

BNeurich: Bayesian Networks for Patient Specific Pathway Enrichment by Integrating Multi-Omics Data with Partial Overlaps

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1st supervisor: Prof. Dr. Martin Hofmann-Apitius

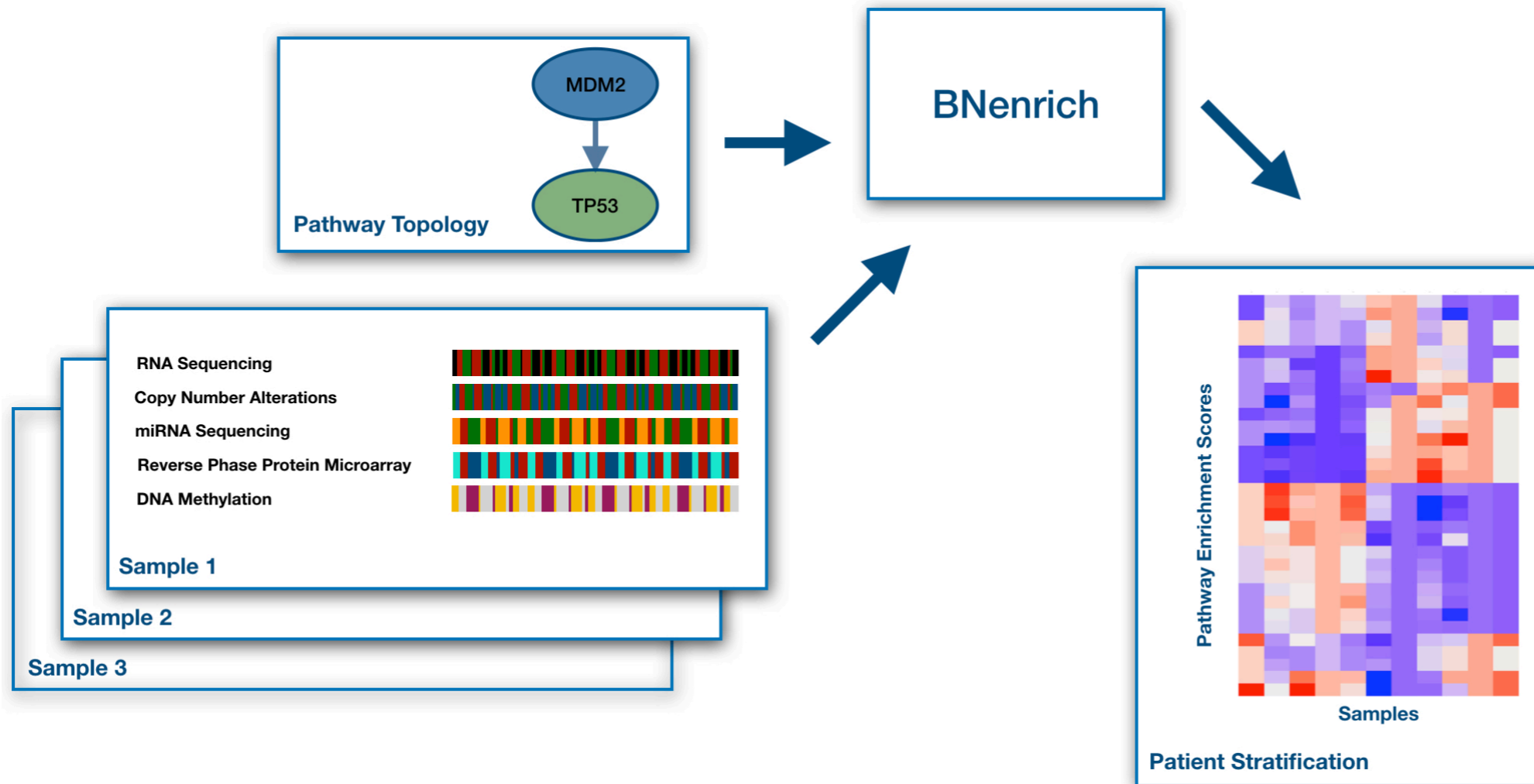
2nd supervisor: Prof. Dr. Holger Fröhlich

Motivation

BNenrich: Bayesian Networks for Patient Specific Pathway Enrichment by Integrating Multi-Omics Data with Partial Overlaps

- The idea of systems biology: *“the whole is greater than the sum of the parts^{*}”*
- The characterization of patient level diversity can be conceptualized via pathway topologies as alterations often involve common pathways
 - Enables patient stratification → personalized medicine
- It is important to deal with the heterogeneity in the coverage of omics data types to be able to utilize all the available resources rather than coupled samples
- Bayesian Network has been applied in data integration over a decade and showed successful results

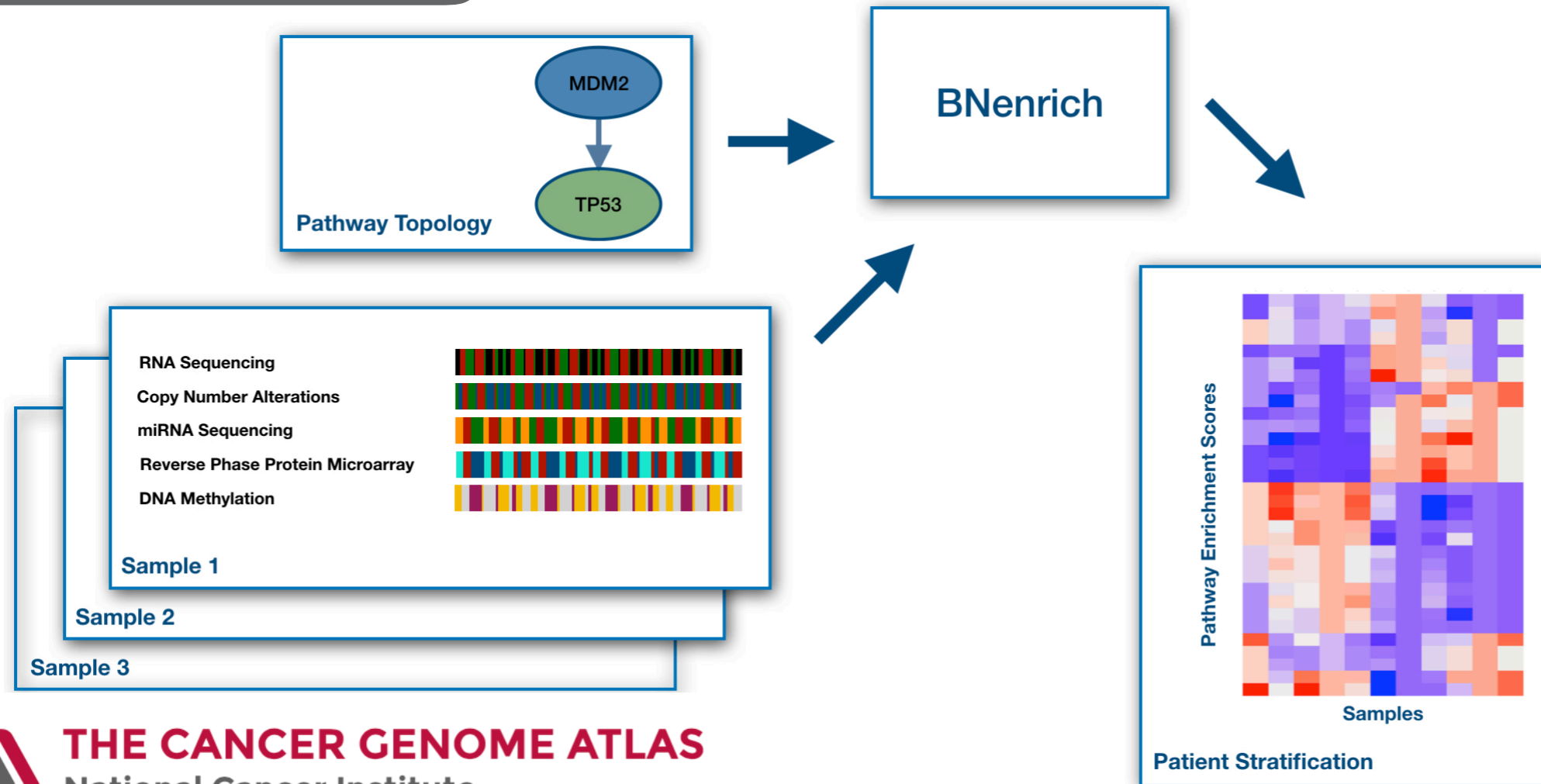
Overview of the Methodology



- The method measures the agreement of patient's network profile with the other patients' profile to estimate patient-wise enrichment scores

Overview of the Methodology

National Cancer Institute (NCI)
Pathway Interaction Database (PID)



NIH **THE CANCER GENOME ATLAS**
National Cancer Institute
National Human Genome Research Institute

Colorectal adenocarcinoma (COADREAD) (CRC)

Results

1. All the pathways that were declared as significant by BNenrich were found to be related to the disease in the literature

Enriched Pathways

ALK2 signaling events

Endothelins networks

Glypican-1 network

ARF1 pathway_1

EphA forward signaling

IL6-mediated signaling events

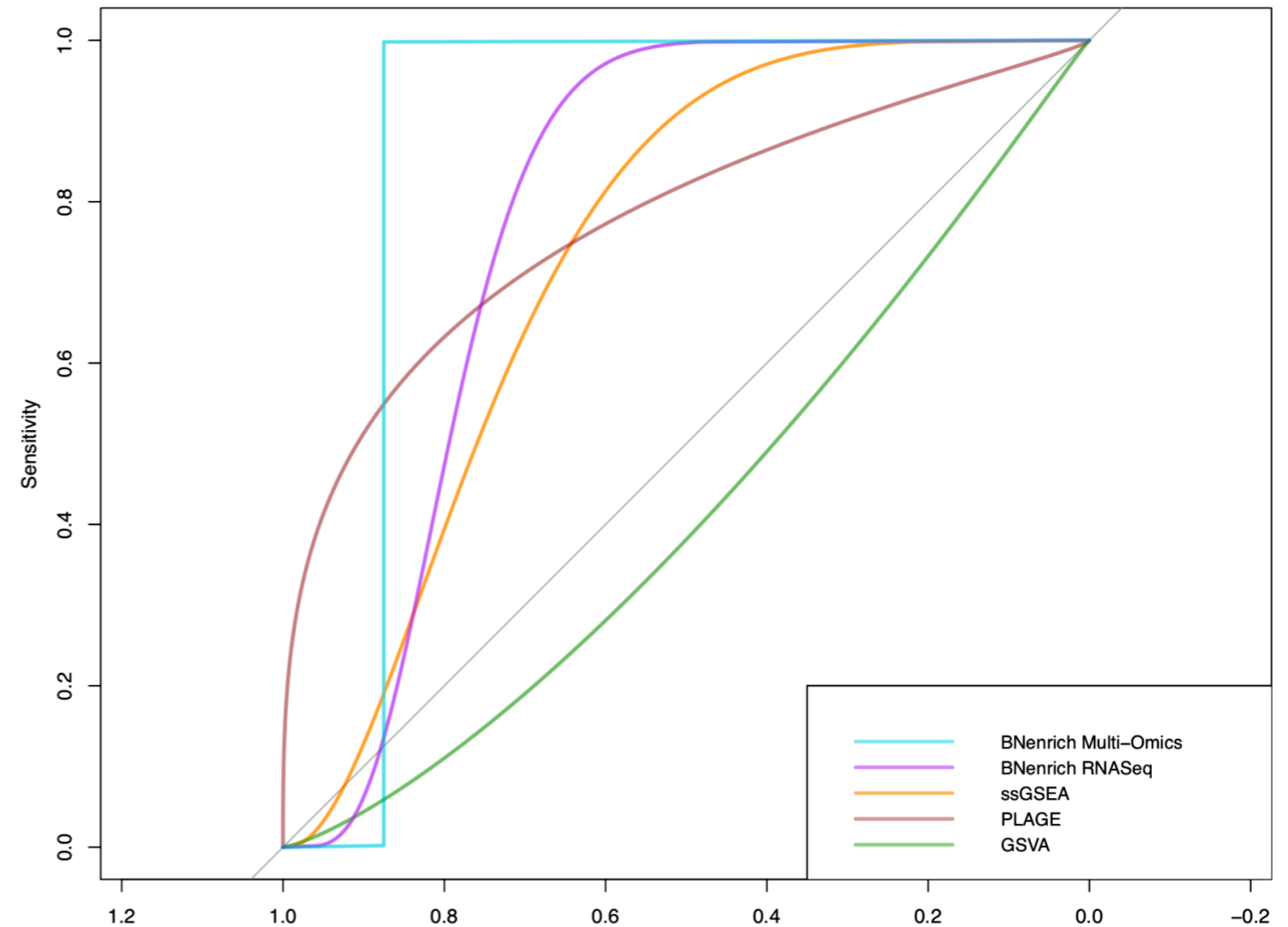
Thromboxane A2 receptor signaling_1

IL8- and CXCR1-mediated signaling events_2

Results (cont.)

2. Diagnostic accuracy (sensitivity-specificity)

- BNeurich showed the best performance of accuracy when tested with the above mentioned pathways

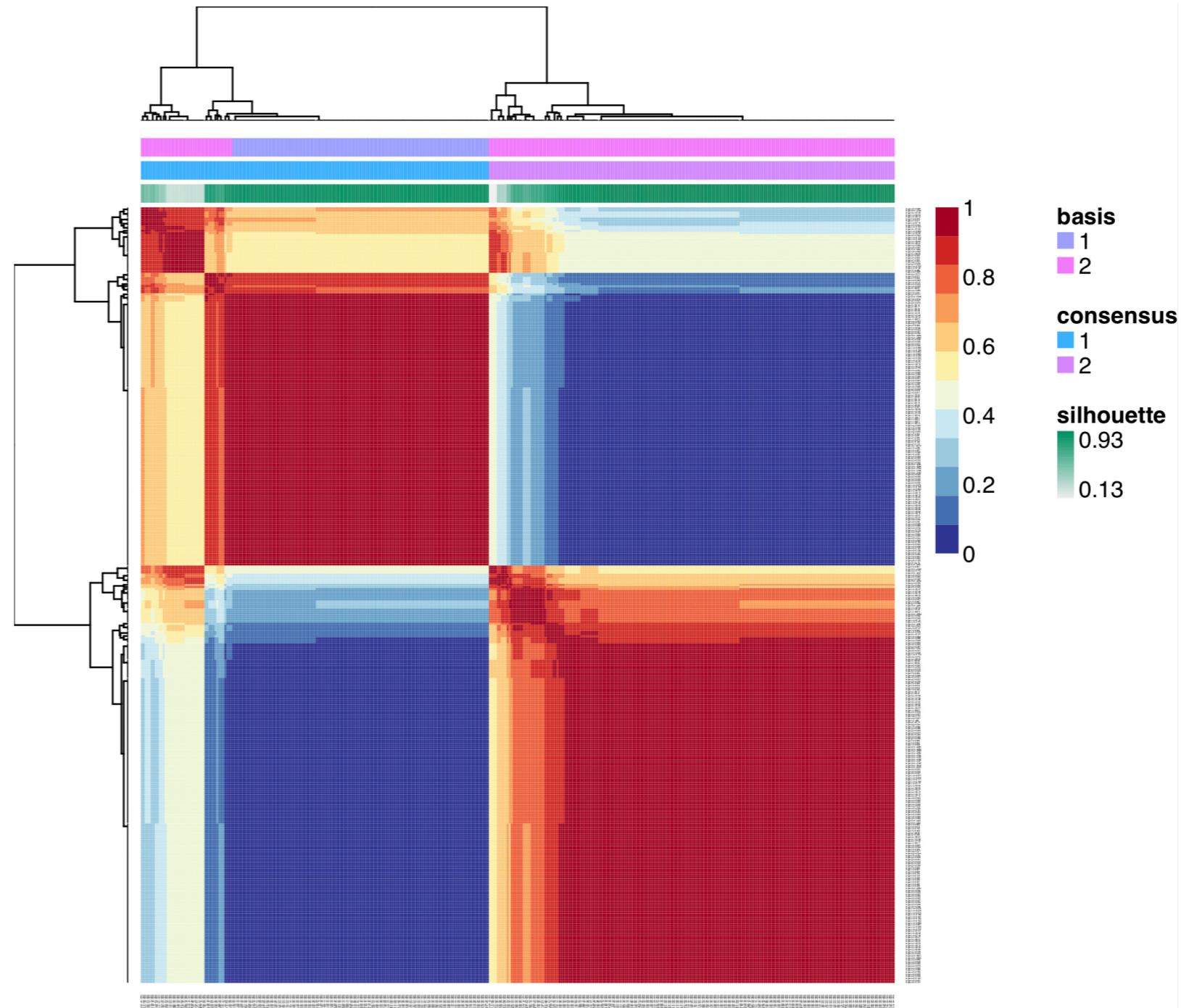


	BNeurich Multi-Omics	BNeurich RNAseq	ssGSEA	GSVA	PLAGE
AUC Scores	0.9062	0.7812	0.7812	0.3906	0.7969
95 % CI	0.7182-1	0.5093-1	0.5429-1	0.09101-0.6902	0.5569-1

Results (cont.)

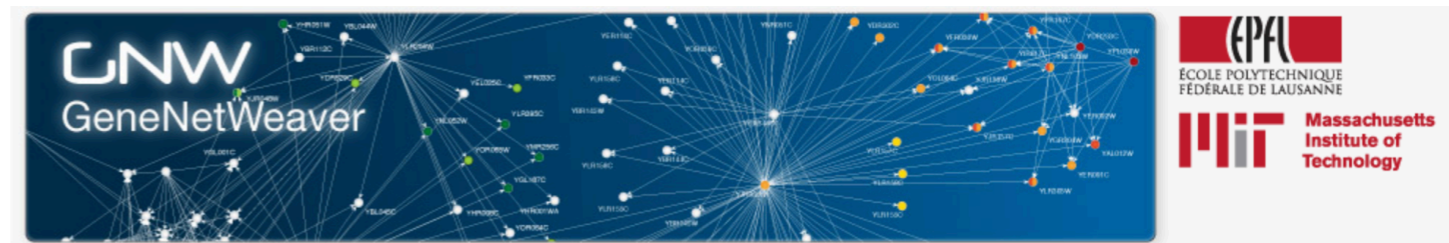
3. Clear patient stratification

- Non-negative Matrix Factorization (NMF) clustering



Future Outlook

- The method needs to be further evaluated on more datasets: TCGA Breast Cancer Dataset
- Better understanding about the sensitivity and specificity of the method: study with simulated data



Thank you!