Name: Rupam Bhattacharyya

Affiliation: Department of Biostatistics, University of Michigan

Current Status: PhD Student, Second Year

Attached Documents:

1. Unofficial Transcript (Proof of academic status),

2. Presentation Poster.

THE UNIVERSITY OF MICHIGAN – ANN ARBOR

Unofficial Transcript - Not an Official Transcript

Bhattacharyya,Rupam
UM ID: 65143773 UIC: 9430895847
Uniqname: RUPAMB

Date: May 5, 2020

Citizen: Non-Resident Alien
Visa: F1

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United States

Fall 2018		Rackham	Grade	Hours	MSH	CTP	MHP
BIOSTAT	653	Appl Stat III:ANOVA	A+	3.00	3.00	3.00	12.90
BIOSTAT	666	Num Meth H Gen	A+	3.00	3.00	3.00	12.90
BIOSTAT	801	Advanced Inference I	A	3.00	3.00	3.00	12.00
BIOSTAT	810	Appr to Resp Biostat	S	1.00	0.00	1.00	0.00
BIOSTAT	830	Adv Topics Biostat	A	3.00	3.00	3.00	12.00
Term Total		**GPA: 4.000**		**13.00**	**12.00**	**13.00**	**49.80**
Cumulative Total		**GPA: 4.000**			**12.00**	**13.00**	**49.80**

Winter 2019		Rackham	Grade	Hours	MSH	CTP	MHP
BIOSTAT	646	Mol Gen&Epigen Data	A-	3.00	3.00	3.00	11.10
BIOSTAT	699	Anl Bio Invest	B+	4.00	4.00	4.00	13.20
BIOSTAT	802	Advanced Infer II	A+	3.00	3.00	3.00	12.90
Term Total		**GPA: 3.720**		**10.00**	**10.00**	**10.00**	**37.20**
Cumulative Total		**GPA: 3.954**			**22.00**	**23.00**	**87.00**

Fall 2019		Rackham	Grade	Hours	MSH	CTP	MHP
BIOSTAT	606	Intro Biocomputing	S	1.00	0.00	1.00	0.00
BIOSTAT	625	Comp with Big Data	A-	3.00	3.00	3.00	11.10
BIOSTAT	880	Stat Analysis	A	3.00	3.00	3.00	12.00
EPID	515	Genetics in Pub Hlth	A	3.00	3.00	3.00	12.00
EPID	633	Intr Math Model Epid	A+	3.00	3.00	3.00	12.90
Term Total		**GPA: 4.000**		**13.00**	**12.00**	**13.00**	**48.00**
Cumulative Total		**GPA: 3.970**			**34.00**	**36.00**	**135.00**

Winter 2020		Rackham	Grade	Hours	MSH	CTP	MHP
BIOSTAT	830	Adv Topics Biostat	A	3.00	3.00	3.00	12.00
BIOSTAT	830	Adv Topics Biostat	A	3.00	3.00	3.00	12.00
EPID	516	Genetics in Epid	A+	4.00	4.00	4.00	17.20
Term Total		**GPA: 4.000**		**10.00**	**10.00**	**10.00**	**41.20**
Cumulative Total		**GPA: 4.000**			**44.00**	**46.00**	**176.20**

Academic Statistics for Rackham		**MSH**	**CTP**	**MHP**
Total to Date	**GPA: 4.000**	**44.00**	**46.00**	**176.20**

Program Action History: **Biostatistics Doc**
04/07/2018 Matriculation
Biostatistics PhD

Remarks
05/13/2019 Successful completion of the Foundations of Public Health Practice requirement in May 2019

Academic Previous Experience

Indian Statistical Institute	WB, India
Bachelor Equivalent	01/01/2019

End of Unofficial Transcript

TransPRECISE: Personalized Network Modeling of the Pan-Cancer Patient and Cell Line Interactome

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Introduction

The Problem

- **Precision Medicine:** Optimizing treatment to each individual patient.
- Large and informative datasets available.

Patients	ICGC, TCGA, TCPA
Cell Lines	CCLE, MCLP, GDSC
Drugs	NCI60, LINCS, DepMap

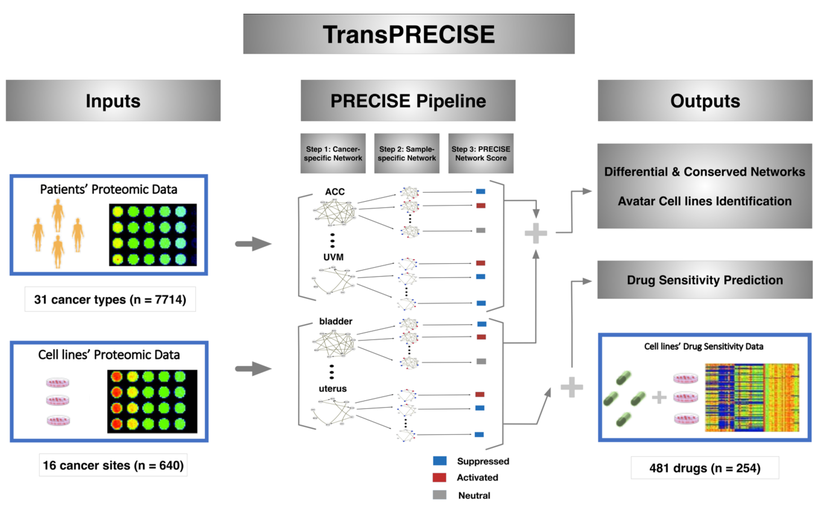
Challenges

- Bridge anticancer pharmacological data to large-scale omics.
- Utilize patient heterogeneity in clinical decision-making.

Features

- Interaction of genes and accumulation of small effects in functional pathways.
- Variation between (and possibly within) cancer lineages.
- Variation across model systems.

Datasets and Methods



- **Data Sources:** Patients – The Cancer Proteome Atlas (TCPA), Cell Lines – M D Anderson Cell Lines Project (MCLP), Drugs – Genomics of Drug Sensitivity in Cancer (GDSC).
- Twelve functional pathways used – including apoptosis, breast reactive, cell cycle, EMT, hormone signaling, RAS/MAPK, RTK.

Published Paper: SCAN ME

R Shiny App: SCAN ME

Model Formulation

$\mathbf{y}_{xi}$: expressions for protein i, x = cancer type for cell lines/patients.

$$\mathbf{y}_{xi} = \sum_{j \neq i} \beta_{ij}\mathbf{y}_{xj} + \epsilon_i = \mathbf{Z}_{xi}\boldsymbol{\beta}_i + \boldsymbol{\epsilon}_i,\ \boldsymbol{\epsilon}_i \sim N_n(\mathbf{0}_n, \sigma_i^2 I_n),$$

$$\boldsymbol{\beta}_i | g \sim N_{p-1}\left(\mathbf{0}_{p-1}, \sigma_i^2\left(\frac{1}{g}Z_i^T Z_i\right)^{-1}\right), g = n;\ p(\sigma_i) \propto \sigma_i^{-1}.$$

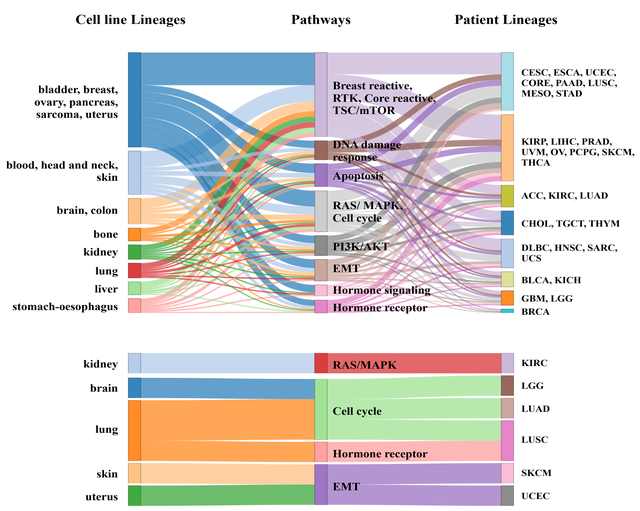
TransPRECISE scores based on inclusion probabilities computed as:

$$\kappa_j^* := \frac{1}{p}\sum_{i=1}^{p} p_{ij}^*(C_i + 1),\ * = +, - \text{ or } 0,$$

(activated, suppressed or neutral), C_i = connectivity of protein i.

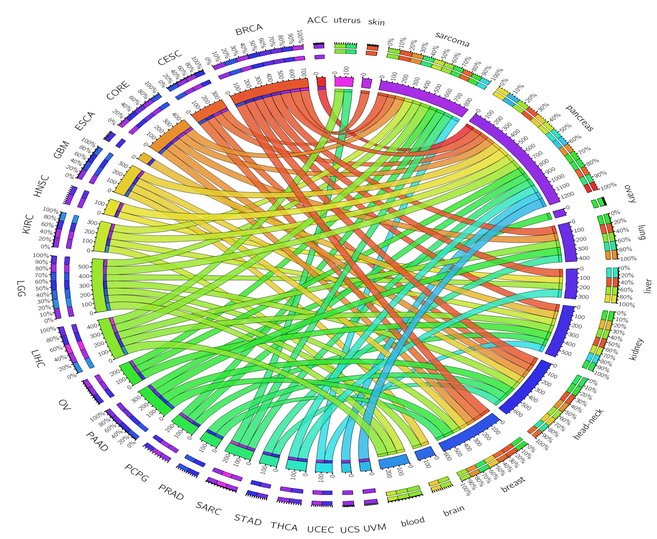
Results

Patient-Cell Line Network Similarity



Ovary and uterus cell lines were connected via the **hormone signaling** pathway to **BRCA**.

Bladder cell lines were connected to **BLCA** via the **core reactive** pathway.



sarcoma-SARC (green), **kidney-KIRC** (light green), **breast-BRCA** (orange), among other pairs, had highly correlated TransPRECISE scores.

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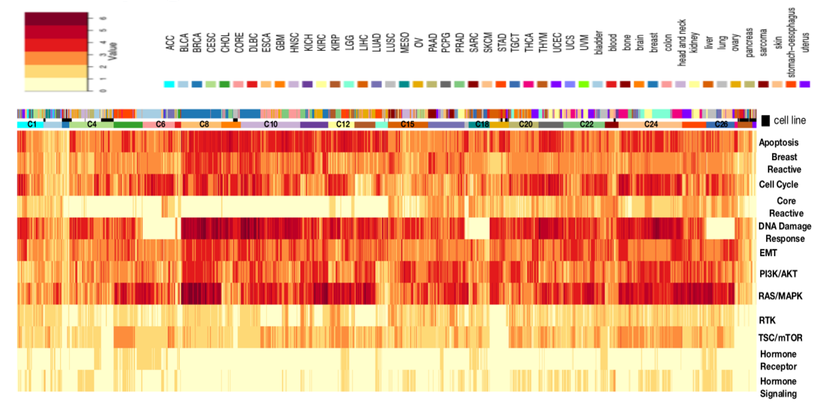
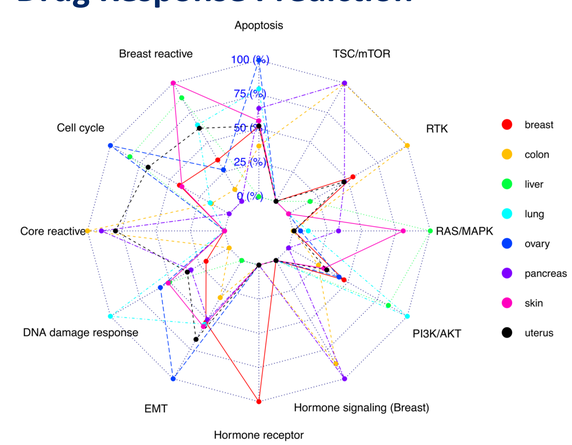
Results

Identifying Avatar Cell Lines



Hierarchical clustering on TransPRECISE pathway activity scores yielded cluster **C4** and **C15** with high fidelity of lineages.

Drug Response Prediction



Pathways exhibit predictive affinity to certain cell line cancer types. Examples:

RTK and **TSC/mTOR** in **colon**, **RAS/MAPK** in **liver**.

Drugs on clinical trials exhibit high predicted response rates for relevant cancers.

Patient Cancer	Drug (Proportion of patients with > 0.5 sensitivity)	Top 3 Pathways
BRCA	Ibrutinib (100%)	RAS/MAPK, PI3K/AKT, EMT
CORE	Lapatinib (100%)	RAS/MAPK, Cell cycle, EMT

Future Research

- More proteins and pathways can be included, thanks to larger datasets, e.g. Clinical Proteomic Tumor Analysis Consortium(CPTAC).
- Extensions to data from other model systems (Patient-Derived Xenografts, organoids, …) is a viable option.
- Other omics or trans-omics data may also be used in the regression modeling step.

Acknowledgements

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References

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3. Li J, Zhao W, Akbani R, et al: Characterization of Human Cancer Cell Lines by Reverse-phase Protein Arrays. Cancer Cell 31:225-239, 2017