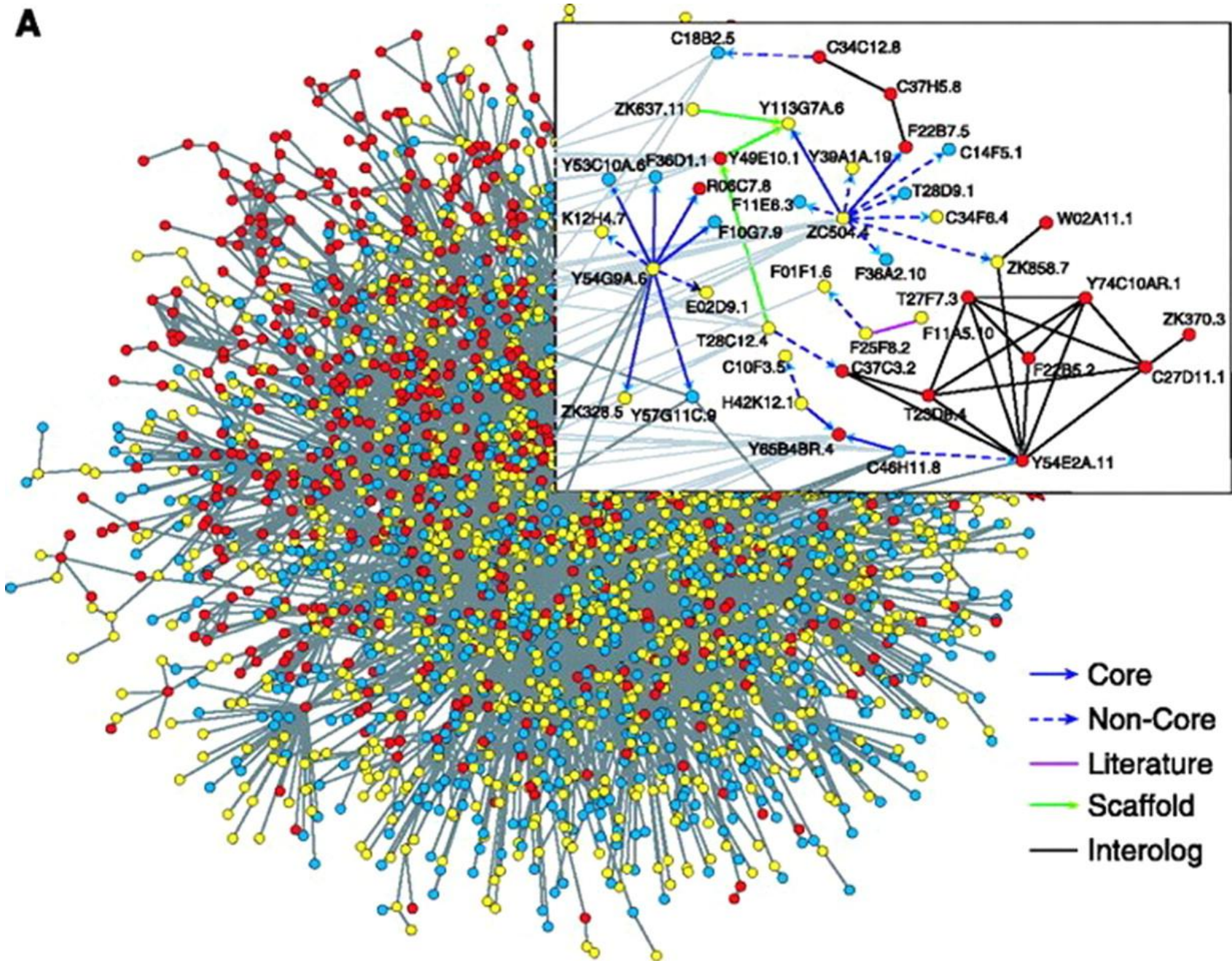


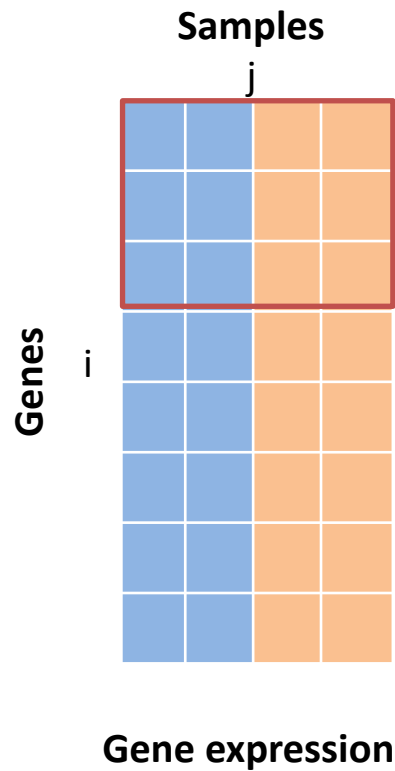
A

Y113G7A.6
Y49E10.1
Y39A1A.19
F22B7.5
C14F5.1
T28D9.1
C34F6.4
W02A11.1
ZK858.7
Y74C10AR.1
ZK370.3
C27D11.1
F27B5.2
Y54E2A.11
C46H11.8
T25Q9.4
C37C3.2
F25F8.2
F11A5.10
T27F7.3
F36A2.10
F01F1.6
ZC504.4
F10G7.9
F11E8.3
R06C7.8
Y53C10A.6
F36D1.1
K12H4.7
Y54G9A.6
E02D9.1
T28C12.4
C10F3.5
H42K12.1
Y65B48R.4
Y57G11C.9
ZK328.5
C18B2.5
C34C12.8
C37H5.8

→ Core
- - - Non-Core
→ Literature
→ Scaffold
— Interolog

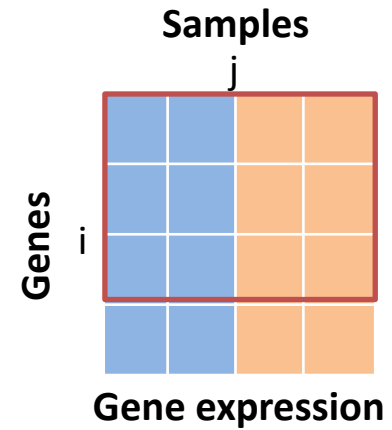


Primary Tumor Metastatic Tumor



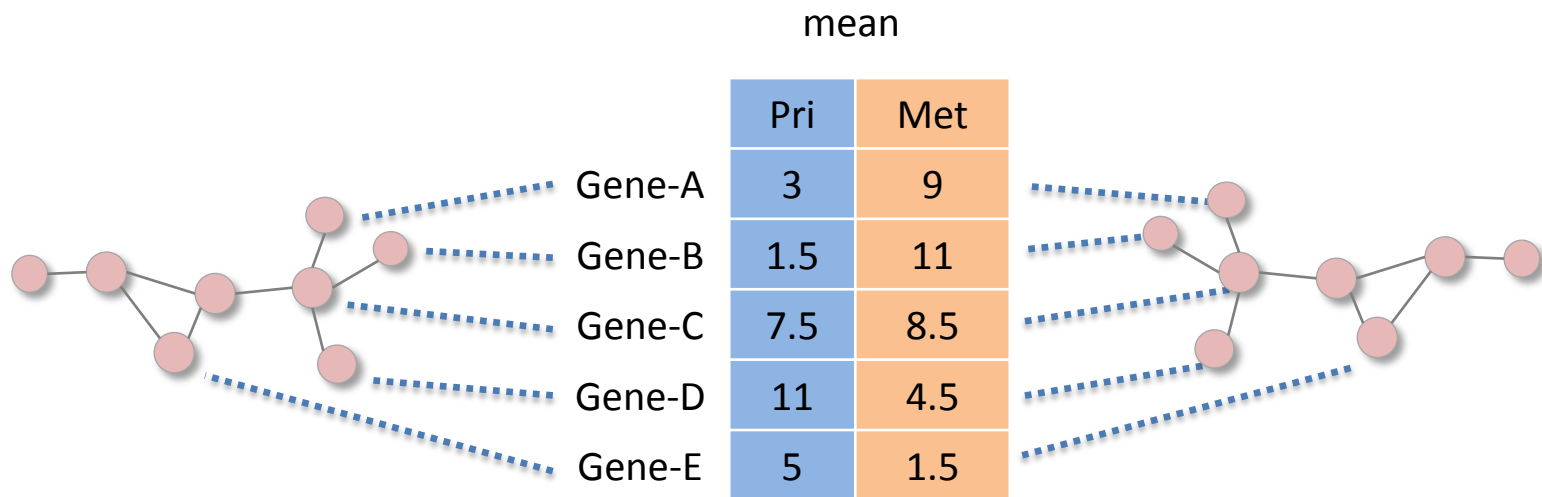
Consider only the genes
that are present in PPI

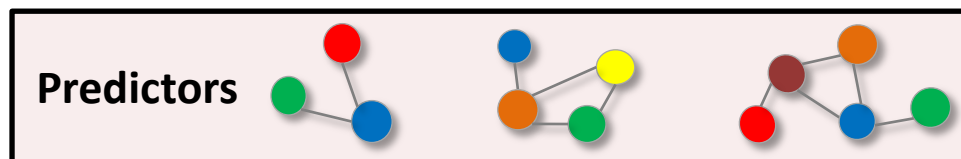
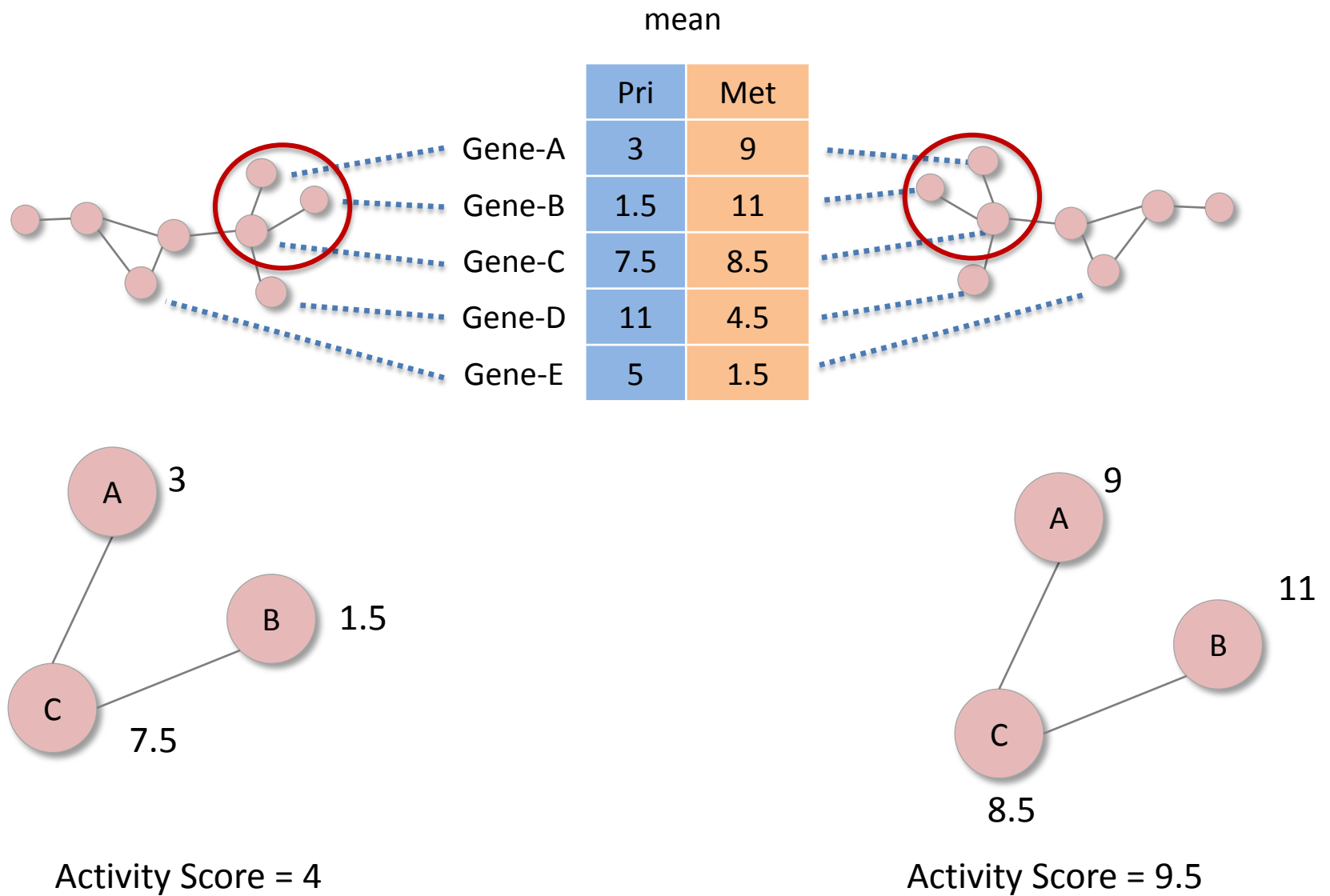
~ 9000 Genes



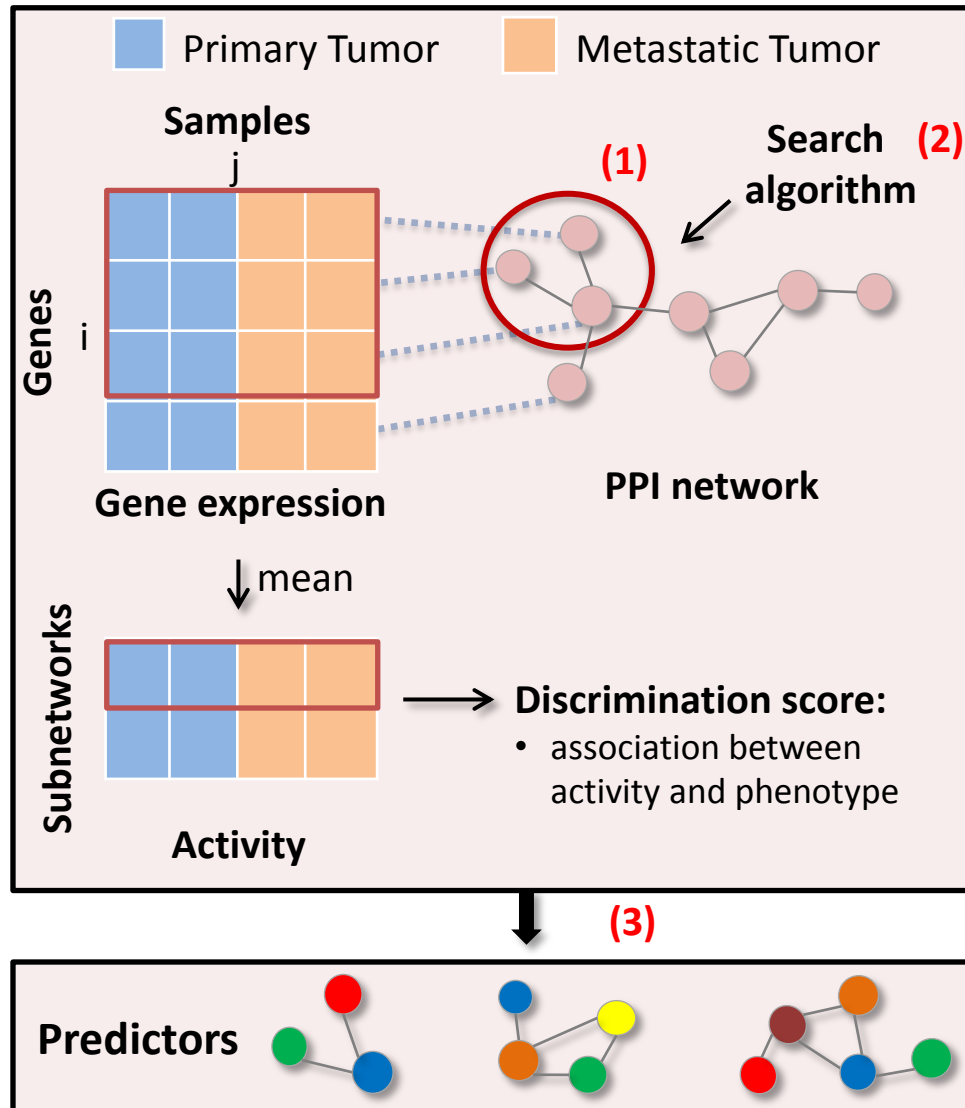
		Samples			
Genes		Pri-1	Pri-2	Met-1	Met-2
	Gene-A	2	4	8	10
	Gene-B	1	2	10	12
	Gene-C	7	8	9	8
	Gene-D	10	12	4	5
	Gene-E	5	5	1	2

Gene expression





Strategy for Identifying Subnetwork Markers



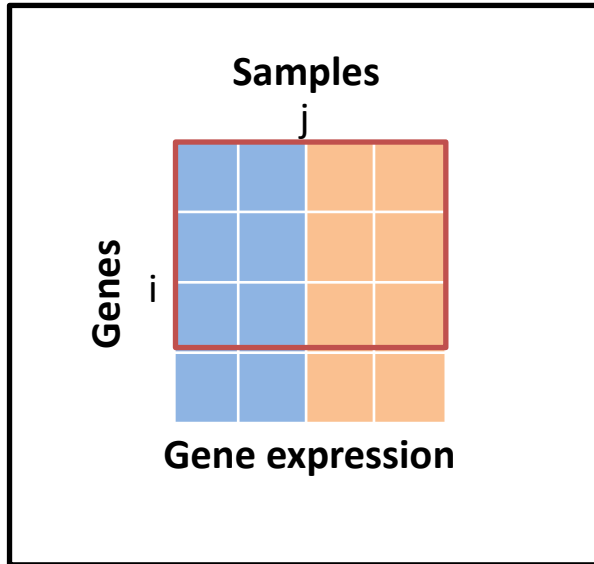
Optimally discriminative subnetwork markers predict response to chemotherapy

Phuong Dao^{1,†}, Kendric Wang^{2,3,†}, Colin Collins^{3,4,*}, Martin Ester¹, Anna Lapuk^{3,*,‡} and S. Cenk Sahinalp^{1,*,‡}

¹School of Computing Science, Simon Fraser University, ²Bioinformatics Training Program, University of British Columbia, ³Vancouver Prostate Centre and ⁴Department of Urology, University of British Columbia

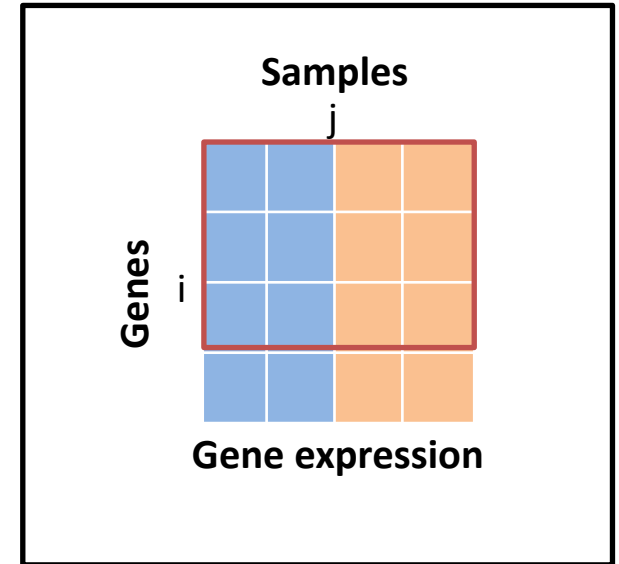
- 1. Data Integration**
Overlay gene expression onto PPI network
- 2. Search**
Find most differentially active subnetworks (search algorithm)
- 3. Marker Selection**
Rank and select top subnetworks as predictors

Training Dataset



Dataset we are processing

Test Dataset



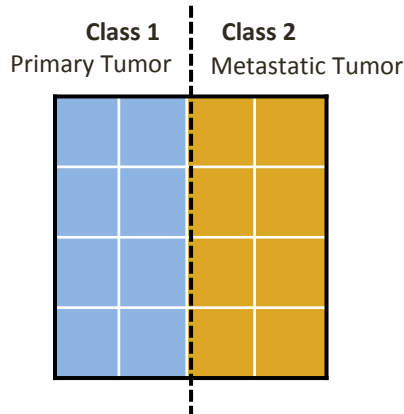
Other dataset
(Already processed)

SubNetwork Markers are Discovered
from Training set



Performance of the SubNetwork
Markers are tested

Classification Performance



		Predicted Class	
		1 (+)	2 (-)
Known Class	1 (+)	True Positive (TP) Primary Tumor Classified Correctly as Primary Tumor	False Positive (FP) Primary Tumor Classified Incorrectly as Metastatic Tumor
	2 (-)	False Negative (FN) Metastatic Tumor Classified Incorrectly as Primary Tumor	True Negative (TN) Metastatic Tumor Classified Correctly as Metastatic Tumor

Matthews Coefficient Correlation (MCC):

- used as a measure to determine the quality of the classifiers
- returns a value between -1 and +1
 - +1 : perfect prediction,
 - 0 : random prediction
 - -1 : total disagreement between prediction and observation

$$MCC = \frac{TP \times TN - FP \times FN}{\sqrt{(TP + FP)(TP + FN)(TN + FP)(TN + FN)}}$$

Classification Performance with Varying No. of Top Subnetworks

