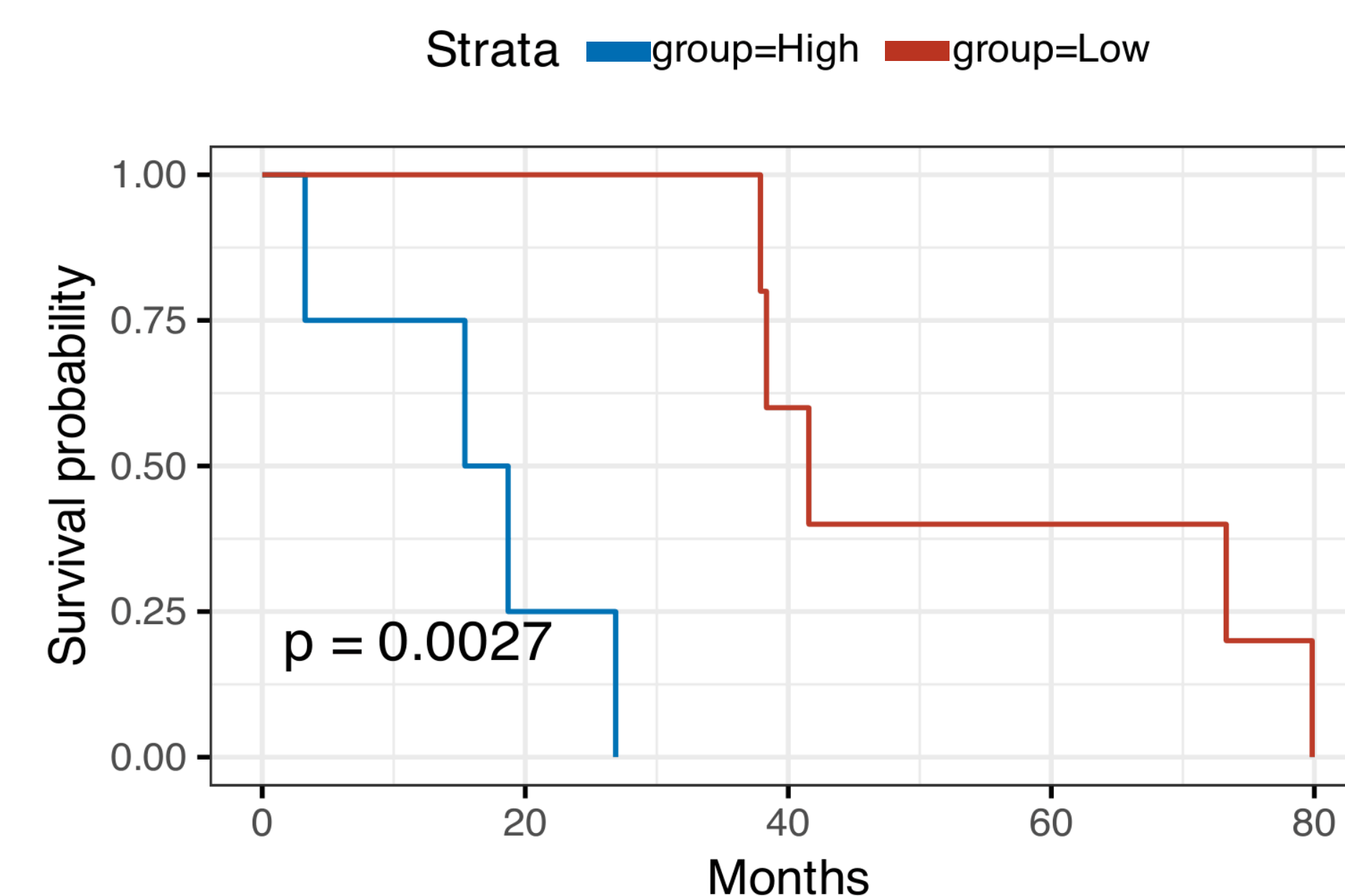
Selected Variables

Variable	Coefficient
NKG2D__in__CD4	-16.846213
IL6__in__CD8	-30.757105
Myel.dist.1__in__B	-4.038059

Predicted Risk Score vs. Survival

Patient #	Risk Score	PFS (months)
24	3.22	3.3
22	1.82	15.4
21	1.65	18.7
15	0.74	26.9
20	0.70	38.3
23	-0.24	37.9
18	-0.87	73.3
16	-3.47	79.8
19	-3.54	41.6

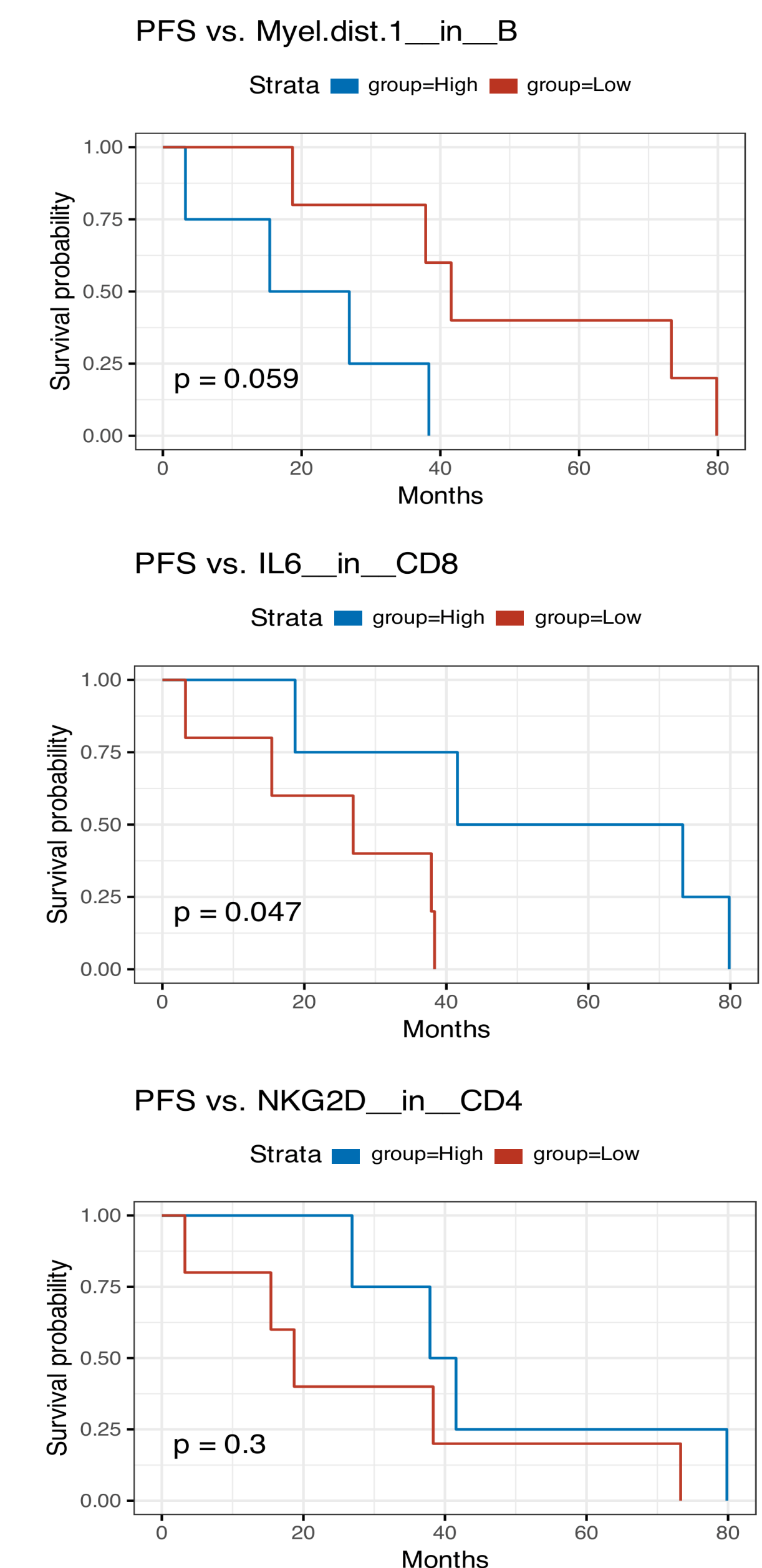
Survival Stratification of Predicted Risk Groups



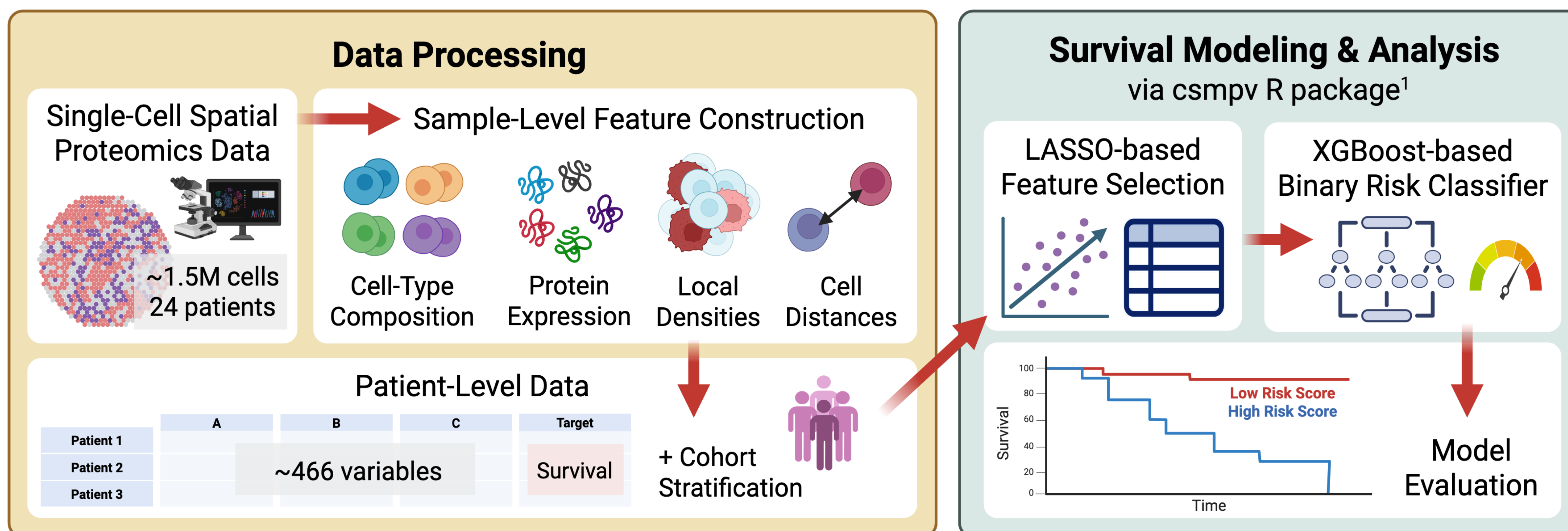
Forest Plot (Cox HRs) for Selected Variables

Variable	N	Hazard ratio	p
NKG2D__in__CD4	9	0.00 (0.00, 1773.77)	0.2
IL6__in__CD8	9	0.00 (0.00, 6123.89)	0.1
Myel.dist.1__in__B	9	0.02 (0.00, 24447.59)	0.6

Univariate Models of Selected Variables



Methods



Conclusions

- Composite biomarkers produced stronger survival stratification than any individual feature, demonstrating the value of multivariate regression
- Modeling effectively reduced hundreds of variables into a small, informative set of features for patient risk stratification
- Limitations of the analysis included small sample size, need for manual feature filtering, and inconsistent biological interpretability
- Overall, this work enables translation of single-cell spatial proteomics data into practical composite biomarkers that are more feasible for clinical deployment and can improve survival prediction in cancers like GEP-NETs

References

[1] Jiang A (2025). *csmvp: Biomarker Confirmation, Selection, Modelling, Prediction, and Validation*. R package version 1.0.5. Methods figure created with Biorender.com.