

AutoPrognosis

Automating the design of predictive models for clinical risk and prognosis

Mihaela van der Schaar

University of Oxford

The Alan Turing Institute

Acknowledgements

- Ahmed Alaa
- Jinsung Yoon
- Prof. William Zame
- Many clinical collaborators

Research Goal

**Improve Quality and Safety of Healthcare
while Managing Costs
using Machine Learning**

**The Policy
Perspective**



- Population-serving
- Cross-sectional

**The Clinical
Perspective**

- Personalized

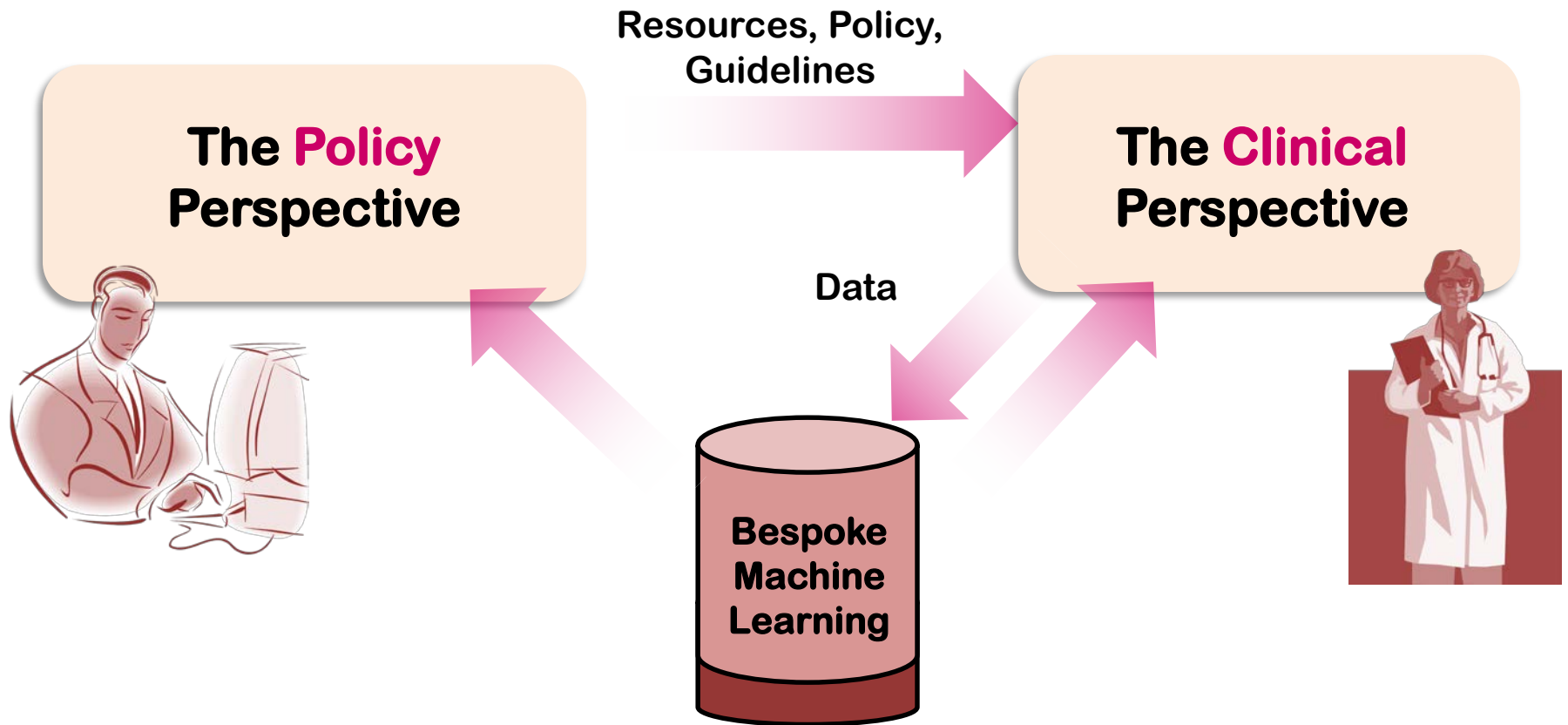


Guidelines, Policies, Standards

**Clinical Decision Support
Actionable Intelligence**

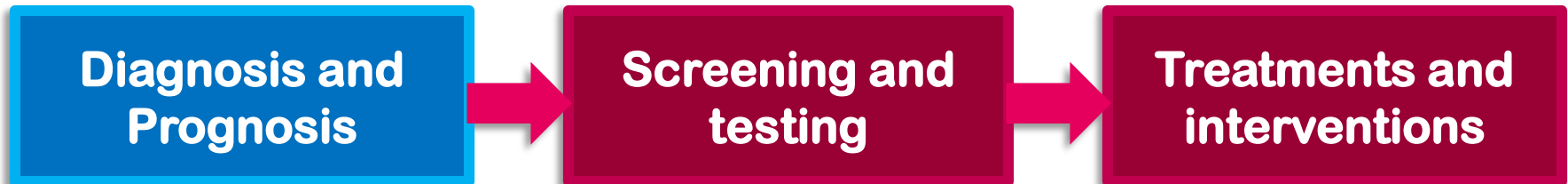
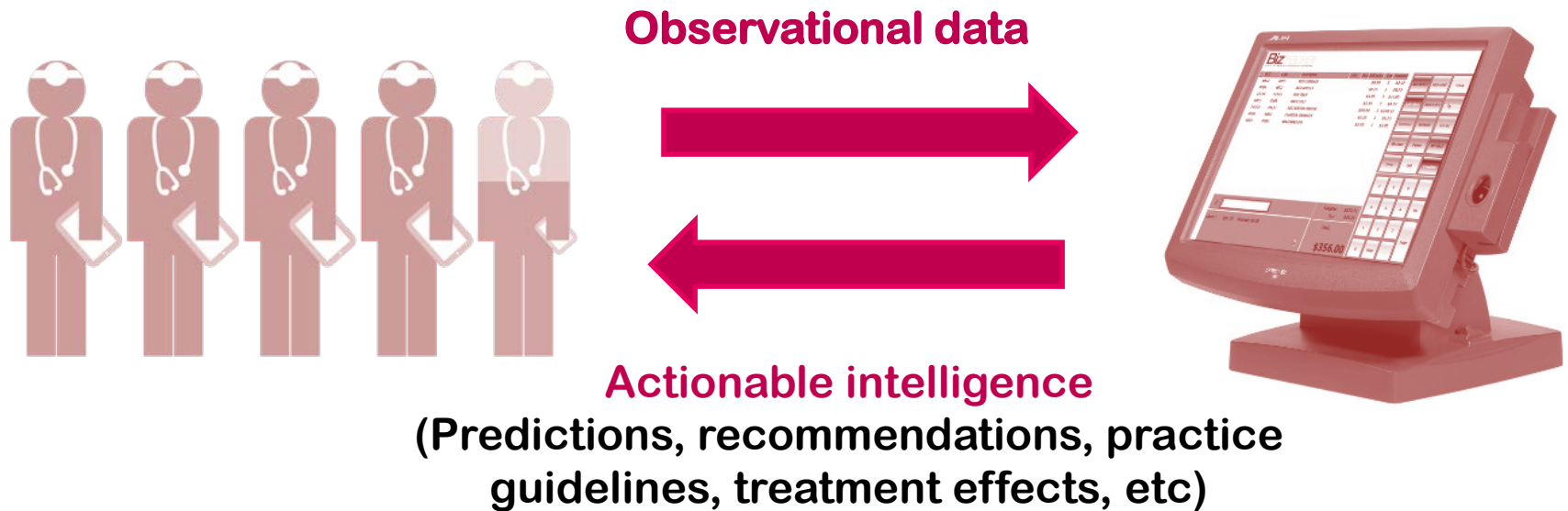
Research Goal

Learning, Co-Evolving, Improving Health Systems



The **Clinical** Perspective: Decision Support Systems to Improve Patient Care

- **Goal:** develop machine learning algorithms to extract **actionable intelligence** in order to improve clinical practice

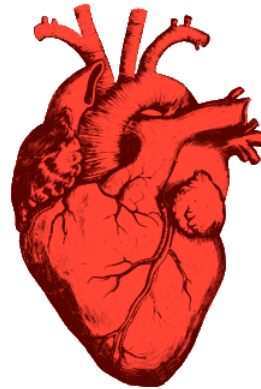


Who should get a heart?

Ann



Bob

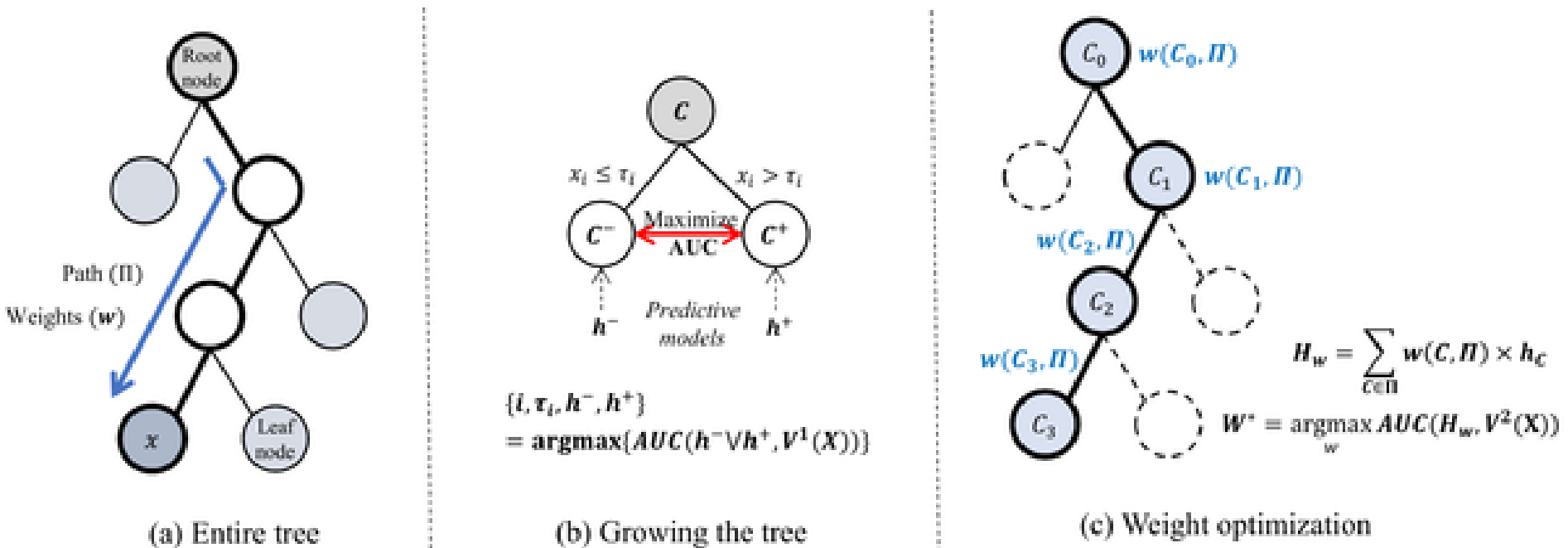


- **Urgency**
 - How long will Ann/Bob survive while waiting?
- **Benefit**
 - How much will Ann/Bob benefit from this heart?

Clinical Risk Scores

- **Urgency: Survival on Wait List**
 - HFSS
 - MAGGIC
 - SHFM
- **Benefit: Survival after Transplantation**
 - DRI
 - IMPACT
 - RSS

Personalized survival predictions via Trees of Predictors (ToPs)

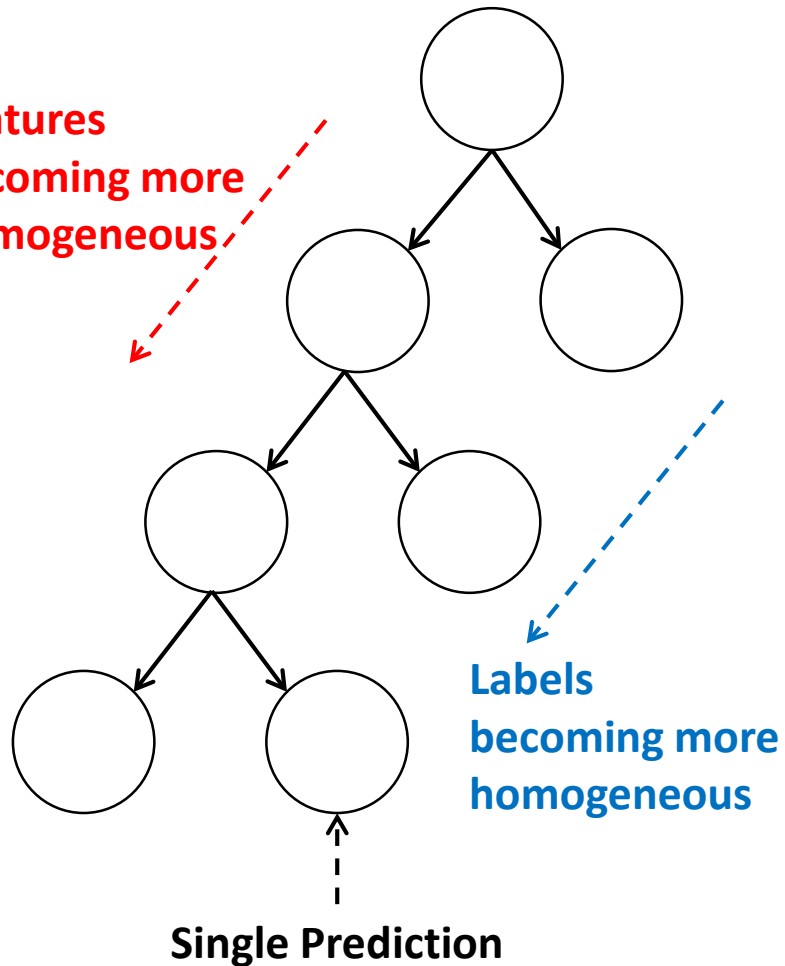


Yoon J, Zame WR, van der Schaar, M. (2018) ToPs: Ensemble Learning with Trees of Predictors. *Trans. on Signal Processing*

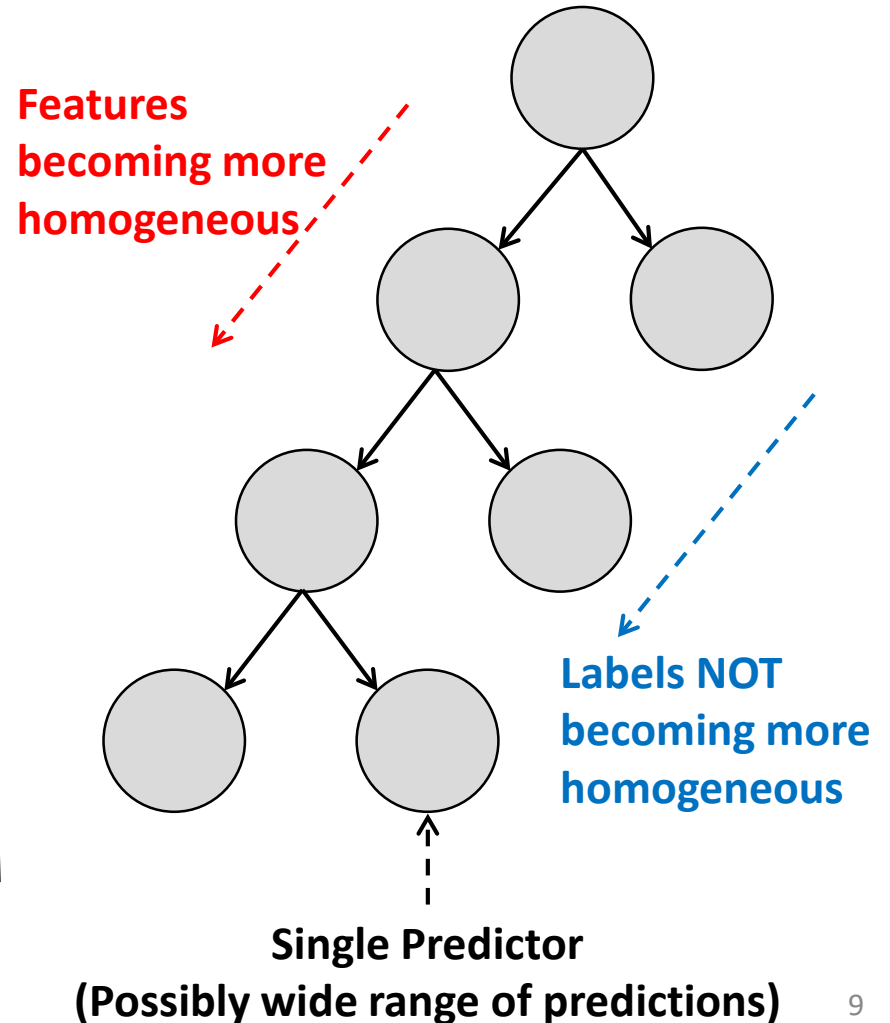
Yoon J, Zame WR, Banerjee A, Cadeiras M, Alaa AM, van der Schaar, M. (2018) Personalized survival predictions via Trees of Predictors: An application to cardiac transplantation. *PLOS ONE* 13(3): e0194985.
<https://doi.org/10.1371/journal.pone.0194985>

ToPs is NOT a regression tree!

Regression Tree



ToPs



Dataset

United Network for Organ Transplantation (UNOS)

- ALL patients registered for heart transplantation in US in 1985-2015
- 35,000+ patients wait-listed but did not receive heart transplant
 - Date of waitlisting + survival
 - 33 features of patients
- 60,000+ patients received heart transplant
 - Date of transplantation + survival
 - 53 features of patients/donors

Performance

Wait-List

	3 months	1 year	3 years	10 years
ToPs/R	0.8467	0.8130	0.7921	0.7897
MAGGIC	0.6298	0.6413	0.6425	0.6290

Post-Transplant

	3 months	1 year	3 years	10 years
ToPs/R	0.6763	0.6637	0.6538	0.6562
IMPACT	0.5808	0.5700	0.5524	0.5308

Survival/Mortality at 3 Months

	Actual Survival	Correctly Predicted (Specificity = .80)	Actual Mortality	Correctly Predicted (Sensitivity =.80)
MAGGIC	4,723	1,984 (37.8%)	2,542	915 (36%)
ToPs/R	4,723	3,212 (68.0%)	2,542	1,754 (69.0%)
Additional Correct Predictions		1,228		839

AFTER A HEART TRANSPLANT WITH SCARY ACCURACY

By **Dana Dovey** On Friday, May 18, 2018 - 12:18



The algorithm may help us make better use of limited available hearts. The first heart used in a heart donation.



Best of
LIPID FORUM 2017
BEYOND STATIN THERAPY: GETTING
THE LOW DOWN ON LDL MANAGEMENT

EARN YOUR CREDIT 

Healio  Cardiologytoday
EducationLab

[Healio](#) > [Cardiology](#) > [HF/Transplantation](#)

IN THE JOURNALS

Algorithm predicts life expectancy in advanced HF

Yoon J, et al. *PLoS One*. 2018;doi:10.1371/journal.pone.0194985.

June 21, 2018



ADD TOPIC TO EMAIL ALERTS



COMMENT



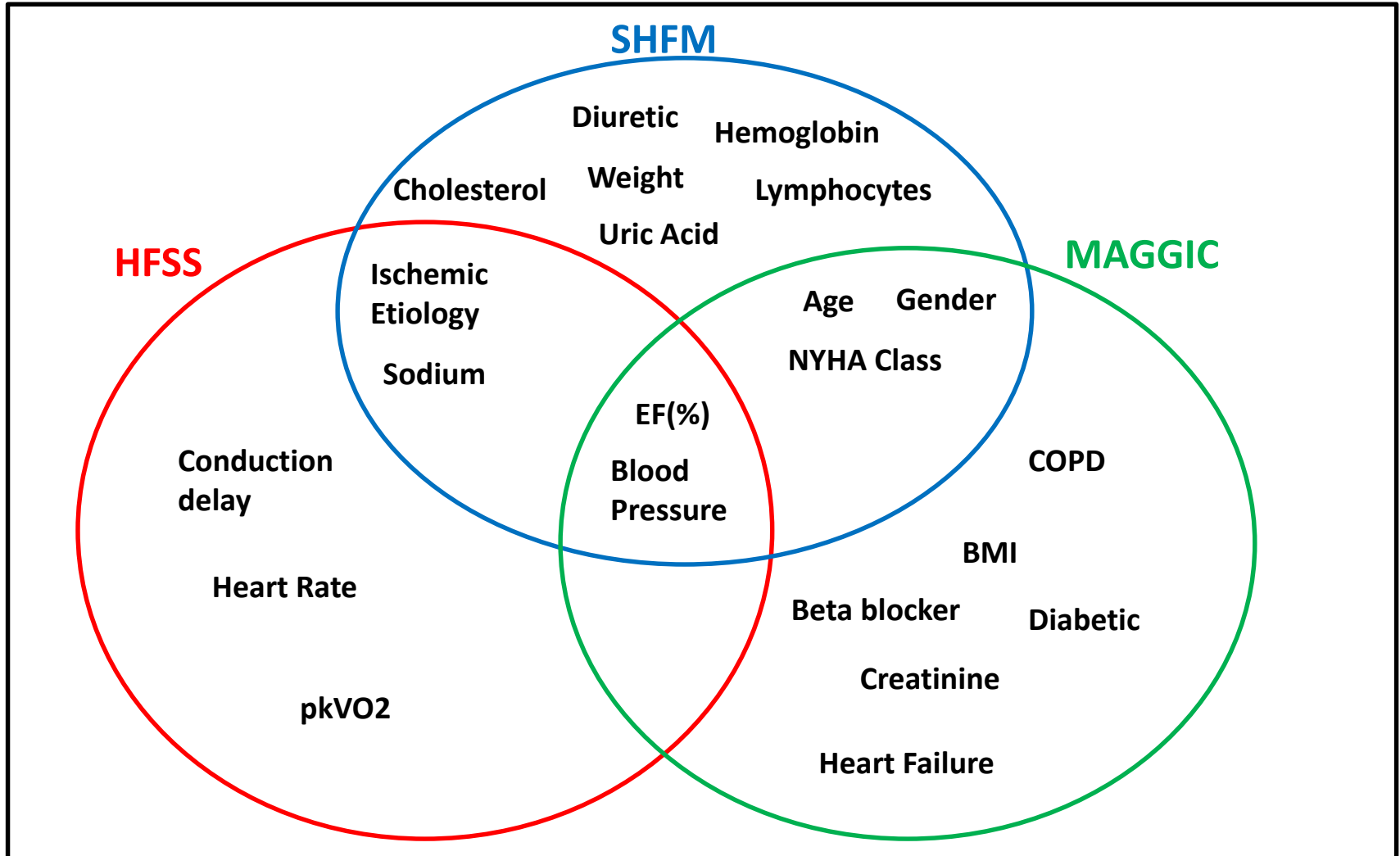
Researchers reported that they developed a new algorithm that more accurately predicts how long patients with advanced HF will survive, regardless of whether they receive a transplant.

“Our work suggests that more lives could be saved with the application of this new machine learning-based algorithm,” **Mihaela van der Schaar, PhD**, Chancellor’s

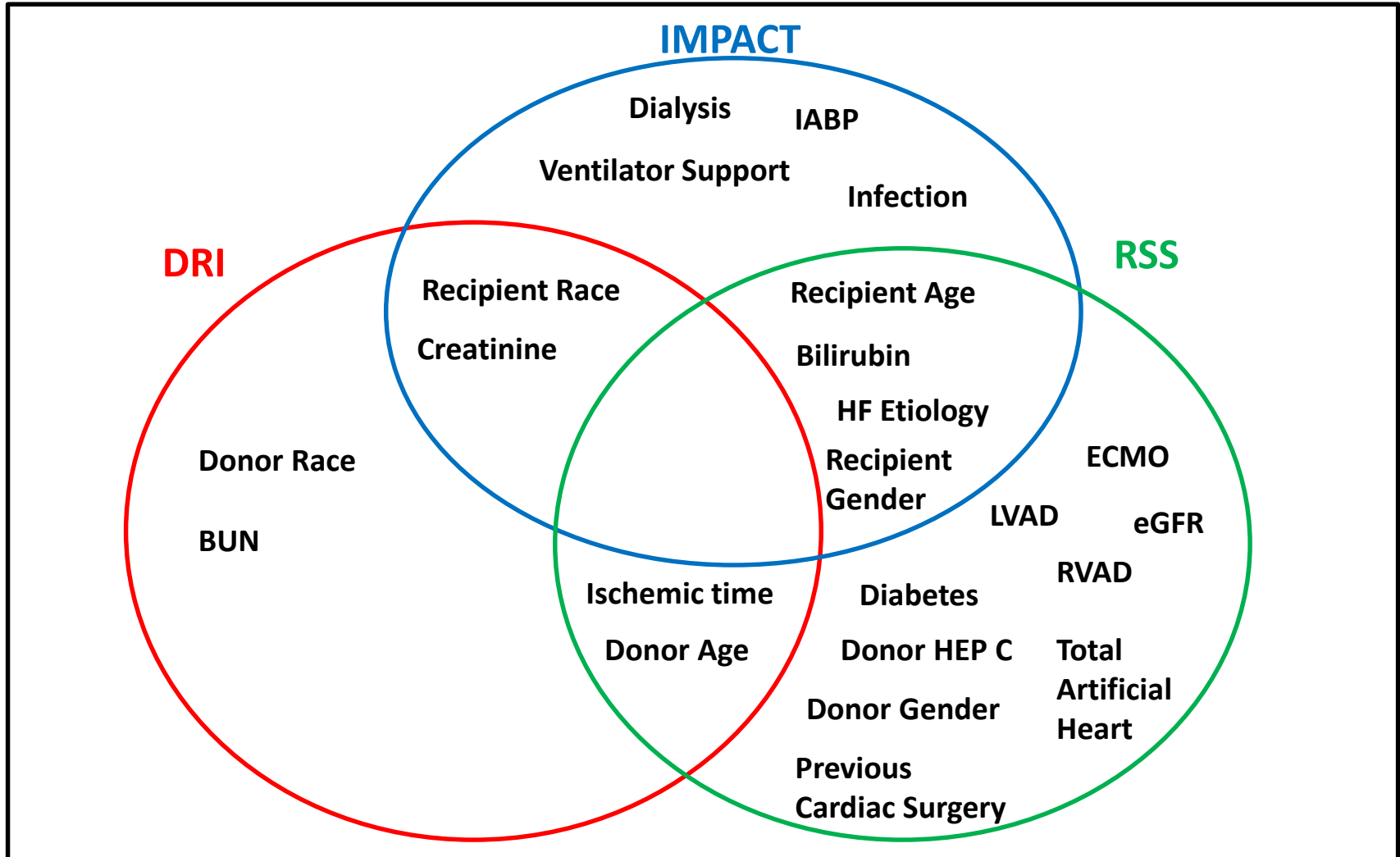
Sources of gain

- Information gain
- Modeling gain

Features used by Clinical Risk Scores (Wait-list)



Features used by Clinical Risk Score (Post-transplantation)



What are the Problems with Clinical Scores?

1. Models are one size-fits-all

- but ... population(s) are very heterogeneous

2. Models are linear

- but ... survival is non-linear: features interact

3. Models are horizon-independent

- but ... long-term survival is different from short-term survival; different features matter for different time horizons

Our Method ToPs – Designed to Solve Problems

1. **Model is individualized**
 - addresses heterogeneous population(s)
2. **Model is non-linear (where needed)**
 - addresses interaction of features
3. **Model is horizon-dependent**
 - addresses differences between long-term survival and short-term survival; different features matter for different time horizons

Interpretability? Tops/R (Regressions as Base Learners)

- Built on
 - Cox Regression
 - Linear Regression
 - Logistic Regression
- Choice of regression model represents interaction of features
- Choice of coefficients represents importance of features
- *Data tells us*
 - how to group/cluster patients
 - which regression model to use for each group/cluster
 - which coefficients to use for each group/cluster
 - how to aggregate predictions

Clinical Decision Support System

University of California Los Angeles

Input Variables

Recipient Variables	Donor Variables	Compatibility Variables
Clinical and demographic features		
Age (years) <input type="text" value="50"/>	Age (years) <input type="text" value="28"/>	Ischemic Time (hour) <input type="text" value="3"/>
Gender <input type="text" value="Male"/>	Gender <input type="text" value="Male"/>	HLA-A Mismatch <input type="text" value="1"/>
Height (cm) <input type="text" value="178"/>	Height (cm) <input type="text" value="181"/>	HLA-B Mismatch <input type="text" value="1"/>
Weight (kg) <input type="text" value="80"/>	Weight (kg) <input type="text" value="83"/>	HLA-DR Mismatch <input type="text" value="1"/>
Diabetes <input type="text" value="Yes"/>	Donor blood group <input type="text" value="A"/>	
Infection <input type="text" value="No"/>	Hep C Antigen <input type="text" value="Yes"/>	
Transfusion <input type="text" value="No"/>	Diabetes <input type="text" value="Yes"/>	
Number of Previous Heart Transplants <input type="text" value="0"/>		
Creatinine ($\mu\text{mol/l}$) <input type="text" value="1.2"/>		
Total Bilirubin ($\mu\text{mol/l}$) <input type="text" value="1.3"/>		
Mean PRA (%) <input type="text" value="5.1"/>		
Blood Type <input type="text" value="A"/>		
Life support		
Ventilator Assist <input type="text" value="No"/>		
ECMO Assist <input type="text" value="No"/>		
LVAD Assist <input type="text" value="No"/>		
Dialysis <input type="text" value="No"/>		
IABP Assist <input type="text" value="Yes"/>		
Total Artificial Heart <input type="text" value="No"/>		
Inotropic Assist <input type="text" value="No"/>		
Other Circulatory Support <input type="text" value="No"/>		
Waiting status and time		
Days in Status 1A (days) <input type="text" value="3"/>		
Days in Status 1B (days) <input type="text" value="9"/>		
Days in Status 2 (days) <input type="text" value="25"/>		

ML Performance Comparisons (Wait-list)

	Algorithms	3-month	1-year	3-year	10-year
	ToPs/R	0.8467	0.8130	0.7921	0.7897
Boosting Methods	AdaBoost	0.8180	0.7865	0.7773	0.7452
	Deep Boost	0.8211	0.7898	0.7731	0.7392
	Logit Boost	0.7449	0.7371	0.7232	0.6776
	XGBoost	0.8243	0.7935	0.7779	0.7456
Tree-based Methods	Decision Tree	0.8188	0.7833	0.7642	0.7440
	Random Forest	0.8239	0.7926	0.7744	0.7280
Other	Neural Nets	0.7881	0.7811	0.7705	0.7412

ML Performance Comparison (Post-transplantation)

	Algorithms	3-month	1-year	3-year	10-year
	ToPs/R	0.6763	0.6637	0.6538	0.6562
Boosting Methods	AdaBoost	0.6506	0.6302	0.6034	0.6155
	Deep Boost	0.6464	0.6347	0.6100	0.6133
	Logit Boost	0.6370	0.6216	0.5961	0.6130
	XGBoost	0.6183	0.6083	0.5877	0.6152
Tree-based Methods	Decision Tree	0.6296	0.6107	0.5895	0.5990
	Random Forest	0.6529	0.6413	0.6113	0.6194
Other	Neural Nets	0.6415	0.6387	0.6101	0.6150

Previous Machine Learning in Prognostic Research

- + High predictive accuracy (for some datasets)
- + Data-driven, few assumptions
- Many algorithms: Which one to choose?
- Many hyper-parameters: Need expertise in data science

AUROC	MAGGIC	UK Biobank	UNOS-I	UNOS-II
Best predictor	0.80 ± 0.004	0.76 ± 0.002	0.78 ± 0.002	0.65 ± 0.001
	NN	GradientBoost	ToPs	ToPs
Best Clinical Score	0.70 ± 0.007	0.70 ± 0.003	0.62 ± 0.001	0.56 ± 0.001
Cox PH	0.75 ± 0.005	0.74 ± 0.002	0.70 ± 0.001	0.59 ± 0.001

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Best Clinical Score	0.70 ± 0.007	0.70 ± 0.003	0.62 ± 0.001	0.56 ± 0.001
Cox PH	0.75 ± 0.005	0.74 ± 0.002	0.70 ± 0.001	0.59 ± 0.001

- Can we predict in advance which method is best?
- Can we do better?
- Many metrics of performance (AUROC, AUPRC, C-index, quality of well-being)

How to do this?

**Many diseases, many
variables, various needs!
All is changing!**



**Can't craft a model for each
disease!**



**Make
Machine Learning
DO the Crafting**

How to do this?

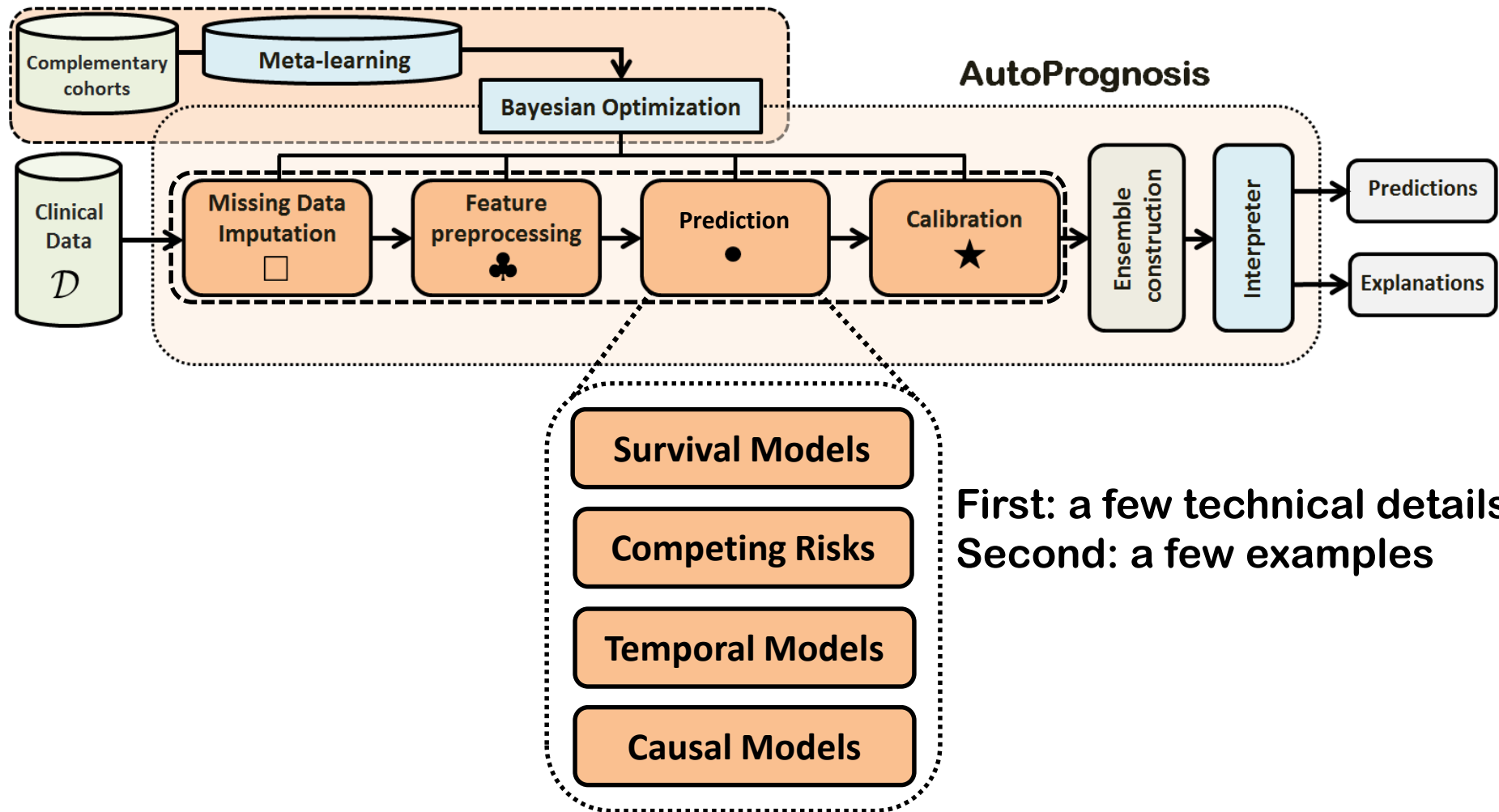
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Make
Machine Learning
DO the Crafting

- **Previous AutoML? Auto-WEKA and Auto-Sklearn**
 - Limited performance gains
 - **Ad-hoc** optimization and ad-hoc meta-learning
 - Simplistic handling of **missing data**
 - Do not capture **uncertainty**
 - Limited to classification problems (**survival, competing risks etc.**)

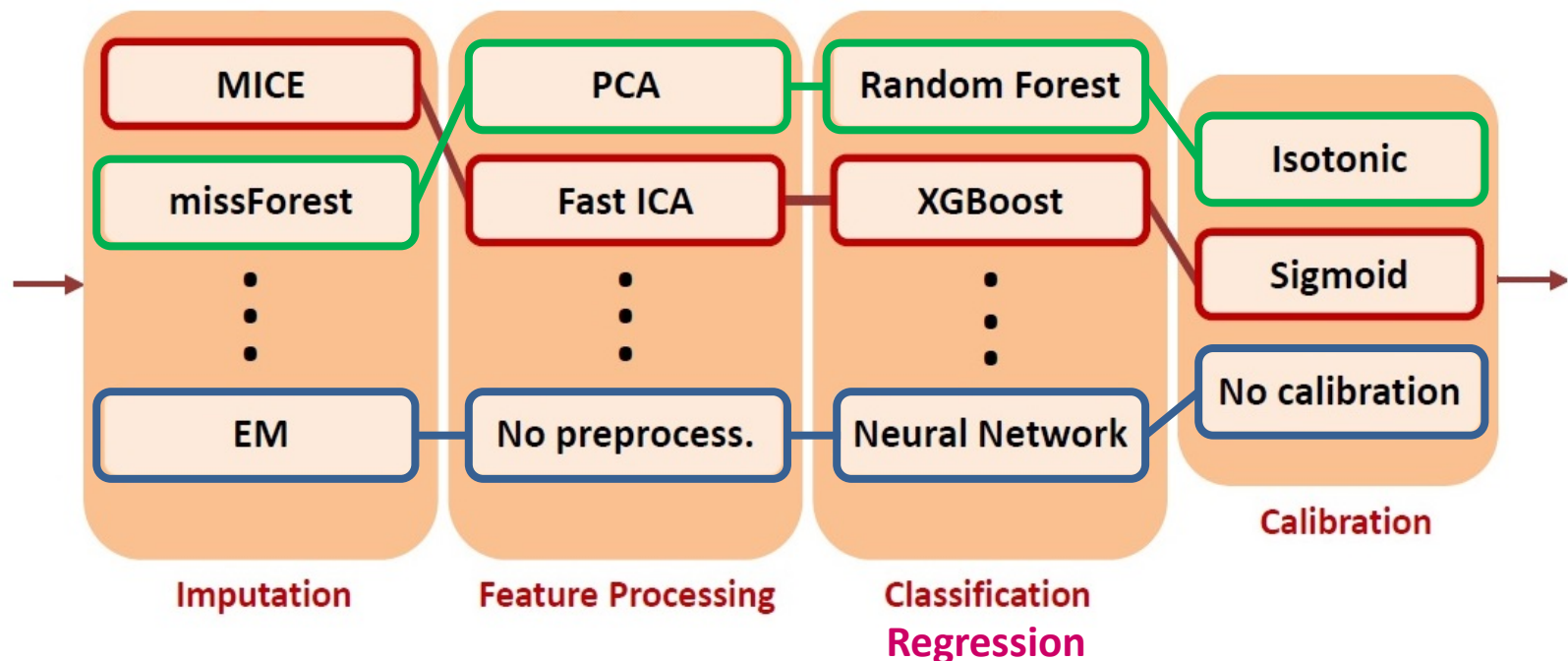
AutoPrognosis: A tool for crafting Prognostic Scores for *Many Diseases*



Principled Bayesian Optimization

We need an entire pipeline!

- Each pipeline is a **path of algorithms!**
- Find the best paths and tune parameters:
A hard optimization problem!

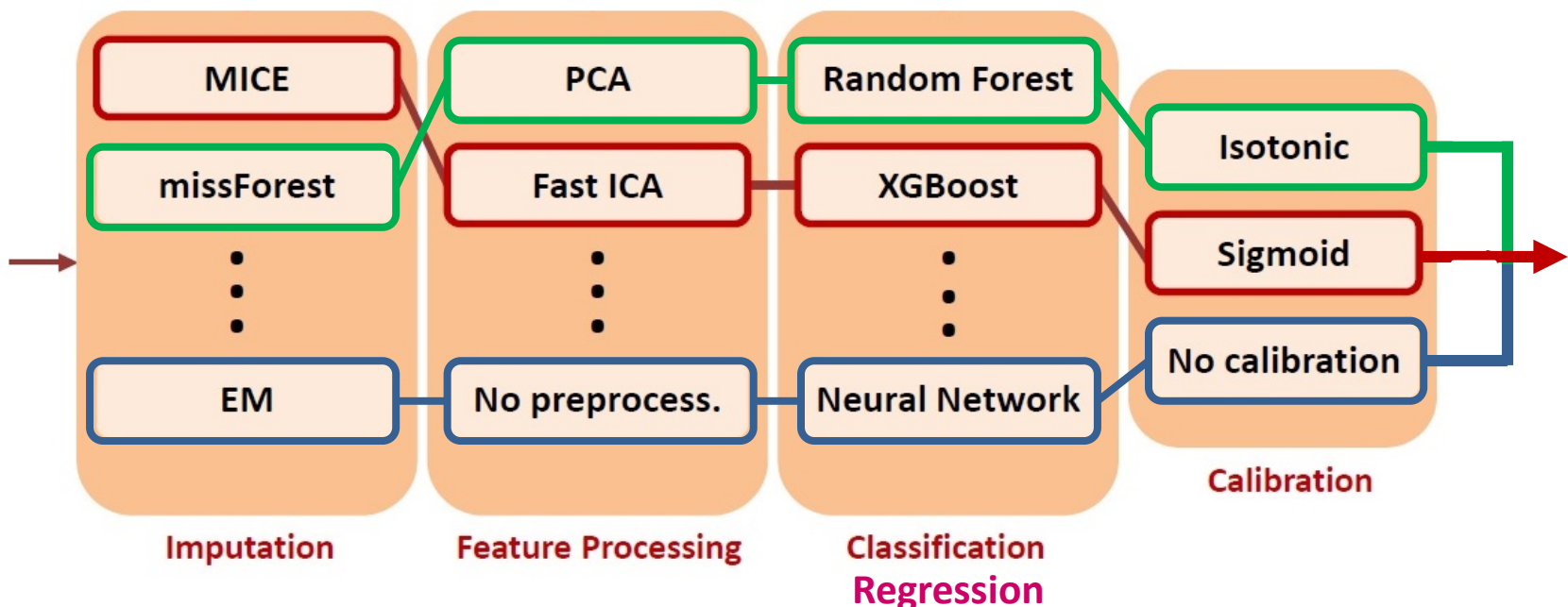


Ensembles

- Instead of the single best pipeline we use an ensemble

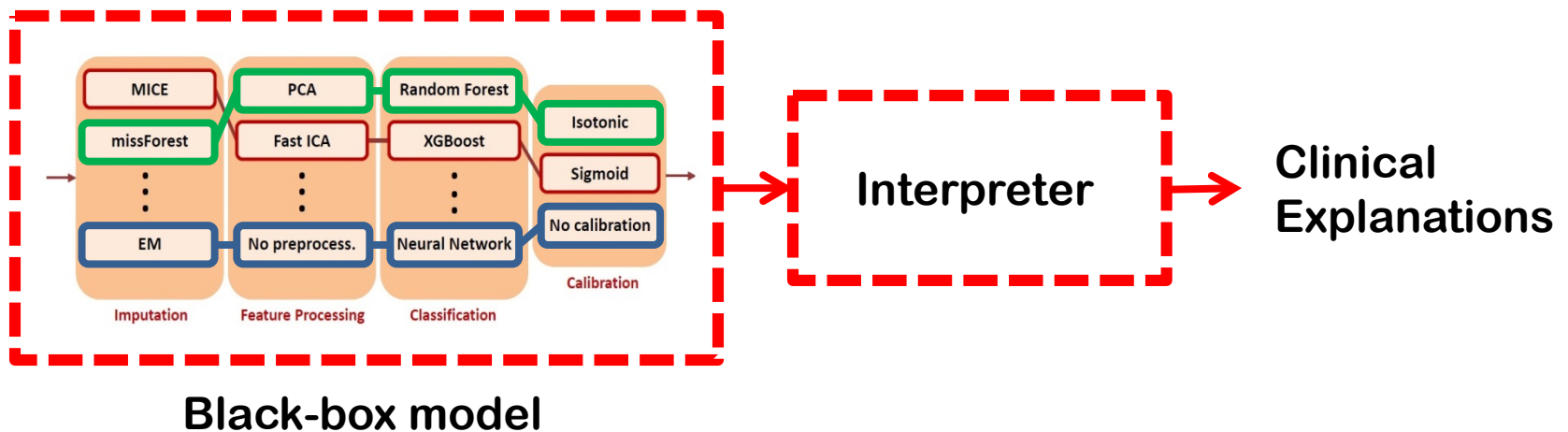
- **Why?**

- **Uncertainty:** finite data set to learn from, so we are not sure which pipeline is “best”
- **Information loss:** using a single pipeline discards useful information from other pipelines



Interpretability

- We don't want simply a **black-box**, we want explanations that users can **interpret**



- Interpreter provides **logical associations**

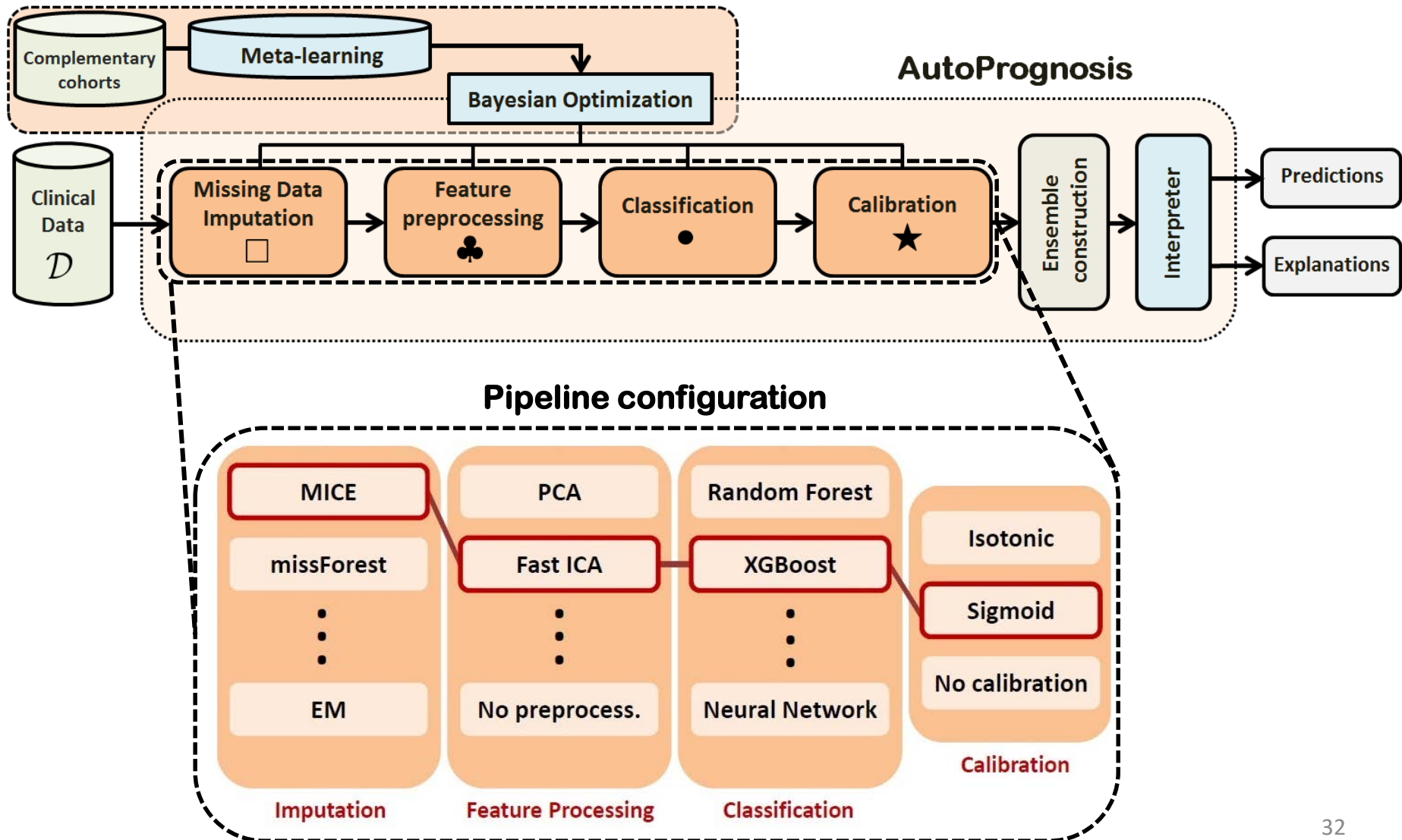
$$\underbrace{C_1 \wedge C_2 \wedge \dots \wedge C_{l(r)}}_{\text{Clinical conditions}} \implies r, \forall r \in \mathcal{R}$$

Risk stratum

\mathcal{R} : risk strata

- **Example:** $\text{Diabetic} \wedge \text{Smoking} \implies \text{High risk for ischemic stroke}$

AutoPrognosis: System Overview



AutoPrognosis: Pipeline Components

- 8 imputation algorithms, 10 feature preprocessing algorithms, 20 classifiers, 3 calibration methods
- MANY hyperparameters in each algorithm
- Total number of hyperparameters = 110

Pipeline Stage	Algorithms				
□ Data Imputation	□ missForest (2) □ Matrix completion (2)	□ Median (0) □ MICE (1)	□ Most-frequent (0) □ GAIN	□ Mean (0) □ None (0)	□ EM (1)
♣ Feature process.	♣ Feature aggro. (4) ♣ R. kitchen sinks (2)	♣ Kernel PCA (5) ♣ Nystroem (5)	♣ Polynomial (3) ♣ Linear SVM (3)	♣ Fast ICA (4) ♣ Select Rates (3)	♣ PCA (2) ♣ None (0)
● Prediction	● Bernoulli NB (2) ● Gaussian NB (0) ● Multinomial NB (2) ● Ridge Class. (1) ● DMGP	● AdaBoost (4) ● XGBoost (5) ● R. Forest (5) ● Bagging (4) ● CMGP	● Decision Tree (4) ● Extr. R. Trees (5) ● Neural Net. (5) ● <i>k</i> -NN (1) ● DeepHit	● Grad. Boost. (6) ● Light GBM (5) ● Log. Reg. (0) ● Surv. Forest (5) ● HBM	● LDA (4) ● L. SVM (4) ● GP (3) ● Cox Reg. (0) ● TOPs
★ Calibration	★ Sigmoid (0)	★ Isotonic (0)	★ None (0)		

Automated Pipeline Configuration (I)

- Imputation algorithms \mathcal{A}_d
Hyperparameters Θ_d
- Feature process. algorithms \mathcal{A}_f
Hyperparameters Θ_f
- Classification algorithms \mathcal{A}_c
Hyperparameters Θ_c
- Calibration algorithms \mathcal{A}_a
Hyperparameters Θ_a
- Set of all pipelines $\mathcal{P} = \mathcal{A}_d \times \mathcal{A}_f \times \mathcal{A}_c \times \mathcal{A}_a$
- Set of all hyperparameters $\Theta = \Theta_d \times \Theta_f \times \Theta_c \times \Theta_a$
- Set of all pipeline configurations \mathcal{P}_Θ
- Combined Pipeline Selection and Hyperparameter optimization problem (CPSH)

$$P_{\theta^*}^* \in \arg \max_{P_\theta \in \mathcal{P}_\Theta} \frac{1}{K} \sum_{i=1}^K \mathcal{L}(P_\theta; \mathcal{D}_{\text{train}}^{(i)}, \mathcal{D}_{\text{valid}}^{(i)})$$

Automated Pipeline Configuration (II)

● **The CPSH problem** $\arg \max_{P_\theta \in \mathcal{P}_\Theta} \frac{1}{K} \sum_{i=1}^K \mathcal{L}(P_\theta; \mathcal{D}_{\text{train}}^{(i)}, \mathcal{D}_{\text{valid}}^{(i)})$

● **Bayesian optimization**

Gaussian process
prior

$$f \sim \mathcal{GP}(\mu(P_\theta), k(P_\theta, P'_\theta))$$

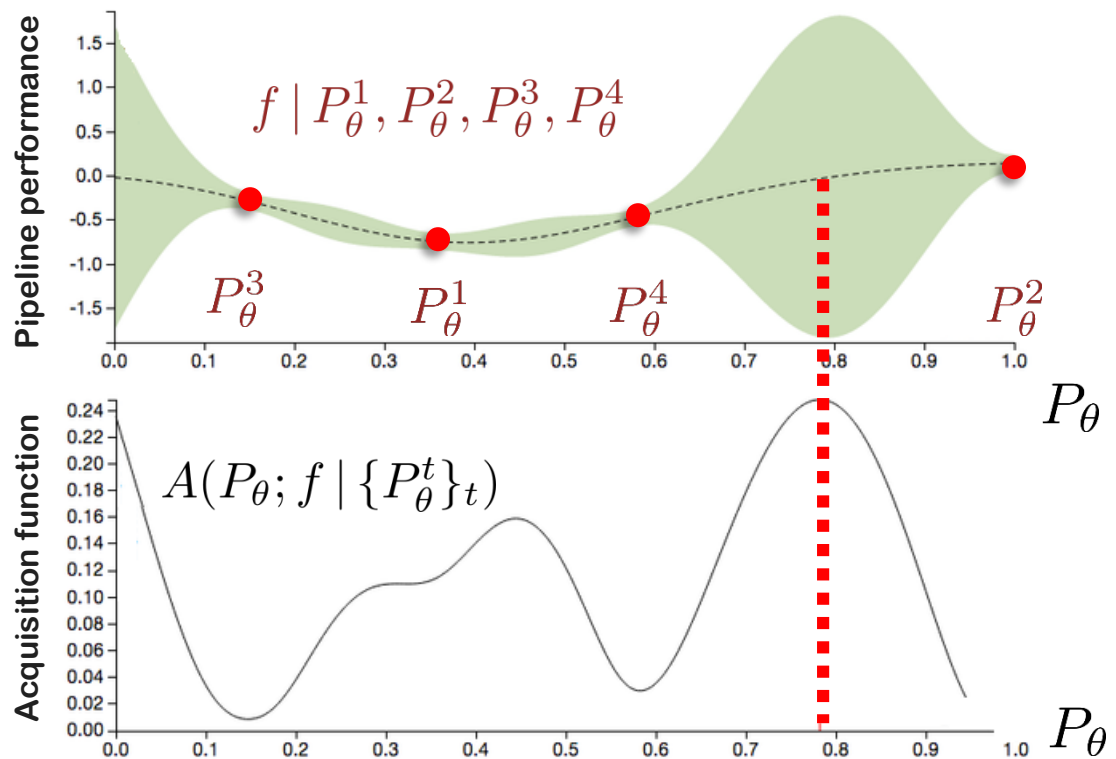
Gaussian process
posterior

$$f | \{P_\theta^t\}_t$$

Select new pipeline via
acquisition function

$$P_\theta^{t+1} = \arg \max_{P_\theta} A(P_\theta; f | \{P_\theta^t\}_t)$$

$$f(P_\theta) = \frac{1}{K} \sum_{i=1}^K \mathcal{L}(P_\theta; \mathcal{D}_{\text{train}}^{(i)}, \mathcal{D}_{\text{valid}}^{(i)}) + \varepsilon$$



The Curse of Dimensionality

- **Statistical** and **computational complexity** of the CPSH problem
- GP BO does not work well for $D > 10$ [Wang, 2013]

Gaussian process prior

$$f \sim \mathcal{GP}(\mu(P_\theta), k(P_\theta, P'_\theta))$$

Gaussian process posterior

$$f \mid \{P_\theta^t\}_t$$

Select new pipeline via acquisition function

$$P_\theta^{t+1} = \arg \max_{P_\theta} A(P_\theta; f \mid \{P_\theta^t\}_t)$$

Sample complexity for non-parametric estimation of α -smooth functions [Stone, 1982]

$$\Theta\left(t^{-\frac{\alpha}{2\alpha+D}}\right)$$

Exponentially many iterations!

Computational complexity of GP posterior
After t iterations [Rasmussen & Williams, 2006]

$$\mathcal{O}(t^3)$$

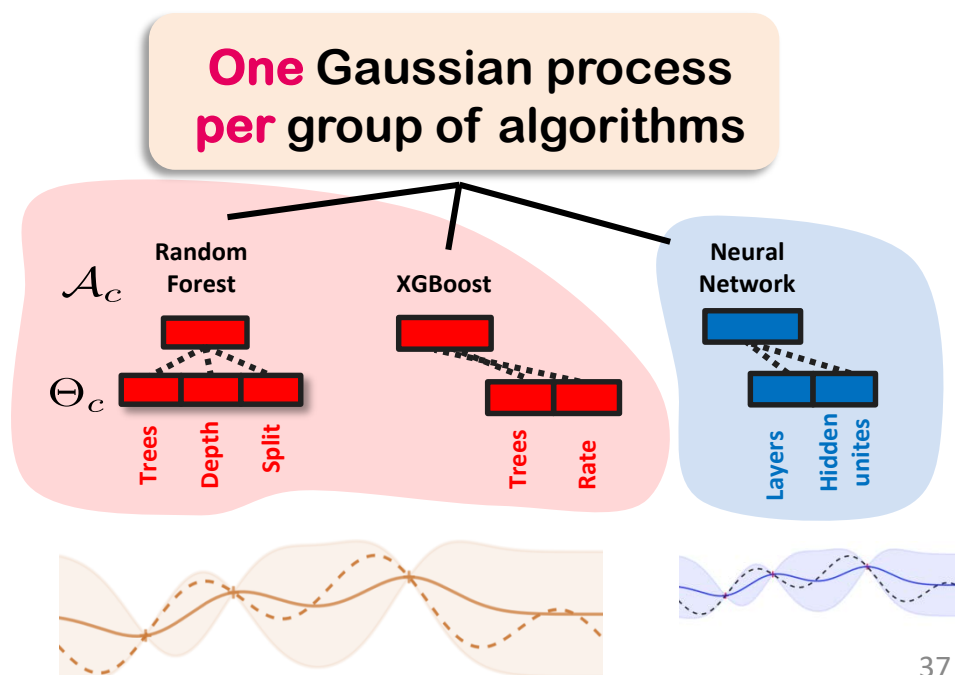
Computational complexity of maximizing acquisition [Snoek, 2015]

$$\mathcal{O}(n^D)$$

Bayesian Optimization with Structured Kernel Learning

- **Main idea:** Some algorithms are “correlated” and some are not => **Correlated** algorithms should be made to **share information**
- Correlation is not known in advance, so must be **learned**
- **Learn** a structured kernel that clusters correlated algorithms:

- Low dimensionality for every cluster
- Relevant information sharing within a cluster



Sparse Additive Gaussian Processes

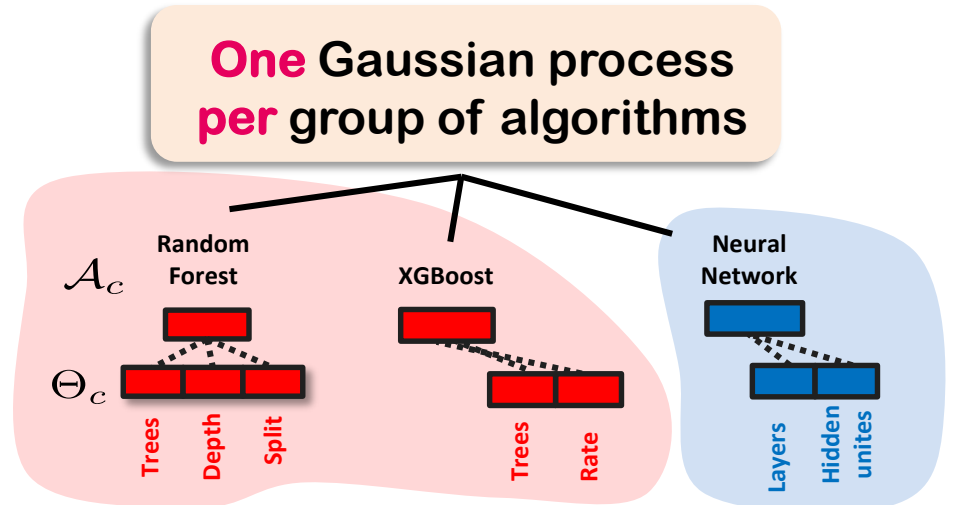
- Decompose high-dimensional GP into sum of low-dimensional components

Λ

Space of all pipelines

$\{\Lambda^{(m)}\}_m$

Partitions of Λ

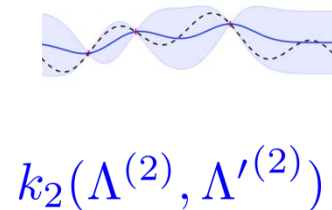
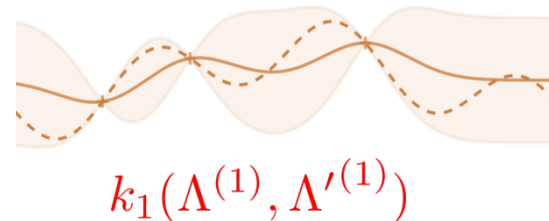


Sparse additive GPs:

$$f(\Lambda) = \sum_{m=1}^M f_m(\Lambda^{(m)})$$

D-dimensional
GP

Low-dimensional
GPs



Structured kernel: $k(\Lambda, \Lambda') = \sum_{m=1}^M k_m(\Lambda^{(m)}, \Lambda'^{(m)})$

Structured Kernel Learning

- Define the variable $z_{v,i} \in \{1, \dots, M\}$: indicator for the subspace allocation for algorithm i in \mathcal{A}_v

Prior on $z_{v,i}$ = Prior on $\{\Lambda^{(m)}\}_m$

- Bayesian inference:

Prior on
decompositions

$$\alpha \sim \text{Dirichlet}(M, \gamma)$$

$$z_{v,i} \sim \text{Multinomial}(\alpha)$$

Compute posterior in
concurrence with BO

$$\mathbb{P}(z, \alpha \mid \{f(P_\theta^t)\}_t, \gamma) \propto \mathbb{P}(\{f(P_\theta^t)\}_t \mid z) \mathbb{P}(z \mid \alpha) \mathbb{P}(\alpha, \gamma)$$

Gibbs Sampling

$$\mathbb{P}(z_{v,i} = m \mid z / \{z_{v,i}\}, \mathcal{H}_t) \propto \mathbb{P}(\mathcal{H}_t \mid z) (|\mathcal{A}_v^{(m)}| + \gamma_m)$$

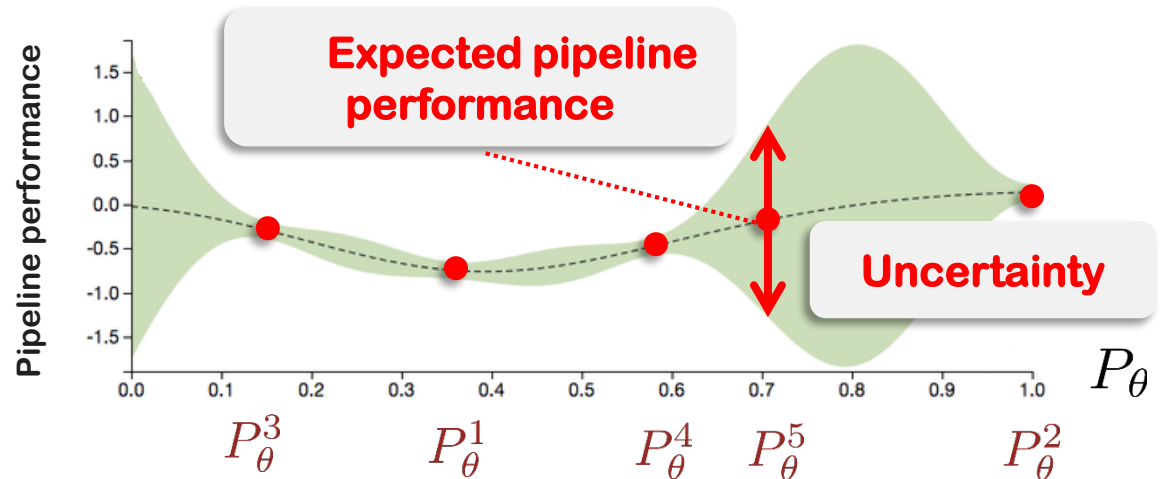
Gumbel-Max Sampler

$$\omega_m \stackrel{\text{i.i.d}}{\sim} \text{Gumbel}(0, 1), m \in \{1, \dots, M\},$$

$$z_{v,i} \sim \arg \max_m \mathbb{P}(\mathcal{H}_t \mid z, z_{v,i} = m) (|\mathcal{A}_v^{(m)}| + \gamma_m) + \omega_m.$$

Post-hoc Ensemble Construction

- Create an ensemble using the posterior distribution of performances

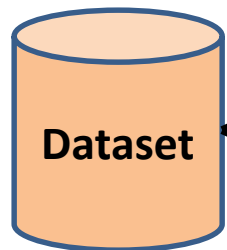


- Bayesian model averaging
- Create a linear combination of pipelines $\sum_i w_i P_\theta^i$
- Weight of every pipeline = empirical probability of it being the best!

$$\begin{aligned} w_i &= \mathbb{P}(P_\theta^{i*} = P_\theta^i \mid \mathcal{H}_t) \\ &= \prod_{j \neq i} \Phi \left((\mu_i - \mu_j) \cdot (\sigma_i^2 + \sigma_j^2)^{-\frac{1}{2}} \right), \end{aligned}$$

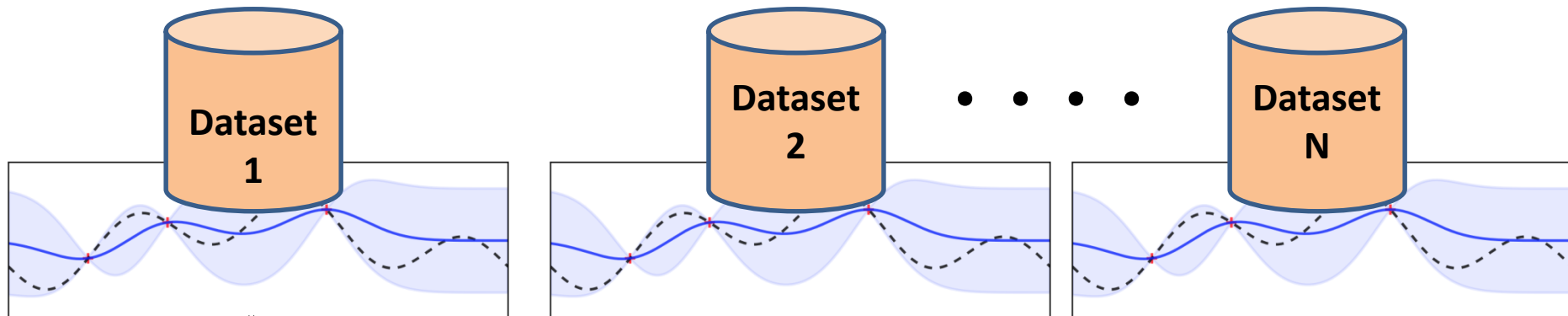
Meta-learning via Empirical Bayes

- For every dataset seen by the system, create meta-features



Statistical meta-features: entropy, size of dataset, number of features, class imbalance, etc.

Clinical meta-features: ICD-10 codes, lab tests, etc



Meta-features

Tuned hyperparameters via empirical Bayes

Match new dataset to old ones using meta-features...

Example 1: **Cystic Fibrosis** (Scientific Reports, 2018)

- **Collaboration with the UK CF trust**

Using cross-sectional observational data for 99% of CF patients in the UK

- **Scarce resources:** donated lungs, surgical resources

- **Questions:**

Who should be referred to a **lung transplant**?

What **guidelines** should be used for referral to a **lung transplant**?

AutoPrognosis: Better Predictions (Out-of-sample)

Prognostic Model	AUC-PR
AutoPrognosis	0.59 ± 0.03
Clinical Practice	0.49 ± 0.02

AUC-PR (Sensitivity-Precision) is the metric of interest!

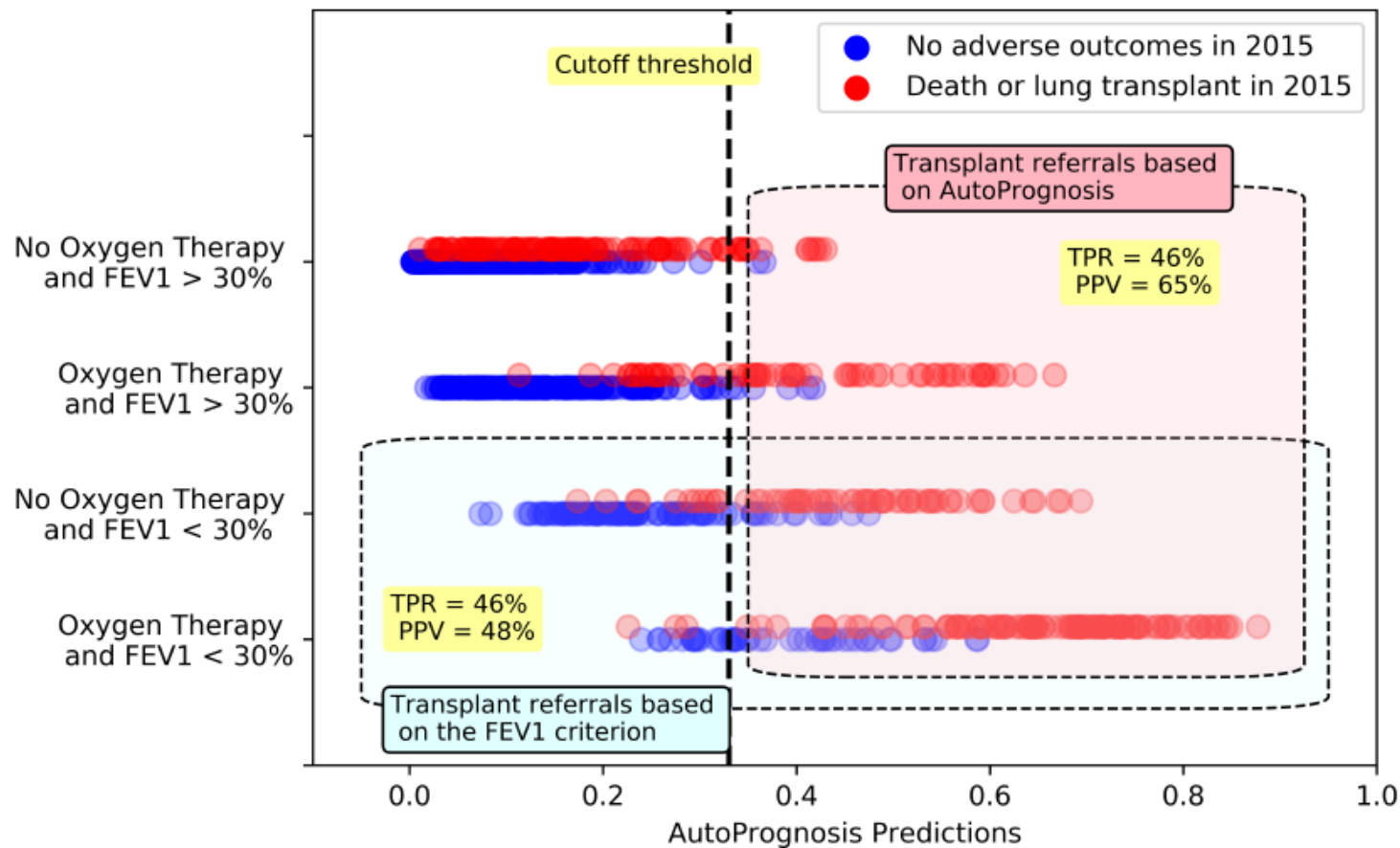
AutoPrognosis: Better Predictions (Out-of-sample)

Prognostic Model	AUC-PR
AutoPrognosis	0.59 ± 0.03
Clinical Practice	0.49 ± 0.02
Auto-WEKA	0.50 ± 0.03
Auto-sklearn	0.51 ± 0.02
Nkam et al., 2017	0.49 ± 0.02
CF-ABLE-UK	0.28 ± 0.04

AUC-PR (Sensitivity-Precision) is the metric of interest!

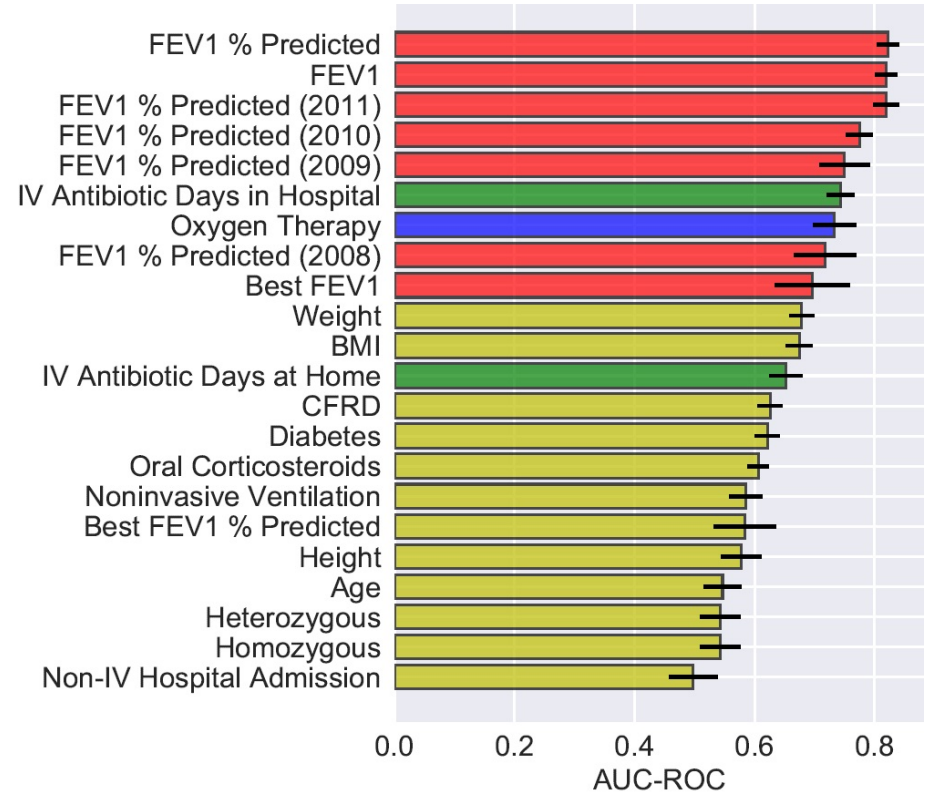
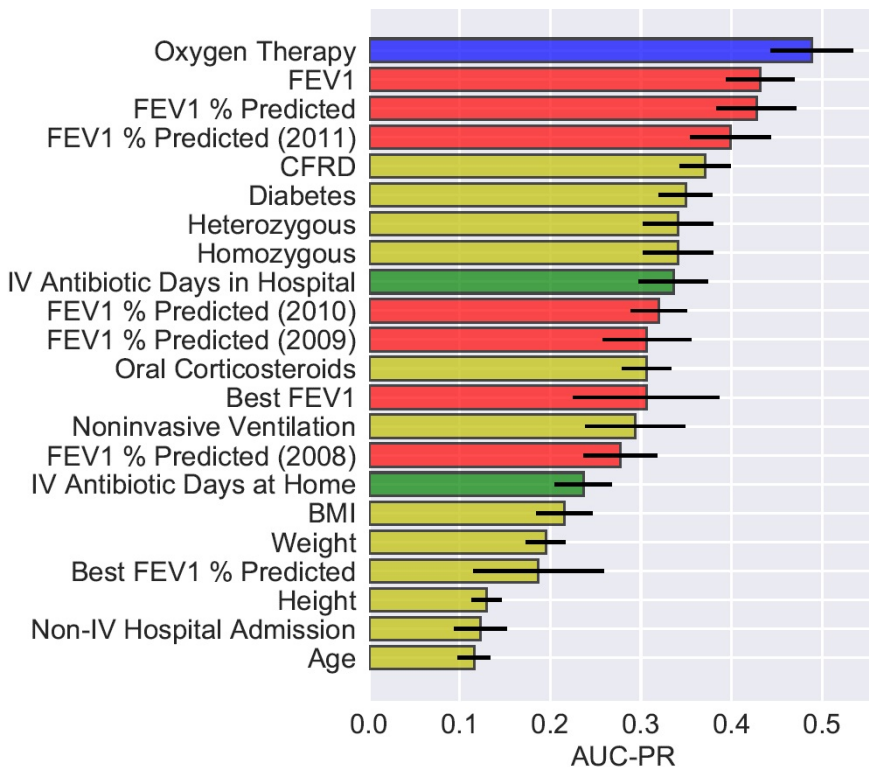
AutoPrognosis at work

- AutoPrognosis learned to stratify the UK CF population in a way that led to a much **more efficient allocation of donor lungs**



AutoPrognosis: Identifying risk factors

● Contribution of different features to predictive accuracy



AutoPrognosis: Risk Stratification

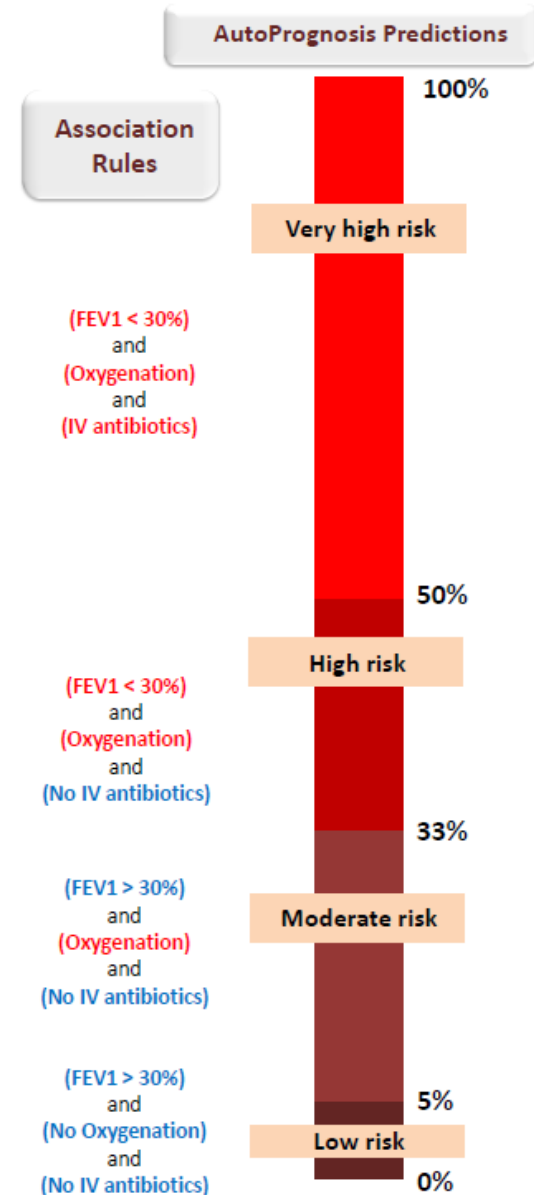
Lung function

Spirometry

Gas exchange

Current practice focuses on **spirometric** variables (FEV1) to make decisions

AutoPrognosis discovers that more refined decisions can be achieved by incorporating variables related to **gas exchange**



AutoPrognosis: Other examples

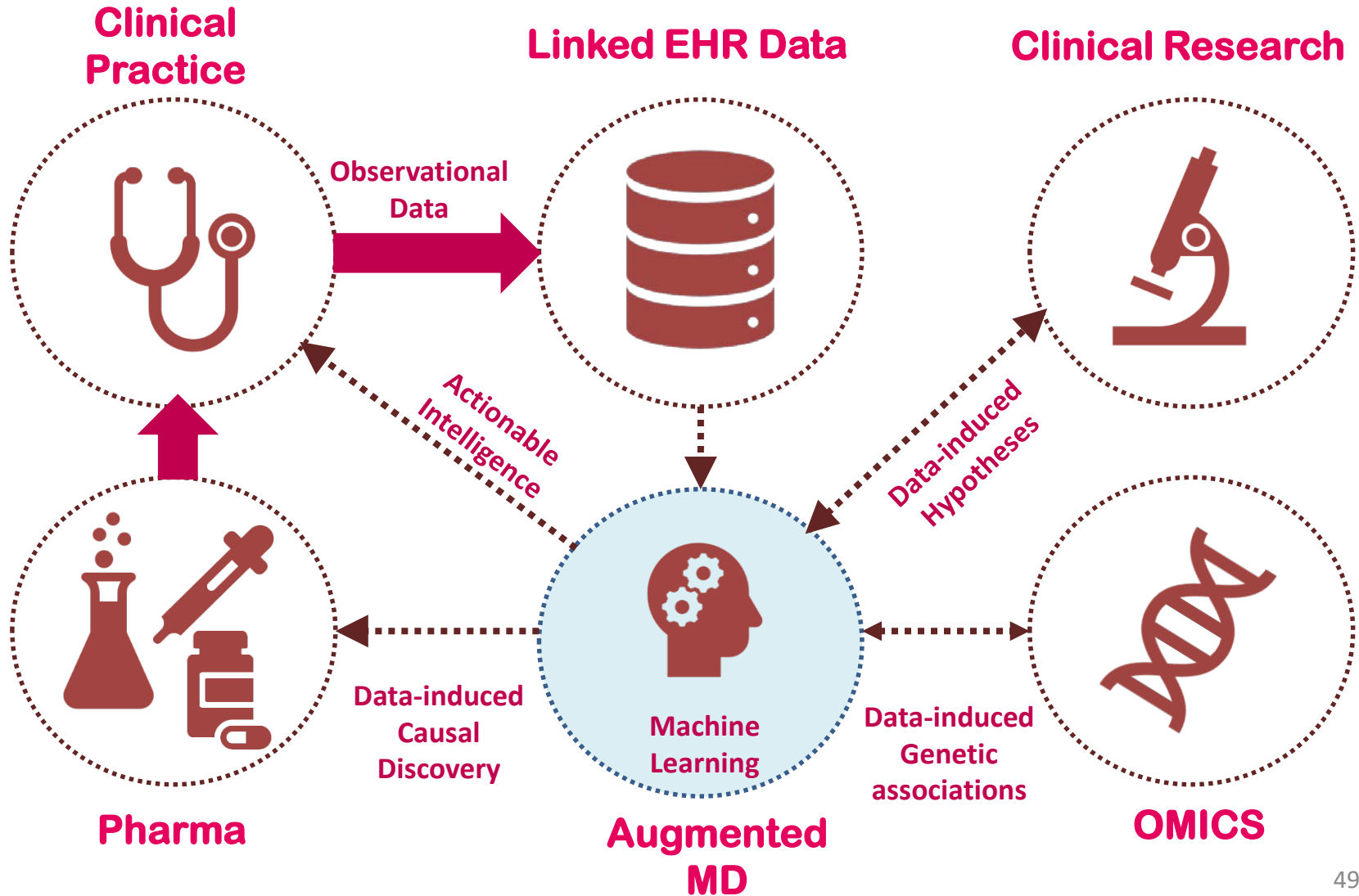
Cardiovascular Disease

Breast Cancer

Dementia

ML+AI:

Enormous potential for transformative impact in medicine




How fast does AutoPrognosis learn?

Theorem

Let the number of algorithms in every subspace be bounded by d . For a Matérn kernel with length-scale parameter ℓ , then the **cumulative regret** of **AutoPrognosis** is given by

$$R(T) = 2^d DT^{\frac{\ell + d(d+1)}{2\ell + d(d+1)}} \log(T)$$

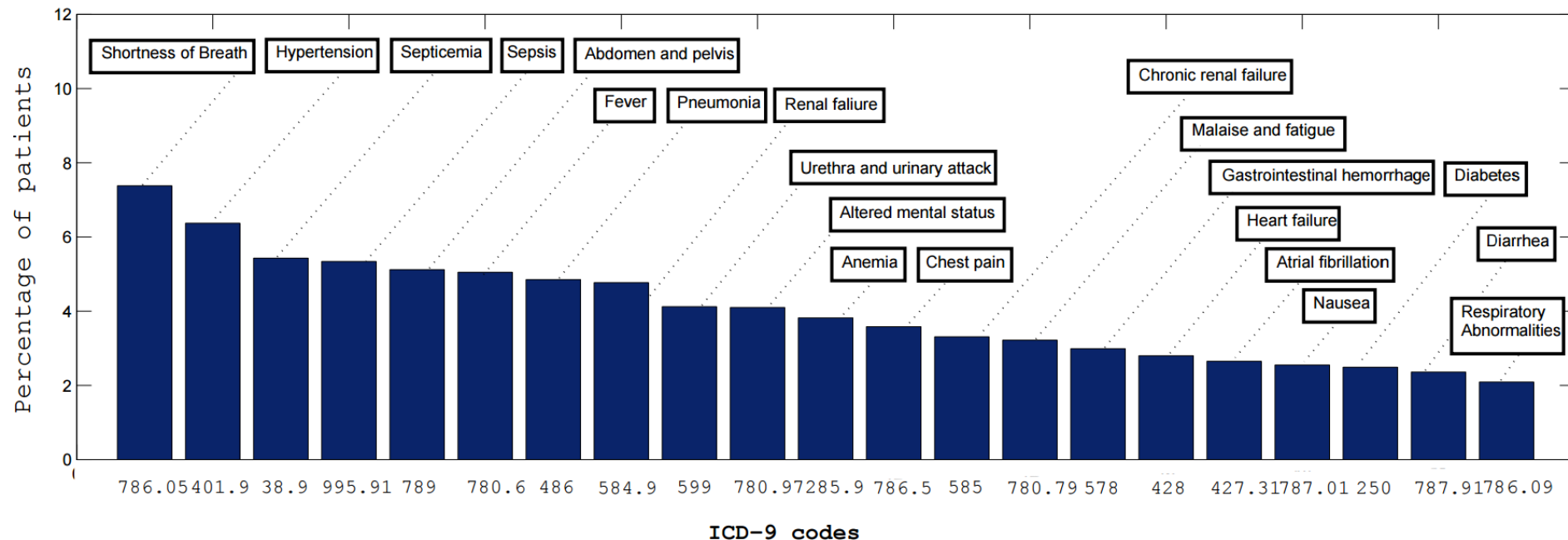
- **Conventional GP-based BO:** $R(T) \sim T$
 - **AutoPrognosis** $R(T) \sim T^{\frac{2}{3}}$  **10-fold improvement
For T = 1000!!**
- (common scenario: $d = 5, \ell = 25$)**

Forecast ICU in practice

- **Hospital:** UCLA Ronald Reagan Medical Center
- **Cohort of 6,094 patients**
 - **Period:** March 2013 ~ June 2015 (tested July 2015 – July 2016)
 - **Age:** 18 ~ 100+ years
 - **Gender:**
 - Male (3,018 patients, 49.5%)
 - Female (3,076 patients, 50.5%)
 - **Length of stay:** 1.5 hours ~ 159 days

Wide Variety of Diagnoses

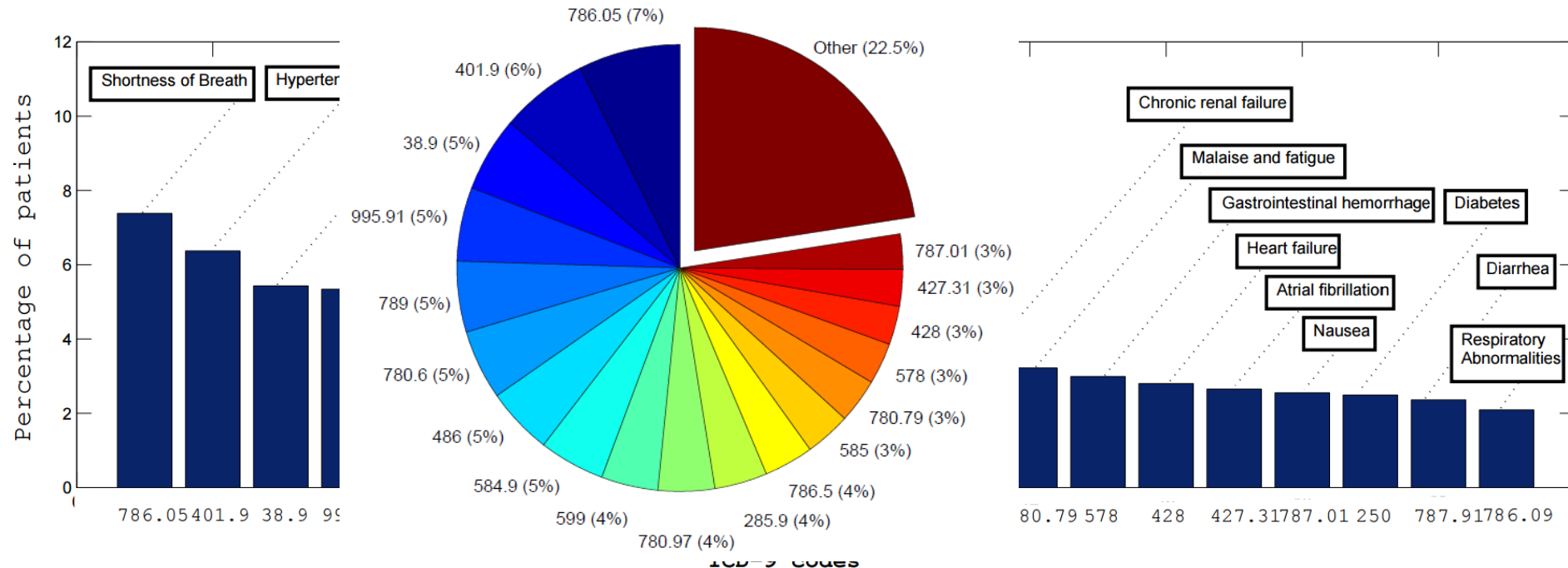
Percentage of patients in **top 20 ICD 9 codes**



Among 6,094 patients, 306 patients (5.0%) admitted to ICU unexpectedly; 5,788 patients (95.0%) discharged

Wide Variety of Diagnoses

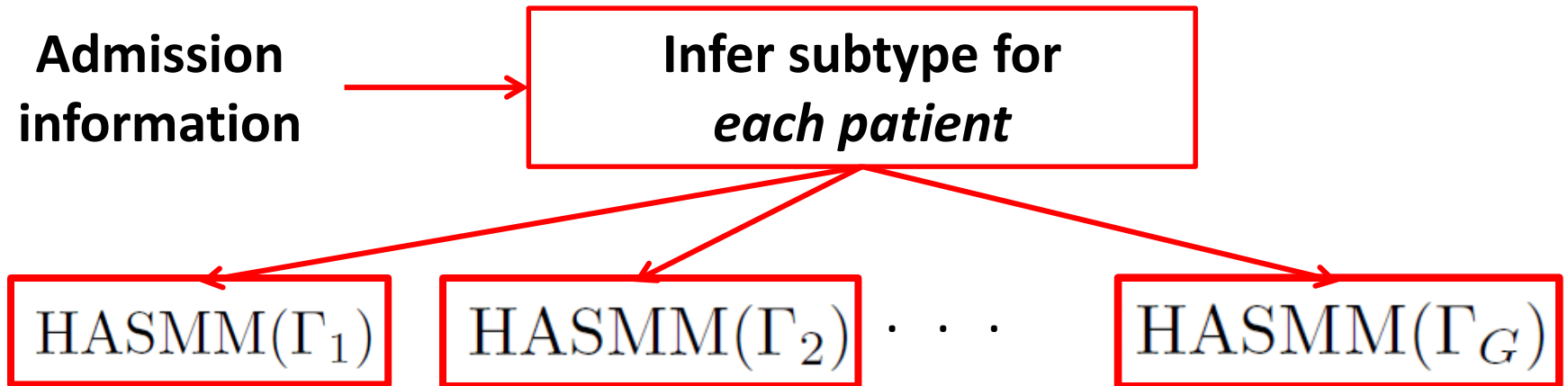
Percentage of patients in top 20 ICD 9 codes



Among 6,094 patients, 306 patients (5.0%) admitted to ICU unexpectedly; 5,788 patients (95.0%) discharged

Subtyping (Phenotyping)

- Discovering the different ways in which a disease manifests in different patients
- Key approach for **personalized medicine**



Performance Metrics

- **TPR** (True Positive Rate, i.e. **Sensitivity**) = True Positive/True ICU Patients
- **TNR** (True Negative Rate, i.e. **Specificity**) = True Negative/True Discharge patients
- **PPV** (Positive Predictive Value, i.e. **Precision**) = True Positive/Predicted ICU Patients
- **NPV** (Negative Predictive Value) = True Negative/Predicted Discharge patients

	Predicted ICU patients	Predicted Discharge patients
True ICU patients	True Positive	False Negative
True Discharge patients	False Positive	True Negative

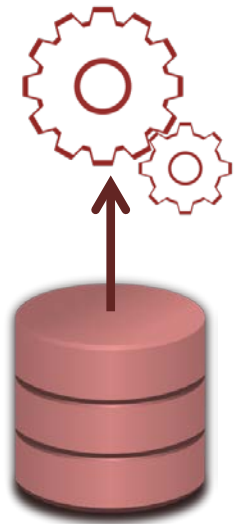
The “Augmented” MD

● Machine learning

...*can't* do medicine!

...*can* provide doctors with **actionable information**!

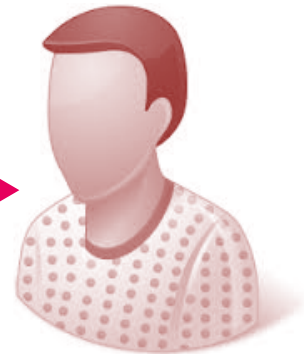
Machine learning algorithms



Personalized risk assessment
Personalized diagnosis and prognosis
Individualized treatment effects
Disease Atlas
Recommendations



Clinical Practice



Application to Cardiovascular Patient Care

- **Preventive care:**

- Meta-analysis Global Group in Chronic Heart Failure (MAGGIC)
- UK bio-bank.

- **Heart-transplant wait-list management:**

- United Network for Organ Sharing

- **Post-transplant care:**

- United Network for Organ Sharing