

Immune Approach To Primary Graft Dysfunction

Exosomes, Proteomics and Machine Learning

Barry Fine MD PhD

Columbia University Medical Center



CUTTING EDGE of TRANSPLANTATION

TRANSPLANT SUMMIT 2019

***NO SIZE FITS ALL:** Uncovering the
Potential of Personalized Transplantation*

Disclosure

Funding: Department of Defense, the NIH and the Gerstner Foundation

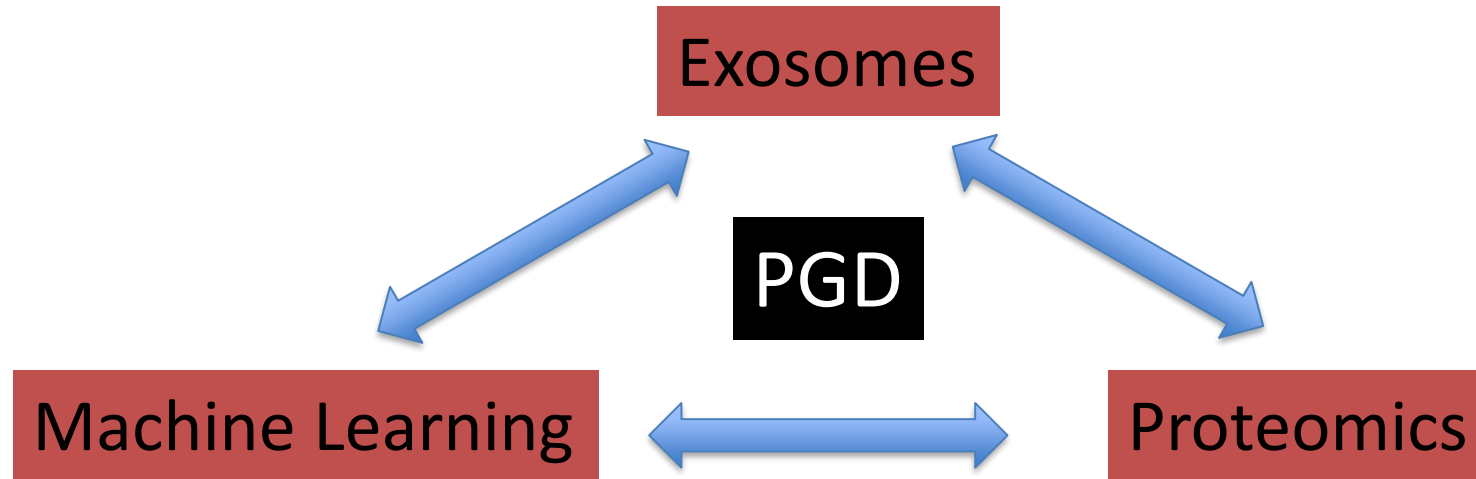
Learning Objectives

1. Delineate the role of proteomics in biomarker discovery as it relates to primary graft failure
2. Understand how we can use machine learning to analyze complex data sets



Nick Giangreco

Three Themes



Primary Graft Dysfunction

ISHLT CONSENSUS

Report from a consensus conference on primary graft dysfunction after cardiac transplantation

Jon Kobashigawa, MD,^a Andreas Zuckermann, MD,^b Peter Macdonald, MD, PhD,^c Pascal Leprince, MD, PhD,^d Fardad Esmailian, MD,^a Minh Luu, MBBS,^a Donna Mancini, MD,^a Jignesh Patel, MD, PhD,^a Rabia Razi, MD, MPH,^a Hermann Reichenspurner, MD, PhD,^f Stuart Russell, MD,^g Javier Segovia, MD, PhD,^h Nicolas Smedira, MD,ⁱ Josef Stehlik, MD, MPH,^j Florian Wagner, MD, PhD^k and on behalf of the Consensus Conference participants

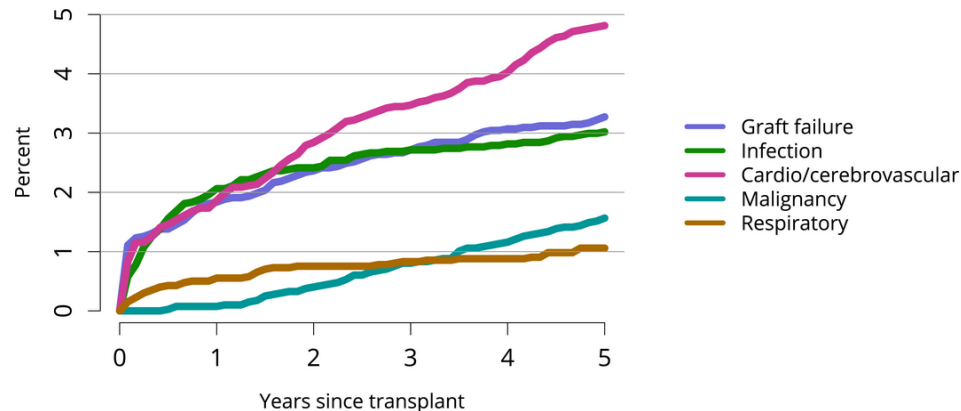
Table 6 Definition of Severity Scale for Primary Graft Dysfunction (PGD)

1. PGD-Left ventricle (PGD-LV):	<i>Mild PGD-LV:</i> One of the following criteria must be met: <i>Moderate PGD-LV:</i> Must meet one criterion from I and another criterion from II: <i>Severe PGD-LV</i>	LVEF $\leq 40\%$ by echocardiography, or Hemodynamics with RAP > 15 mm Hg, PCWP > 20 mm Hg, CI < 2.0 L/min/m ² (lasting more than 1 hour) requiring low-dose inotropes I. One criteria from the following: Left ventricular ejection fraction $\leq 40\%$, or Hemodynamic compromise with RAP > 15 mm Hg, PCWP > 20 mm Hg, CI < 2.0 L/min/m ² , hypotension with MAP < 70 mm Hg (lasting more than 1 hour) II. One criteria from the following: i. High-dose inotropes—Inotrope score $> 10^a$ or ii. Newly placed IABP (regardless of inotropes) Dependence on left or biventricular mechanical support including ECMO, LVAD, BiVAD, or percutaneous LVAD. Excludes requirement for IABP.
2. PGD-right ventricle (PGD-RV):	Diagnosis requires either both i and ii, or iii alone:	i. Hemodynamics with RAP > 15 mm Hg, PCWP < 15 mm Hg, CI < 2.0 L/min/m ² ii. TPG < 15 mm Hg and/or pulmonary artery systolic pressure < 50 mm Hg, or iii. Need for RVAD

BiVAD, biventricular assist device; CI, cardiac index; ECMO, extracorporeal membrane oxygenation; IABP, intra-aortic balloon pump; LVAD, left ventricular assist device; PCWP, pulmonary capillary wedge pressure; RAP, right atrial pressure; RVAD, right ventricular assist device; TPG, transpulmonary pressure gradient.

^aInotrope score = dopamine ($\times 1$) + dobutamine ($\times 1$) + amrinone ($\times 1$) + milrinone ($\times 15$) + epinephrine ($\times 100$) + norepinephrine ($\times 100$)²⁷ with each drug dosed in $\mu\text{g/kg/min}$.

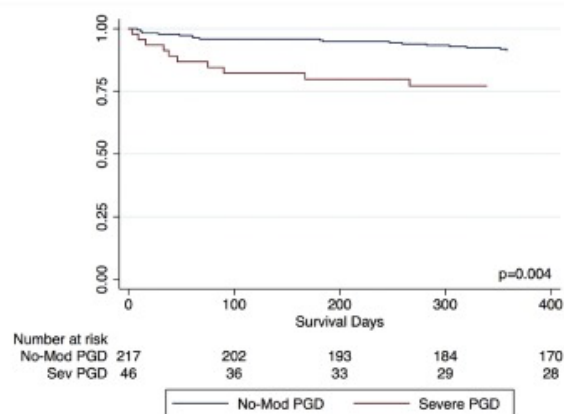
Graft dysfunction within 24 hours of transplant without a discernible cause such as rejection, pHTN, infection, etc...



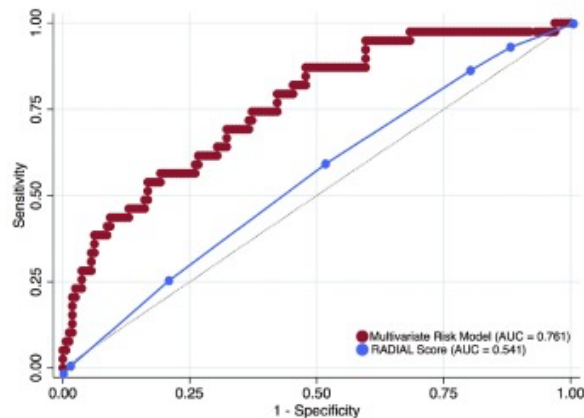
OPTN
2016

Primary Graft Dysfunction – Clinical Impact

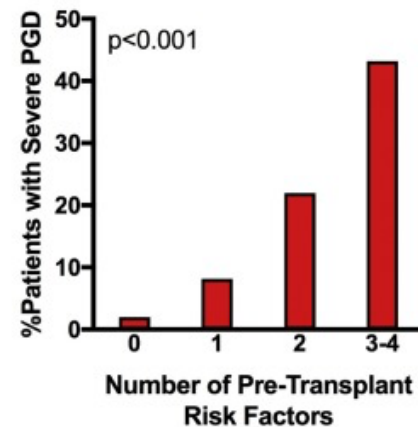
A Kaplan Meier Survival Analysis: Impact of Severe PGD on Post-HT Outcomes in BTT Patients



A Receiver Operating Characteristic Analysis

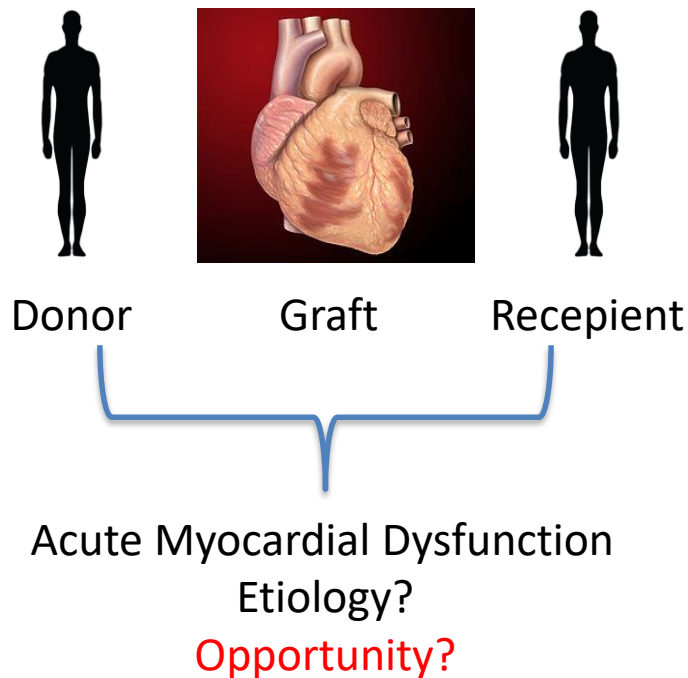


B Percent of BTT Patients with Severe PGD Stratified by Number of Pre-Transplant Risk Factors



Truby et al JHLT 2018

Primary Graft Dysfunction - Etiology



Primary Graft Dysfunction – Precision Medicine



Donor

“an emerging approach for disease treatment and prevention that takes into account individual variability in genes, environment, and lifestyle for each person”

-NIH

Primary Graft Dysfunction – Precision Medicine



Donor

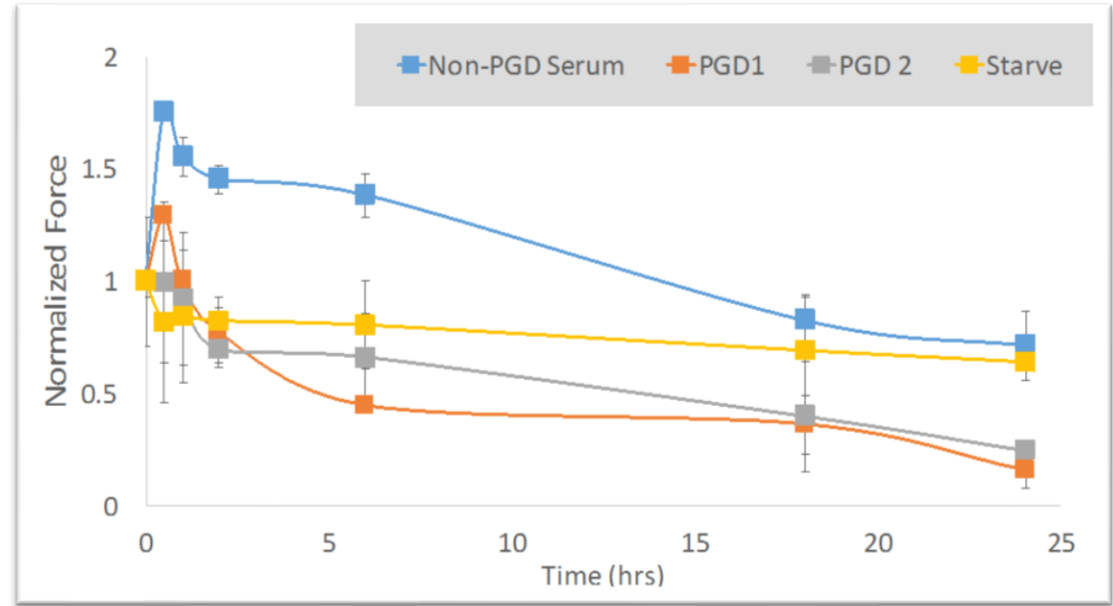
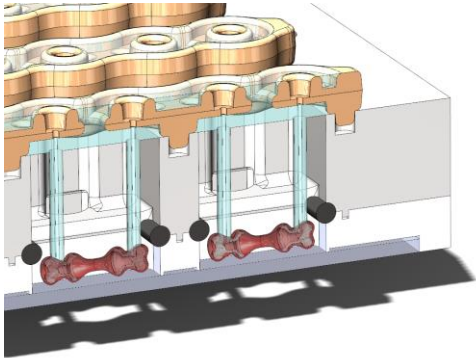
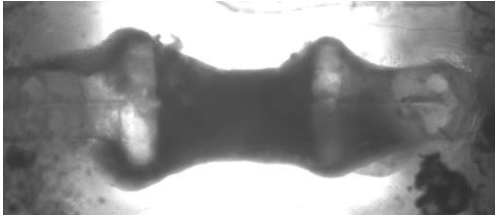
“an emerging approach for disease treatment and prevention that takes into account individual variability in genes, environment, and lifestyle for each person”

-NIH

Hostile Donor?

Circulating factors in the blood of transplant recipients impede cardiomyocyte function at the cellular level, leading to overall organ dysfunction.

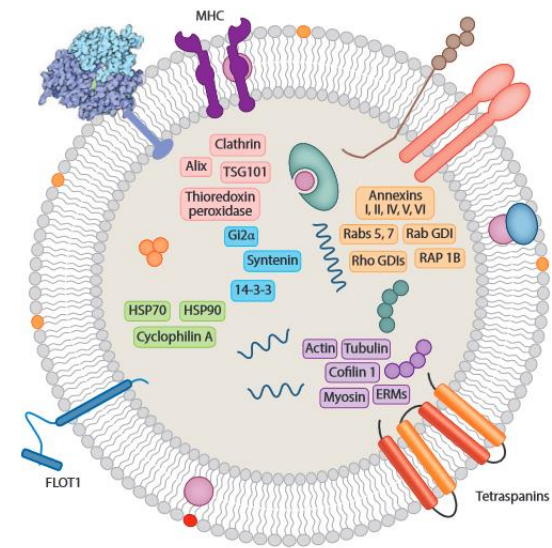
Primary Graft Dysfunction – Hostile Donor



Exosomes

Characterize the “Hostile Milieu” Hypothesis

- Small 30-120nm cell derived vesicles that are likely present in all body fluids
- Released by cells as MVB merge with the cytoplasmic membrane
- Complex cargo including miRNA, mRNA, proteins and specialized lipids
- Delivered to recipient cells through endocytosis and have
- Burgeoning understanding of the role of exosomes in disease



Origin

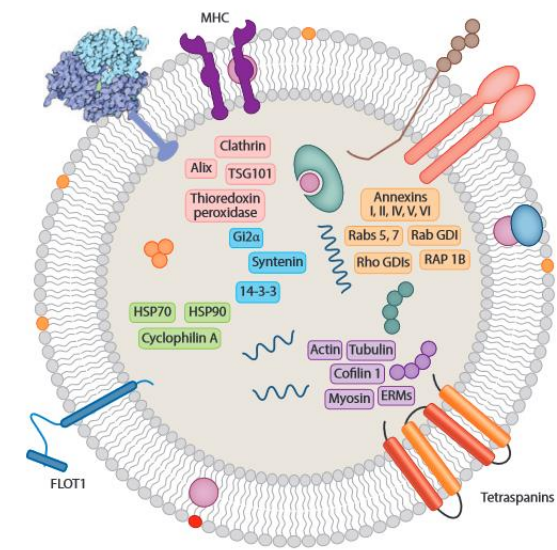
DC and B cells
Tumors
Vasculature
Pathogens
Adaptive Immunity

Physiological Role

Metastasis,
MS and TIA
Prions

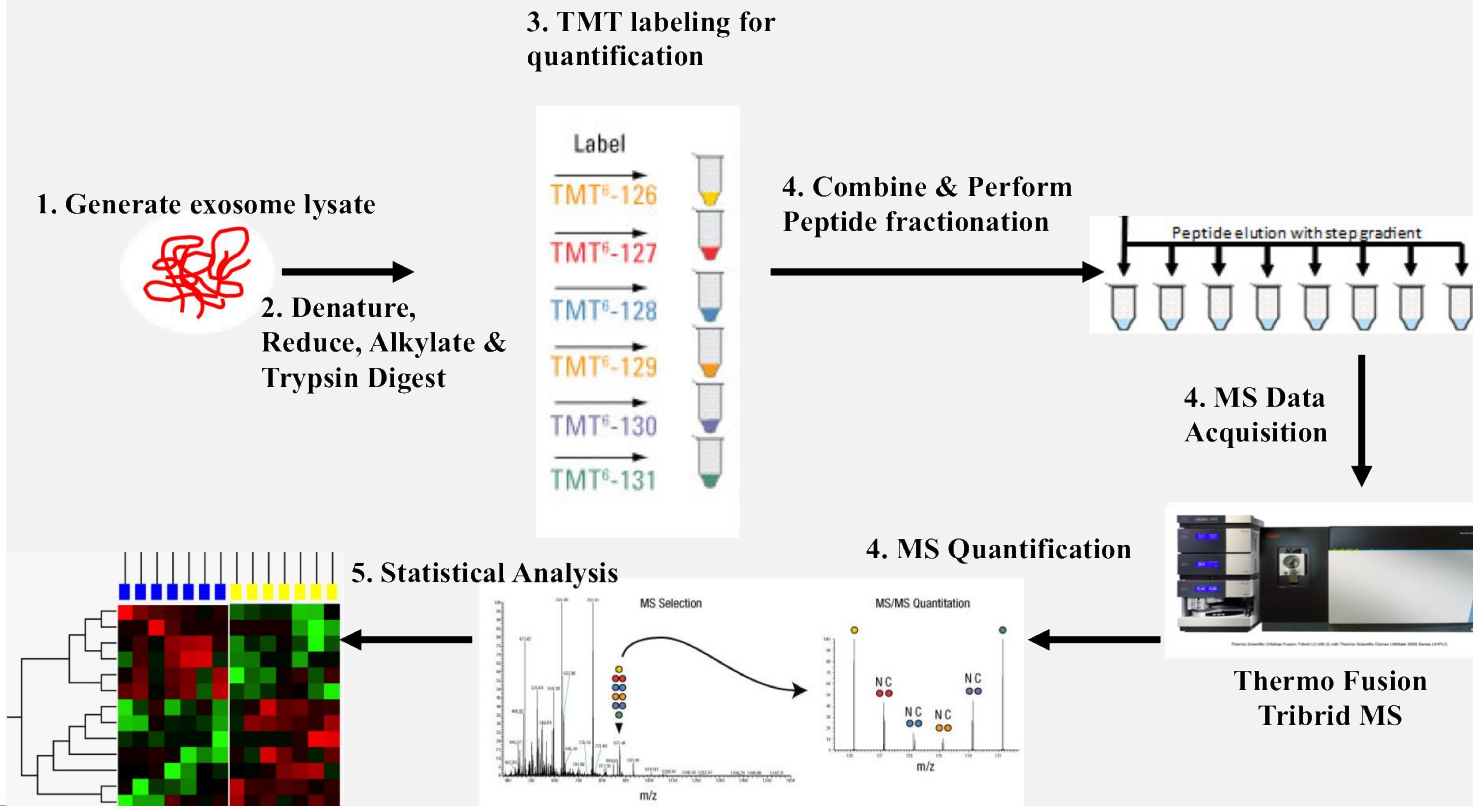
Exosomes

- Can be rapidly isolated using immuno-affinity methods or ultrafiltration from accessible fluids (blood/urine)
- Secreted in both normal and pathological states
- Exosomal miRNA have been shown to be clinically relevant biomarkers for multiple cancers
- Exosomal proteins have been found to be potentially useful biomarkers in cancer, neurological disease and kidney disease
- Importantly, cargo is very **stable** compared to proteins and RNA in serum

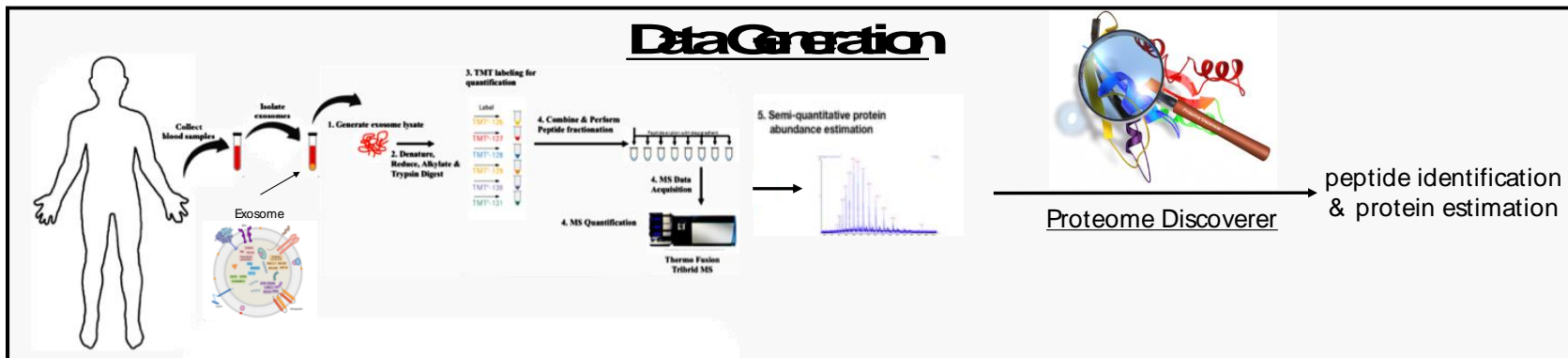


Protein	Disease Biomarker
Fetulin-A	AKI
EGFRvIII	Glioblastoma
Phospho-Tau	Alzheimers
α -synuclein	parkinsons

Proteomics on Pre-Transplant Serum Exosomes

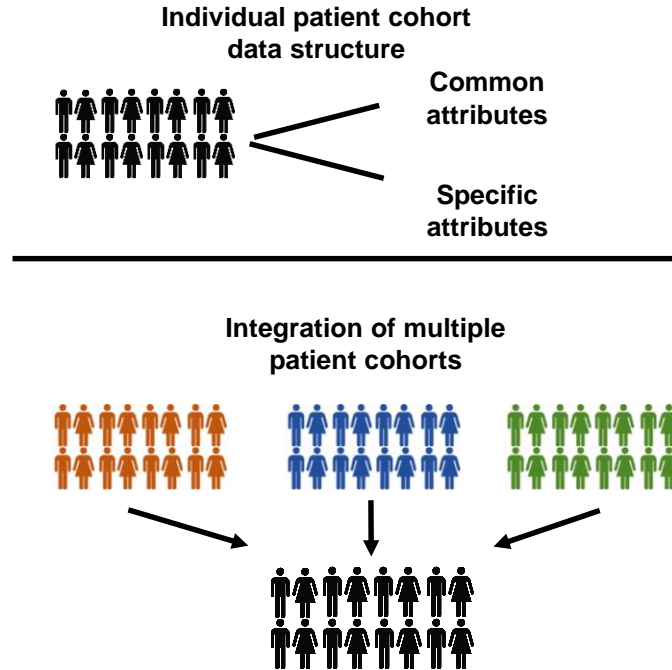


Workflow



cohorts

<https://github.com/ngiangre/cohorts>



cohorts is:

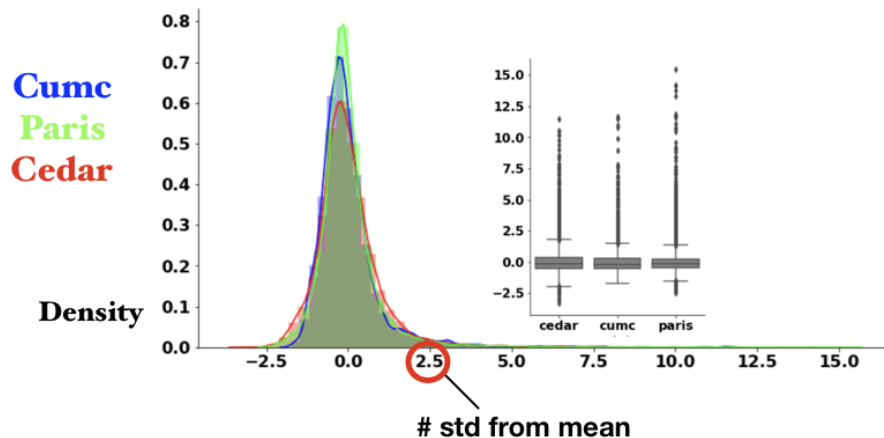
- Modular
 - Each cohort is its own data structure
- Customizable
 - Each cohort has attributes for individual and integrative cohort analyses
- Flexible
 - Can use built in functions and use custom code leveraging the cohort attributes

Proteomics

There are two questions we can try to answer with proteomics

1. Mechanistic: Do the proteins tell us something about PGD. Is there a pathway discernible in differential protein analysis?
2. Classification: Can we use a protein or a set of proteins to help us predict PGD. Are there “features” can correctly classify transplant candidates at high risk versus those at low risk of PGD

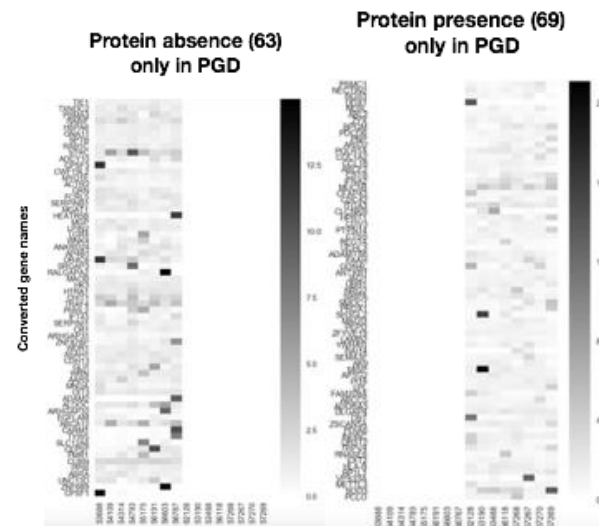
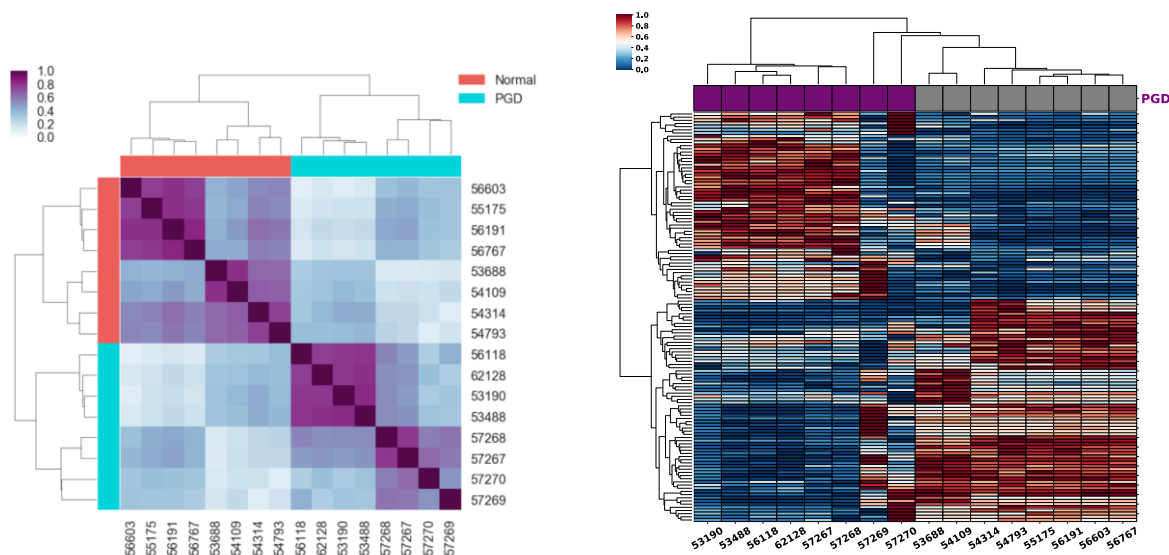
Data distribution



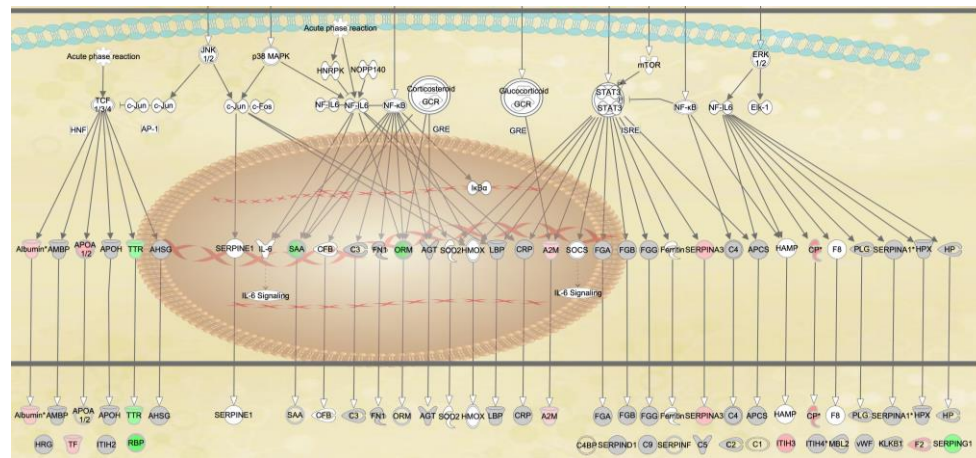
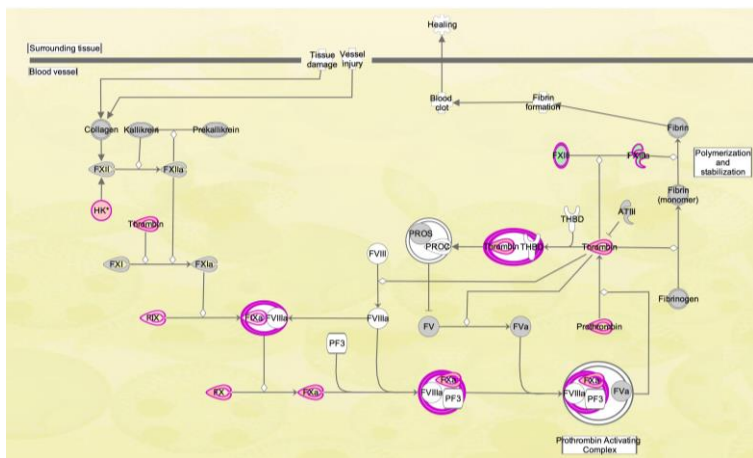
	# Data Files	# Proteins	# Replicates	# Samples	# Groups
Columbia	2	1204	64	16	5
Cedar-Sinai	2	729	150	44	7
Paris	2	934	108	29	8

Prospective Cohort - Columbia

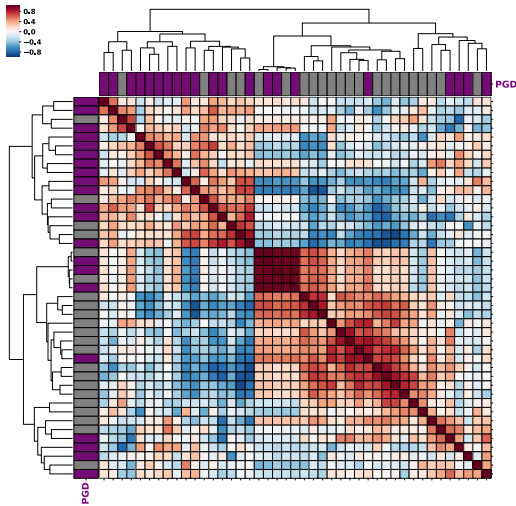
PGD Patients Have Different Exosome Proteomics Prior to Transplant



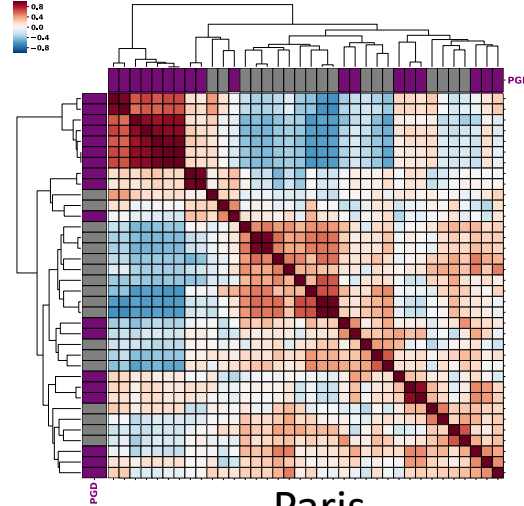
PGD Patients Have Different Exosome Proteomics Prior to Transplant



Retrospective Cohort – Cedars and Pitie Salpetriere

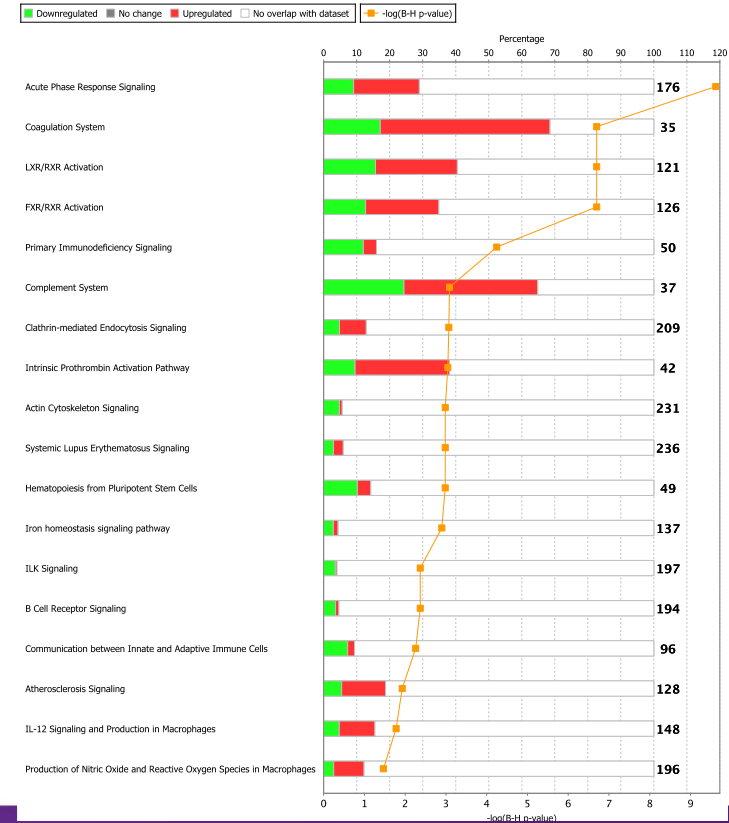


Cedars



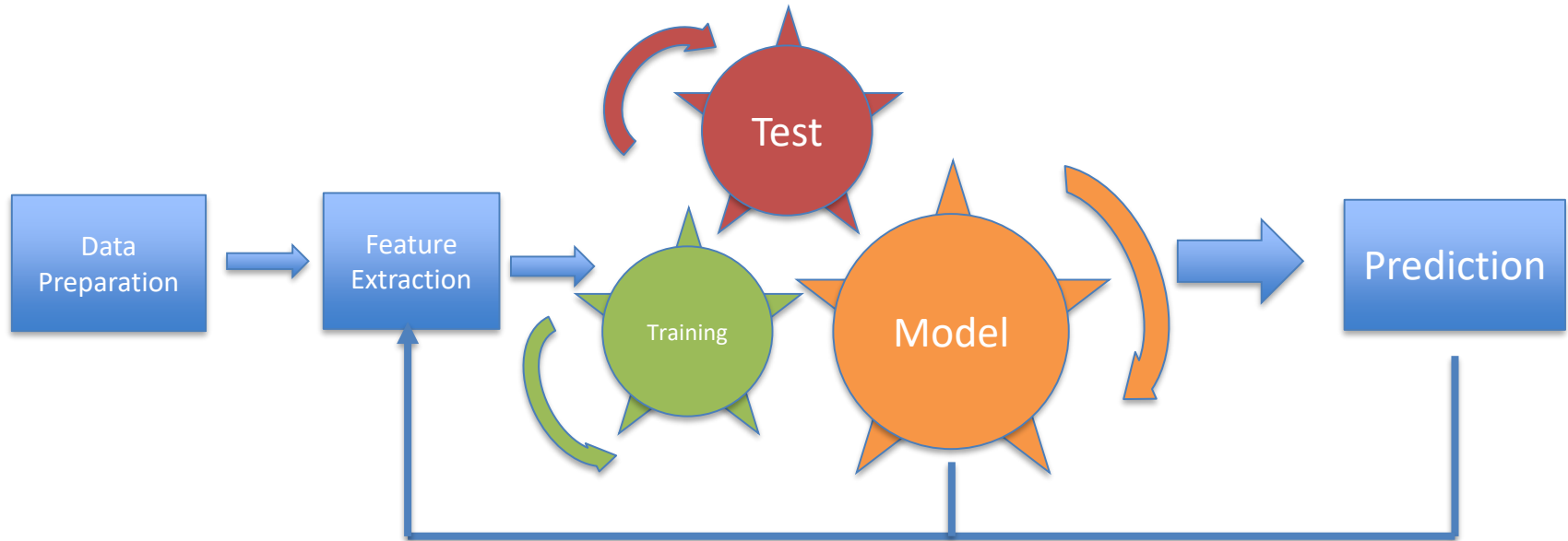
Paris

Low Correlation
Small number of differential proteins
PGD did not separate out



Classification – Machine Learning

Machine Learning: Building mathematical models using training data in order to make predictions or decisions on test data without explicitly programmed to perform the task. Important to this is progressive improvement in that task with more data and training.

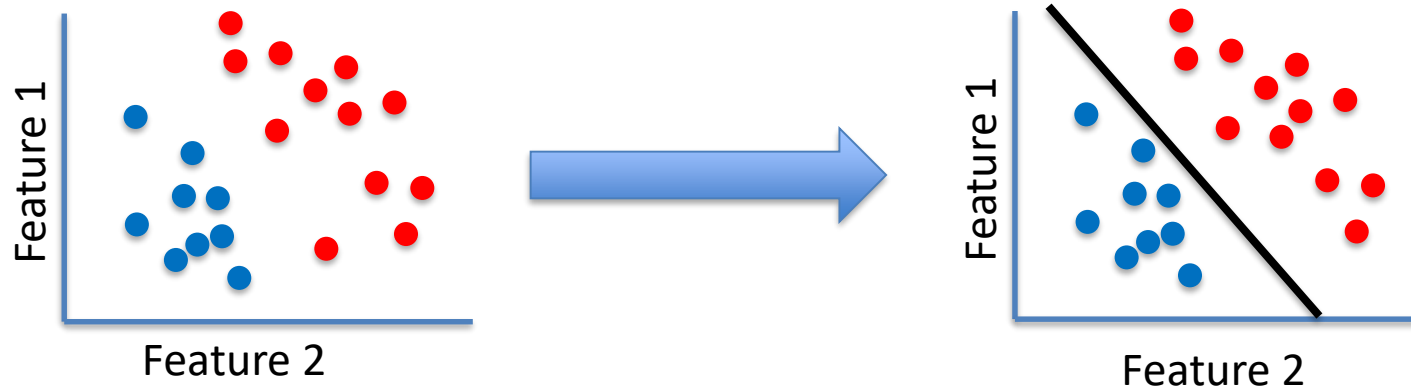


Classification Machine Learning

Different Algorithms

Multidimensional Feature Space

Allows identification of boundaries between two states

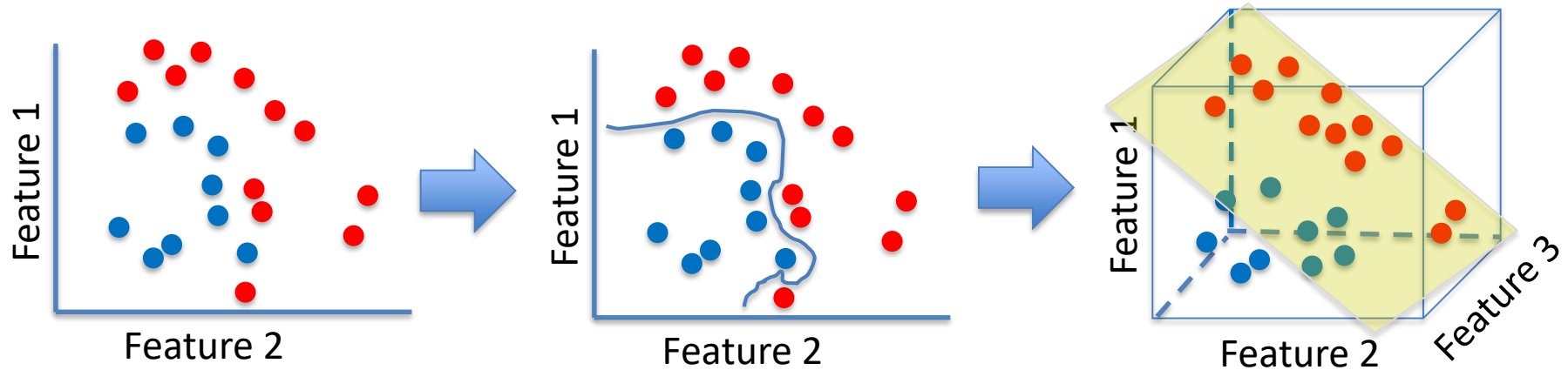


Classification Machine Learning

Different Algorithms

Multidimensional Feature Space

Allows identification of boundaries between two states

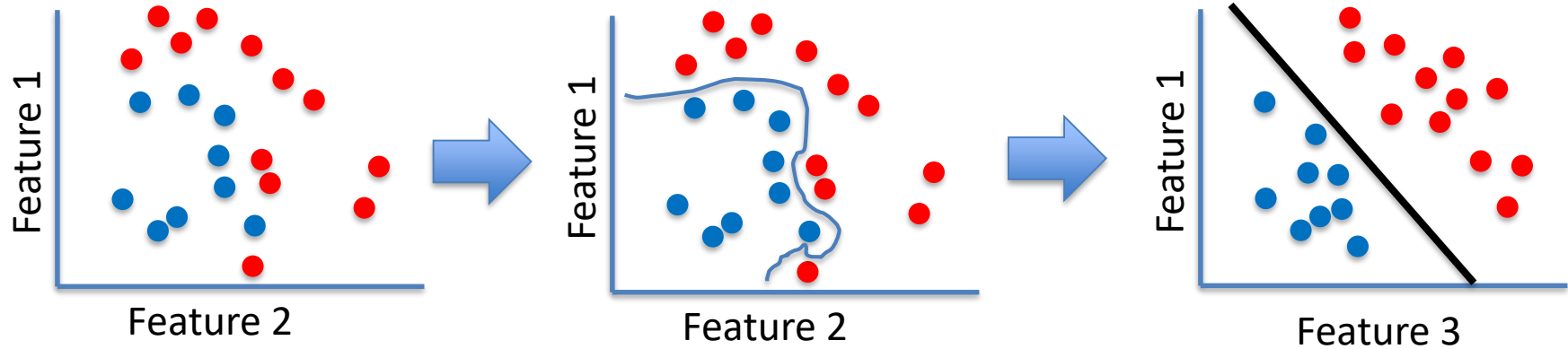


Classification Machine Learning

Different Algorithms

Multidimensional Feature Space

Allows identification of boundaries between two states

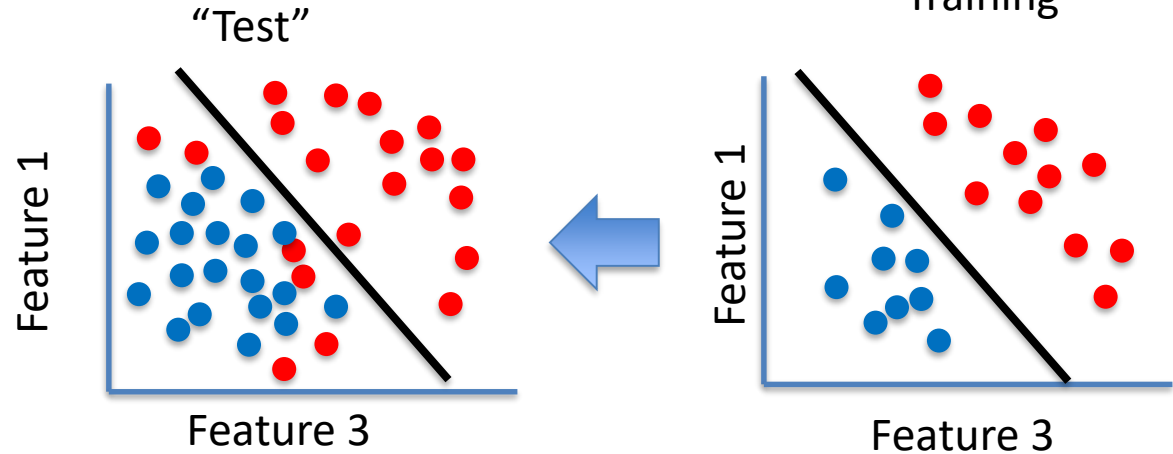


Classification Machine Learning

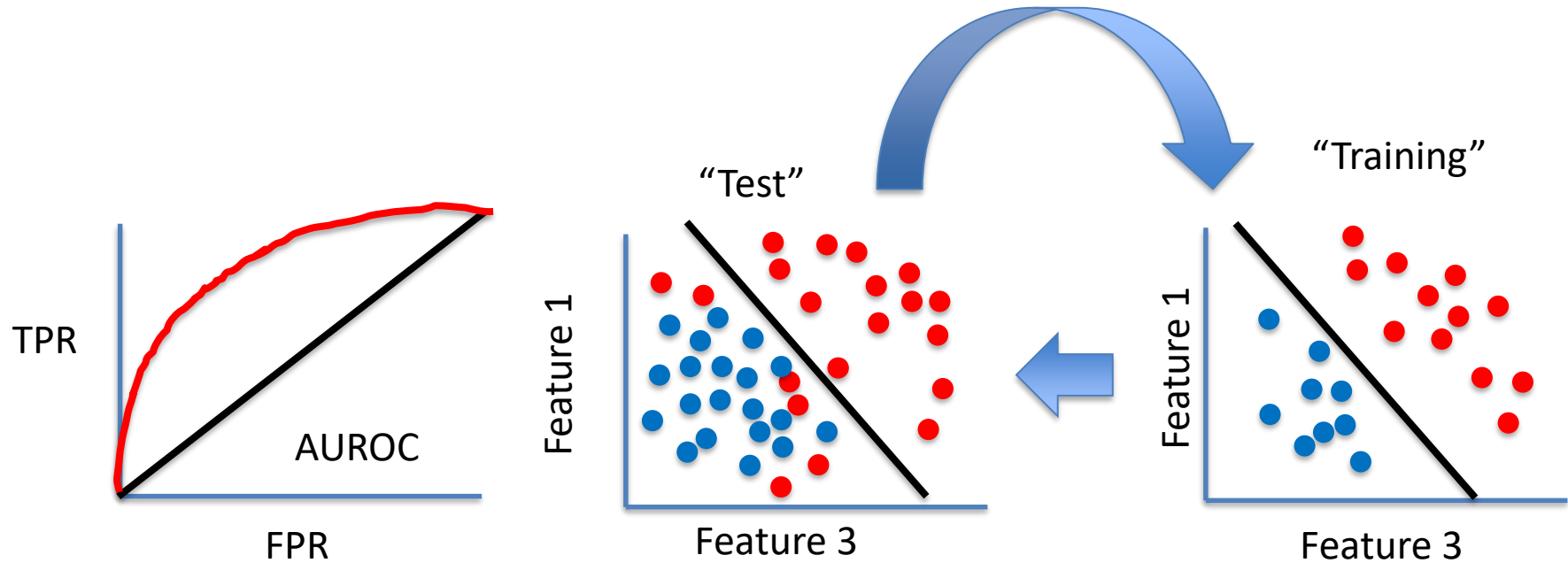
Different Algorithms

Multidimensional Feature Space

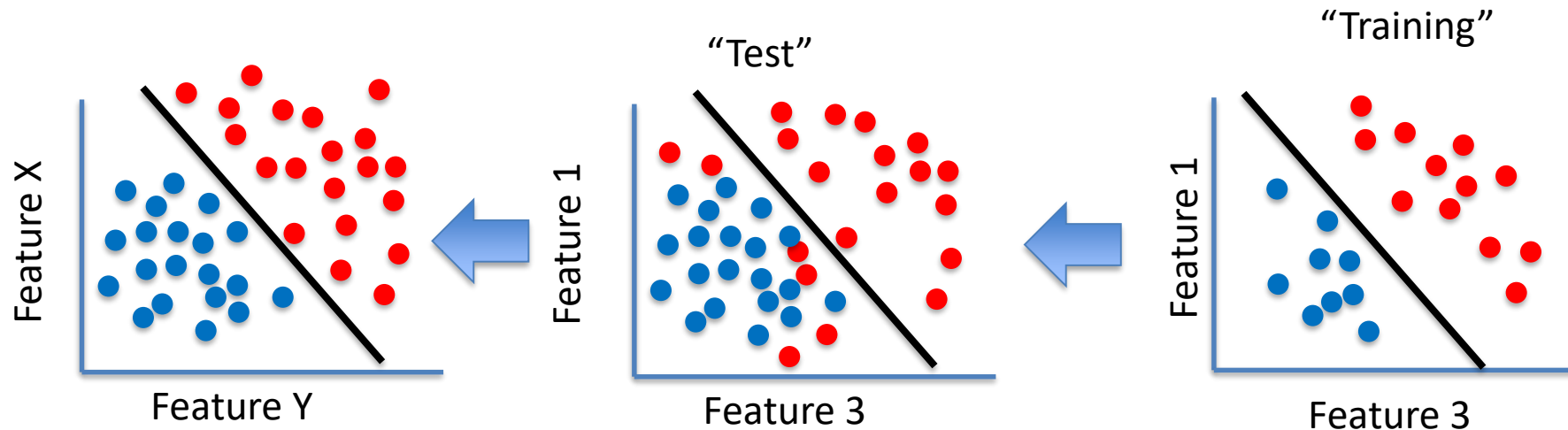
Allows identification of boundaries between two states



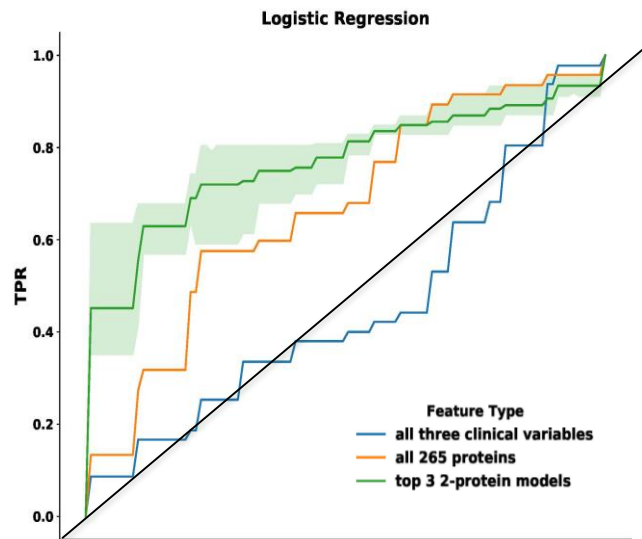
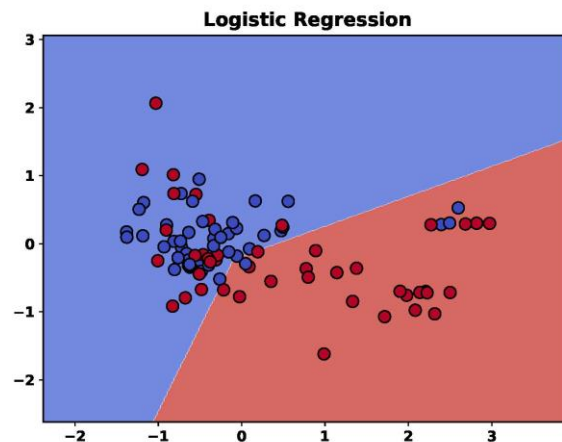
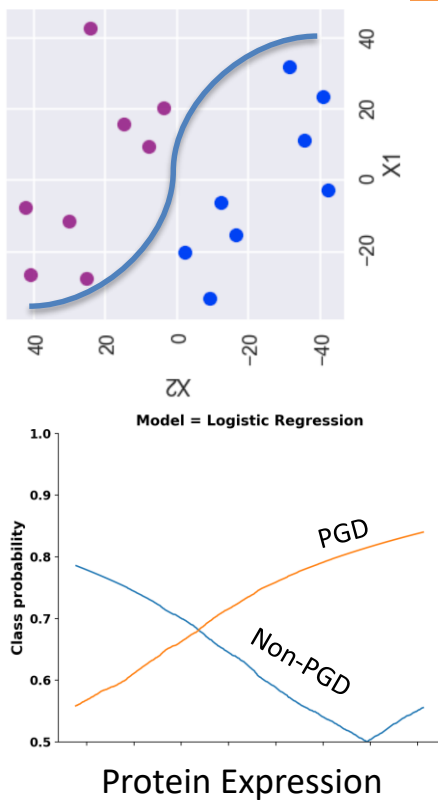
Classification Machine Learning



Classification Machine Learning

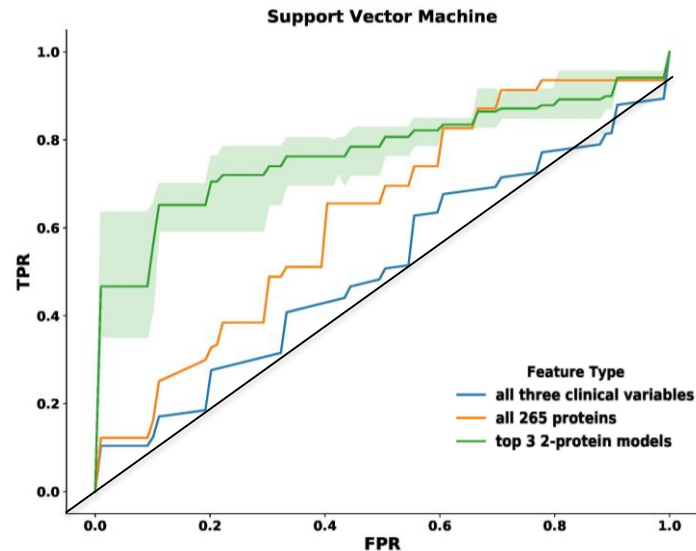
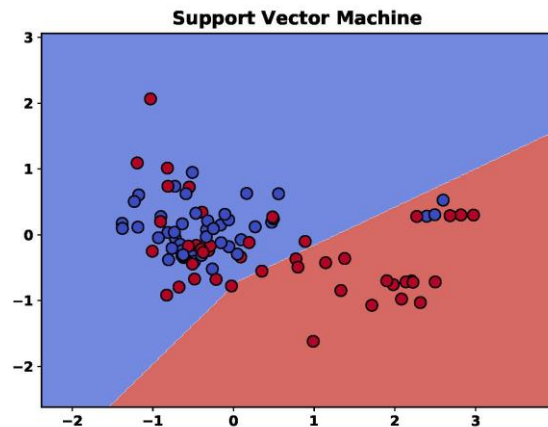
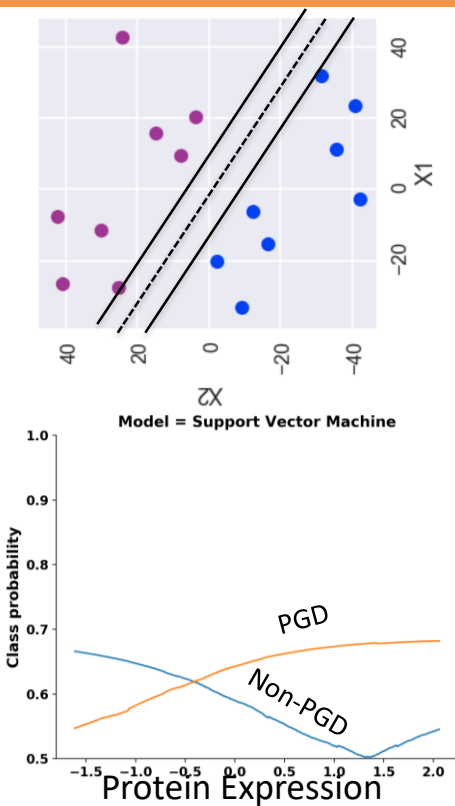


PGD– Prediction Using Logistic Regression



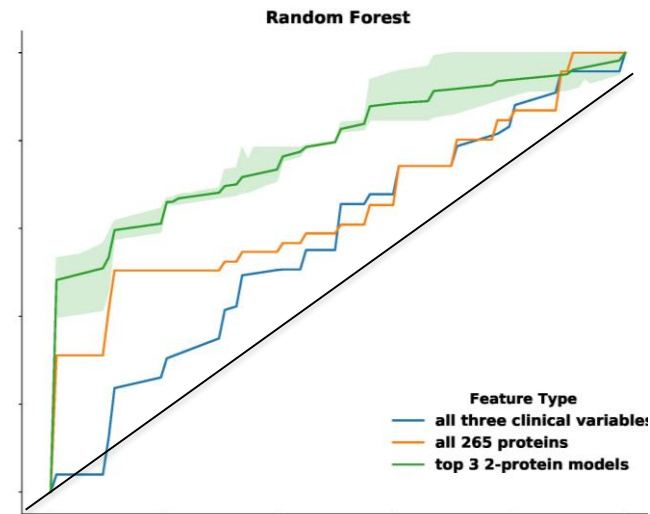
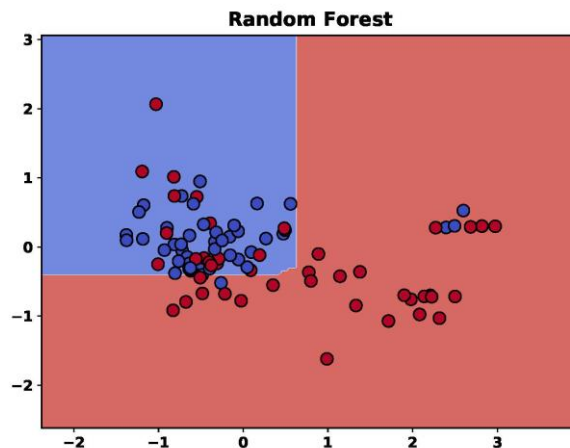
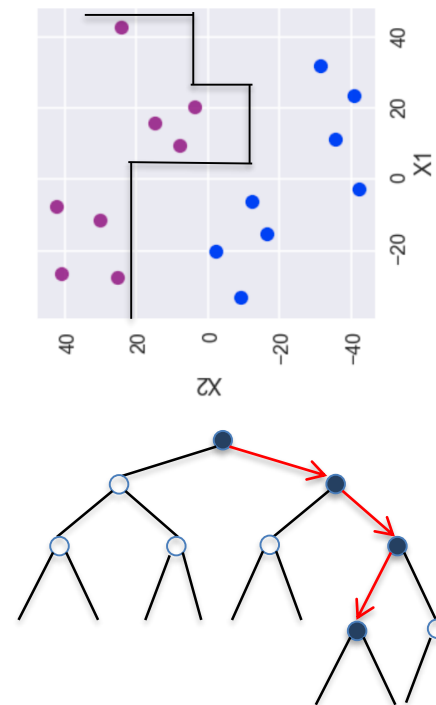
Feature	AUROC	TPR	TNR
Top Two Proteins	0.803	0.57	0.85

PGD– Prediction Using Support Vector Machines



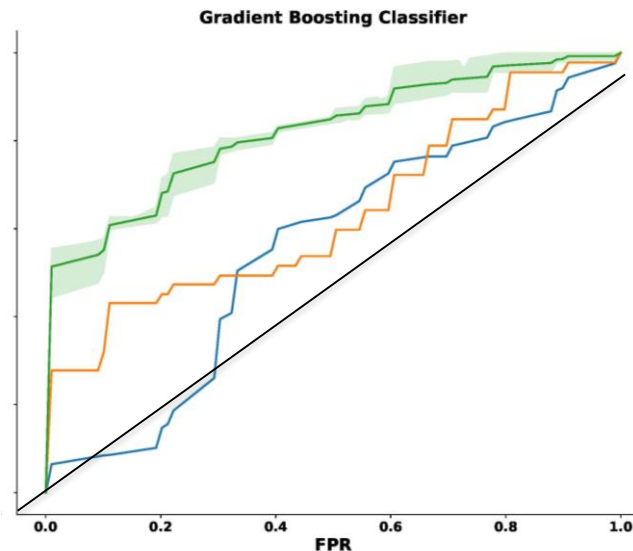
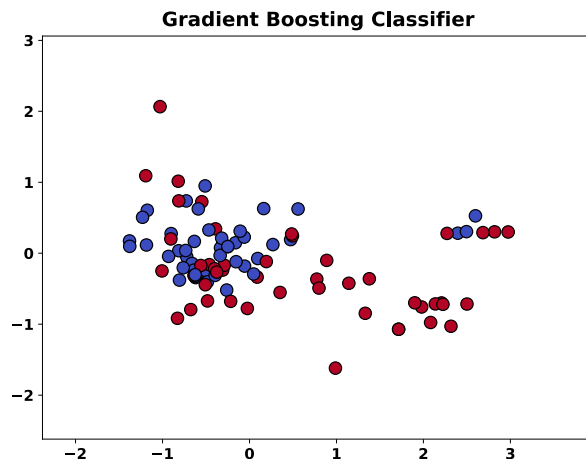
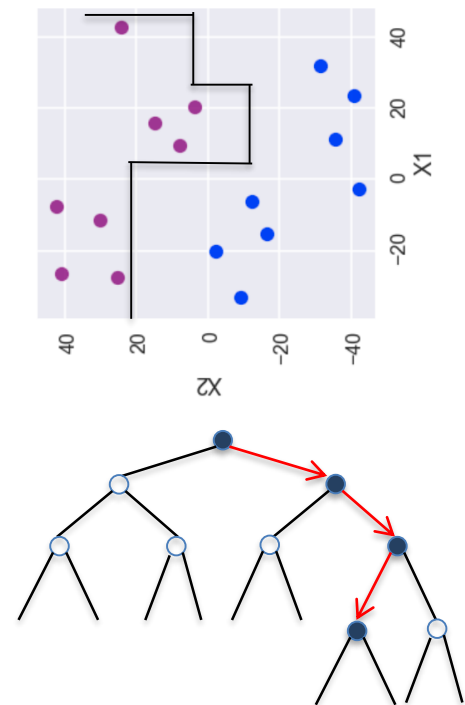
Feature	AUROC	TPR	TNR
Best 2 Protein	0.805	0.681	0.938

PGD– Prediction Using Random Forest



Feature	AUROC	TPR	TNR
Best 2 Protein	0.807	0.660	0.875

PGD– Gradient Boosting

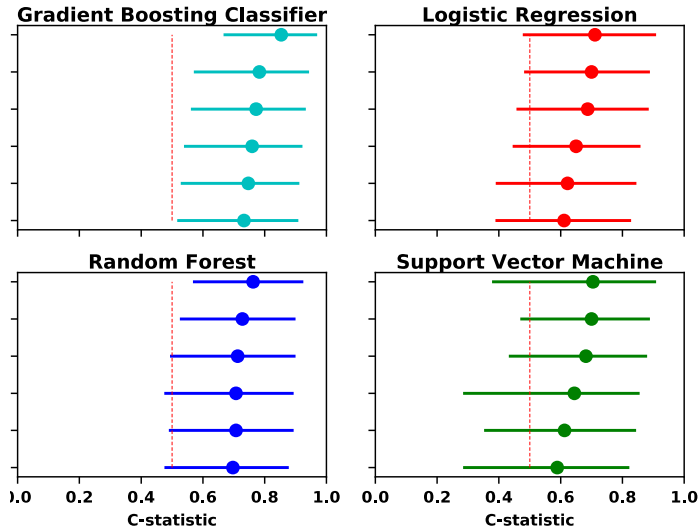


Feature	AUROC	TPR	TNR
Best 2 Protein	0.829	0.72	0.79

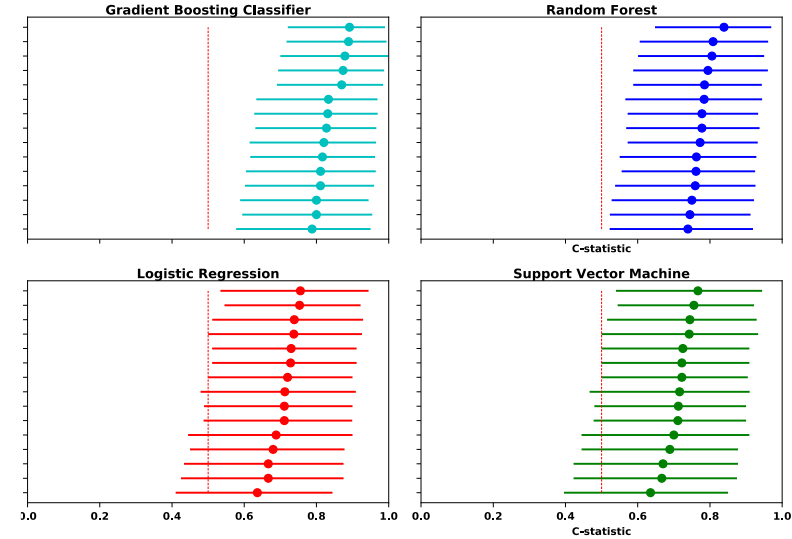
Best boundary may not be clinical

Bootstrapping with Recursive Feature Extraction

Constraint to One Protein

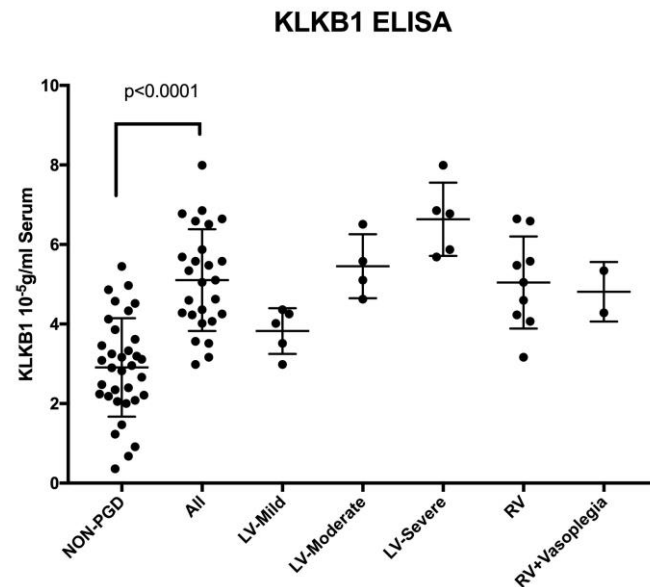
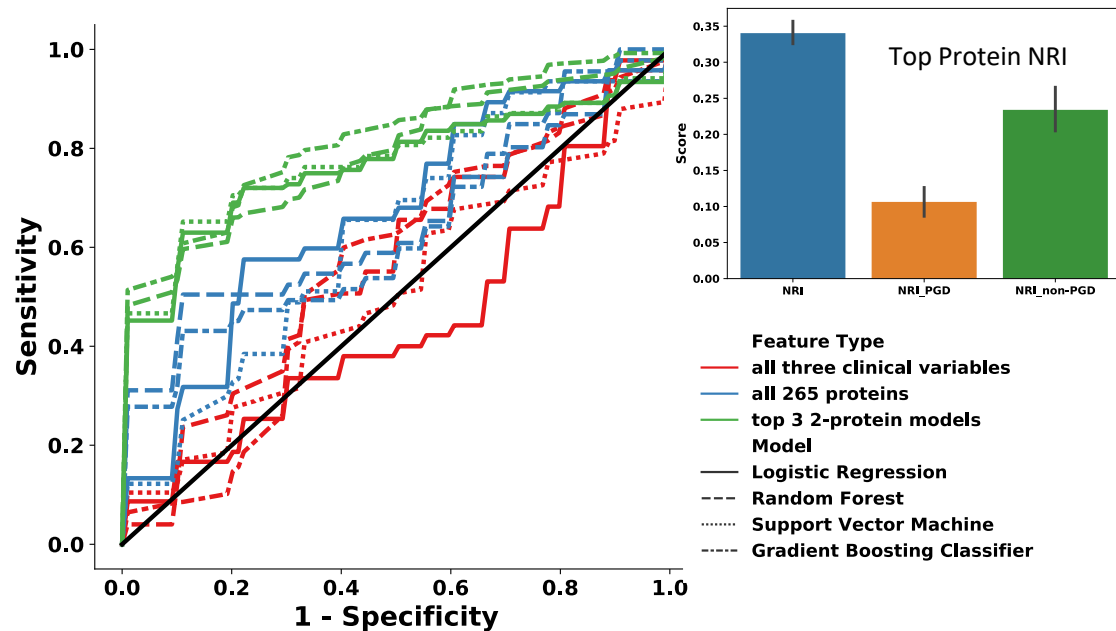


Constraint to Two Protein



More Dimensions → Better Prediction

Overall Prediction Performance



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