



# MATHEMATICAL FRONTIERS

*The National  
Academies of*

SCIENCES  
ENGINEERING  
MEDICINE

[nas.edu/MathFrontiers](https://nas.edu/MathFrontiers)

Board on Mathematical Sciences & Analytics

# MATHEMATICAL FRONTIERS

## 2019 Monthly Webinar Series, 2-3pm ET

**February 12:** *Machine Learning for Materials Science\**

**March 12:** *Mathematics of Privacy\**

**April 9:** *Mathematics of Gravitational Waves\**

**May 14:** *Algebraic Geometry\**

**June 11:** *Mathematics of Transportation\**

**July 9:** *Cryptography & Cybersecurity\**

**August 13:** *Machine Learning in Medicine*

**September 10:** *Logic and Foundations*

**October 8:** *Mathematics of Quantum Physics*

**November 12:** *Quantum Encryption*

**December 10:** *Machine Learning for Text*

*Made possible by support for BMSA from the  
**National Science Foundation**  
**Division of Mathematical Sciences**  
and the  
**Department of Energy**  
**Advanced Scientific Computing Research***

*\* Webinar posted*

# MATHEMATICAL FRONTIERS

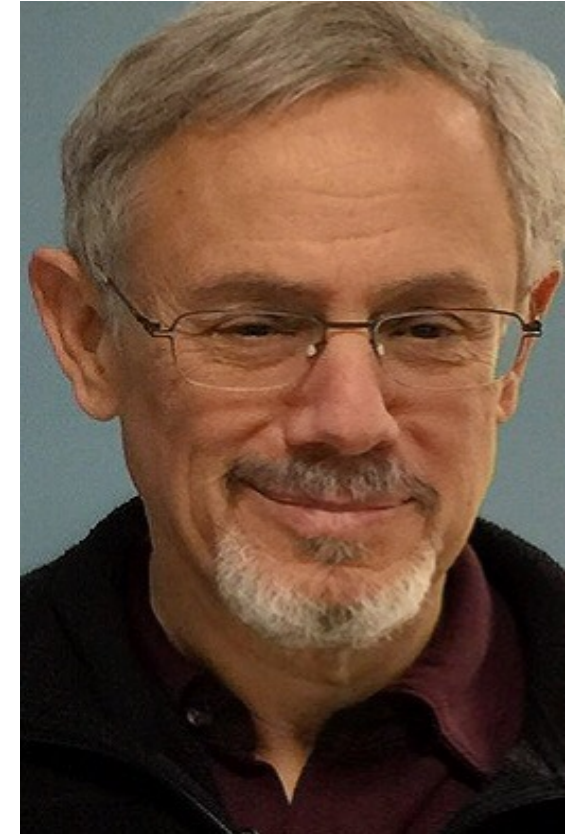
## Machine Learning in Medicine



**Mihaela van der Schaar,  
University of Cambridge,  
Alan Turing Institute, and UCLA**



**Juan Gutierrez,  
University of Georgia**



**Mark Green,  
UCLA (moderator)**

# MATHEMATICAL FRONTIERS

## Machine Learning in Medicine



Mihaela van der Schaar,  
University of Cambridge,  
Alan Turing Institute, and UCLA

*John Humphrey Plummer Professor of Machine Learning,  
Artificial Intelligence and Medicine at University of Cambridge  
Turing Faculty Fellow at the Alan Turing Institute in London  
Chancellor's Professor at UCLA*

**Transforming medicine through  
AI-enabled healthcare  
pathways**



# My research

Develop cutting-edge machine learning and AI theory, methods, algorithms and systems to **deliver effective personalized healthcare**

- 1) **support** clinical decisions for the patient at hand
- 2) **understand** the basis of health and disease
- 3) **inform and improve** clinical pathways, better utilize resources & reduce costs
- 4) **transform** public health and policy

Genomic Data is Big Data



Genome, Transcriptome and Proteome

Clinical Data is Complex Data



“Clinome”, Patient Experience, Risk Factors etc

&

# Goal: deliver decision support for the patient at hand

## Cancer - a useful exemplar

- Common, costly and important group of disorders
- Varied aetiologies, presentations and long-term outcomes
- Complex management affecting multiple clinical systems
- Care delivered through multiple organisations
- Leads in personalised medicine therapeutics & genotype-phenotype correlation



# ML-AIM Predictor for Risk Prognosis

Making more informed and dynamic estimates about cancer survival  
by learning on diagnosis data and patient events over time

[TRY THE DEMO](#)

ML-AIM Predictor (Beta)

ML-AIM PREDICTOR BETA

BREAST CANCERCOLON CANCERLUNG CANCERPROSTATE CANCERHOW IT WORKSCREDITS

Breast Cancer

Input

Diagnosis Information

Input

Pathology Information

Age at Diagnosis

Enter value...

Tumor Size

Enter value...

ER Status

Select one...

HER2 Status

Select one...

Cancer Stage

Select one...

Nodes Involved

Enter value...

Tumor Grade

Select one...

Detected by Screening

Select one...

Vascular Invasion

Enter value...

Distance to Resection

Enter value...

PT

Enter value...

PN

Enter value...

PR

Enter value...

Ki67

Enter value...

B5B

Enter value...

E-cadherin

Enter value...

Pathology Report

de 3, her2 positive,

Select File

Figure Importance

Prediction Horizons →

ity

1.0

0.9

0.8



ML-AIM Predictor (Beta)

ML-AIM PREDICTOR BETA

BREAST CANCERCOLON CANCERLUNG CANCERPROSTATE CANCERHOW IT WORKSCREDITS

Breast Cancer

Input Diagnosis Information

Age at Diagnosis

Enter value...

Tumor Size

Enter value...

ER Status

Select one...

HER2 Status

Select one...

Cancer Stage

Select one...

Tumor Grade

Select one...

Nodes Involved

Enter value...

Detected b

Select one...

Input Pathology Information

Vascular Invasion

Enter value...

Distance to Resection

Enter value...

PT

Enter value...

PN

Enter value...

PR

Enter value...

Ki67

Enter value...

or, Upload Pathology Report

Distance margin: 3mm, grade 3, her2 positive, ki67 negative, ....

Drag-and-Drop or [Select File](#)

Select a patient

Time since Initial Diagnosis (Months)

06121824303642

Mortality Risk over Time

ity

1.0

0.9

0.8

Load or Create New Patient...

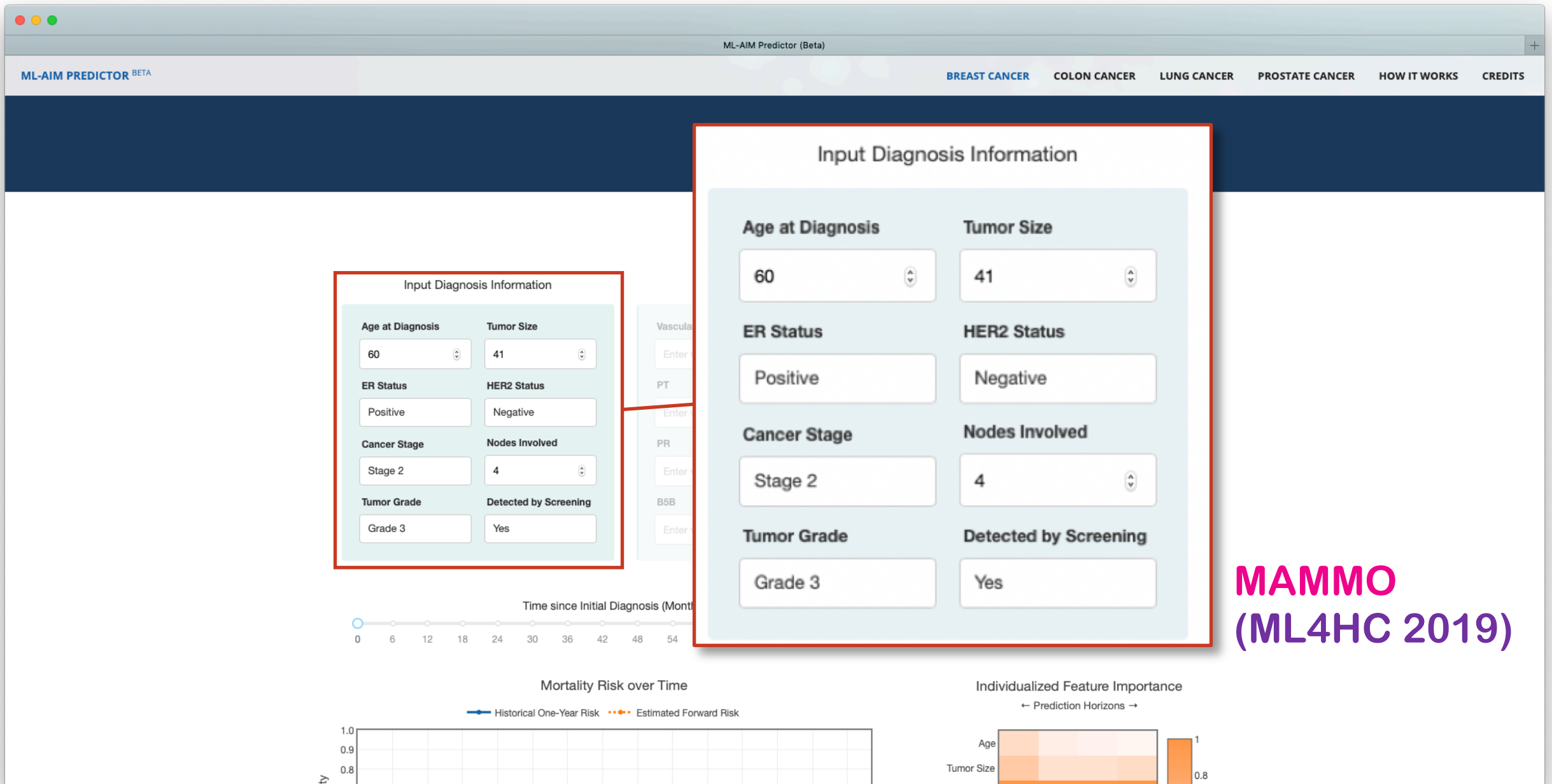
Create New Patient...

Patient 1

Patient 2

Patient 3

Patient 4



ML-AIM Predictor (Beta)

ML-AIM PREDICTOR BETA

BREAST CANCERCOLON CANCERLUNG CANCERPROSTATE CANCERHOW IT WORKSCREDITS

Breast Cancer

Input Pathology Information

Vascular Invasion

N

Distance to Resection

7

PT

X

PN

pn0

PR

N

Ki67

X

B5B

X

E-cadherin

X

or, Upload Pathology Report

marking axillary tail. At approximately 12 o'clock position needle tract with surrounding fat is identified. There is some fibrosis and this area extends up to around 60mm and lies 15mm from the deep margin, 20mm from superior and 60mm from inferior margin. Part C - labelled ""Left sentinel node #2"". A lymph node with surrounding fat measuring

Drag-and-Drop or [Select File](#)

or, Upload Pathology Report

marking axillary tail. At approximately 12 o'clock position needle tract with surrounding fat is identified. There is some fibrosis and this area extends up to around 60mm and lies 15mm from the deep margin, 20mm from superior and 60mm from inferior margin. Part C - labelled ""Left sentinel node #2"". A lymph node with surrounding fat measuring

Drag-and-Drop or [Select File](#)

Patient 3

Mortality Risk over Time

Historical One-Year Risk

Estimated Forward Risk

Individualized Feature Importance

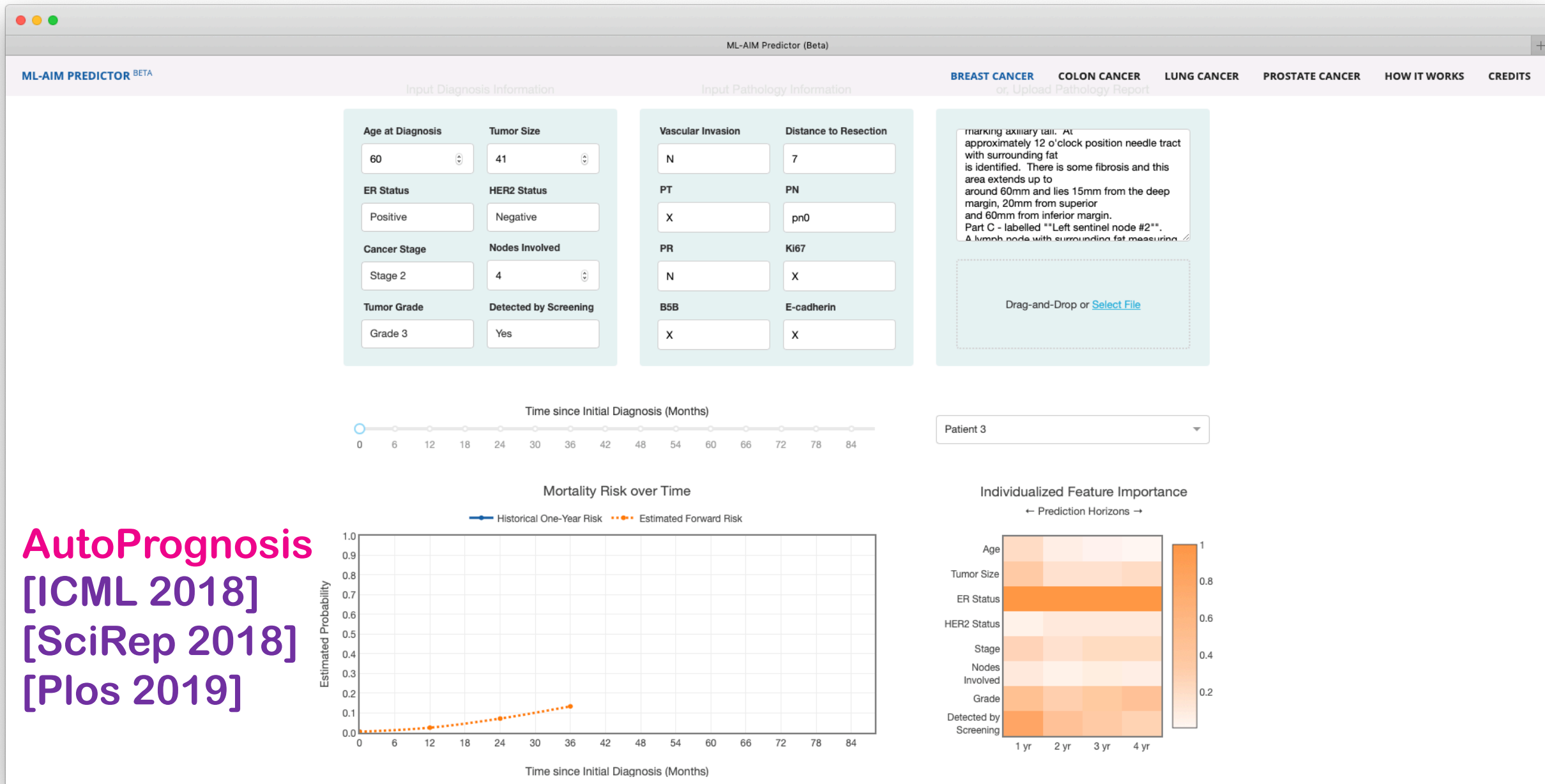
Prediction Horizons

Age

Tumor Size

Upload a pathology report

11

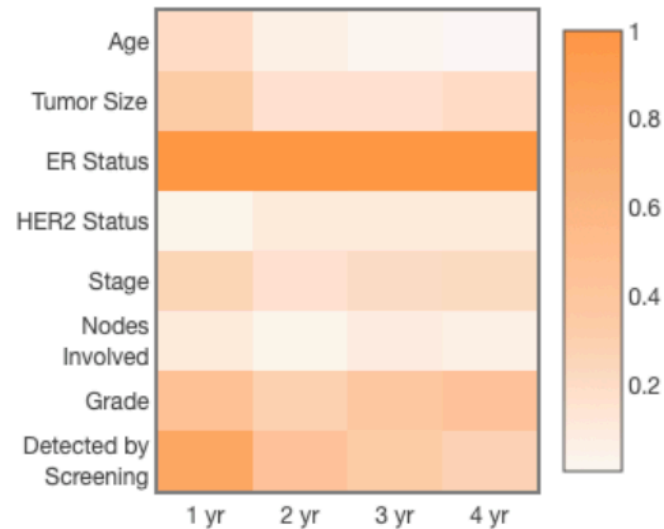


AutoPrognosis  
[ICML 2018]  
[SciRep 2018]  
[Plos 2019]



## Individualized Feature Importance

← Prediction Horizons →



INVASE [ICLR 2019]

Age at Diagnosis

60

Tumor Size

41

ER Status

Positive

HER2 Status

Negative

Cancer Stage

Stage 2

Nodes Involved

4

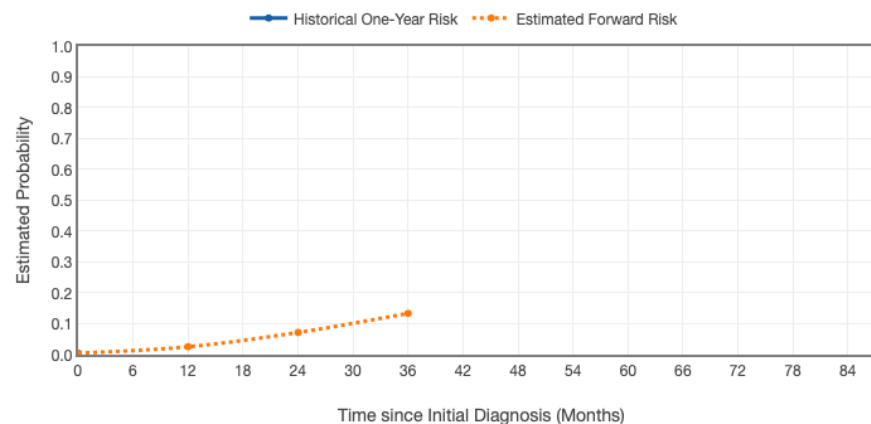
Tumor Grade

Grade 3

Detected by Screening

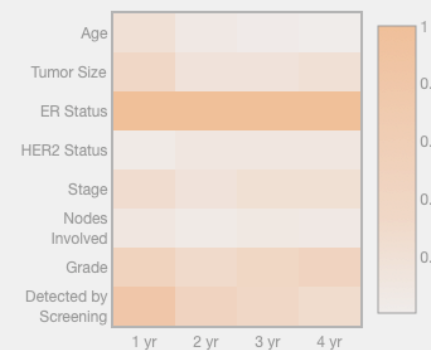
Yes

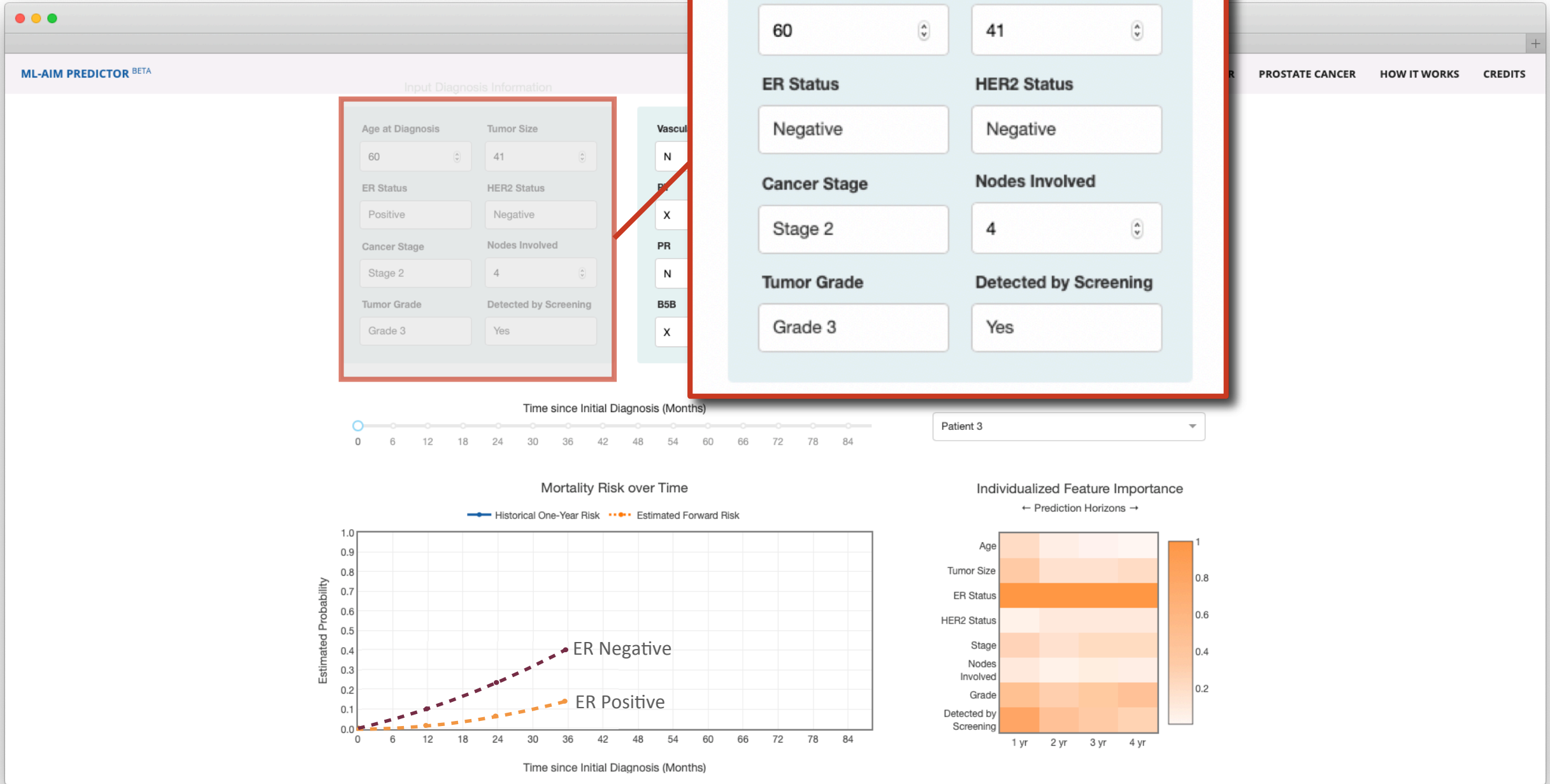
## Mortality Risk over Time

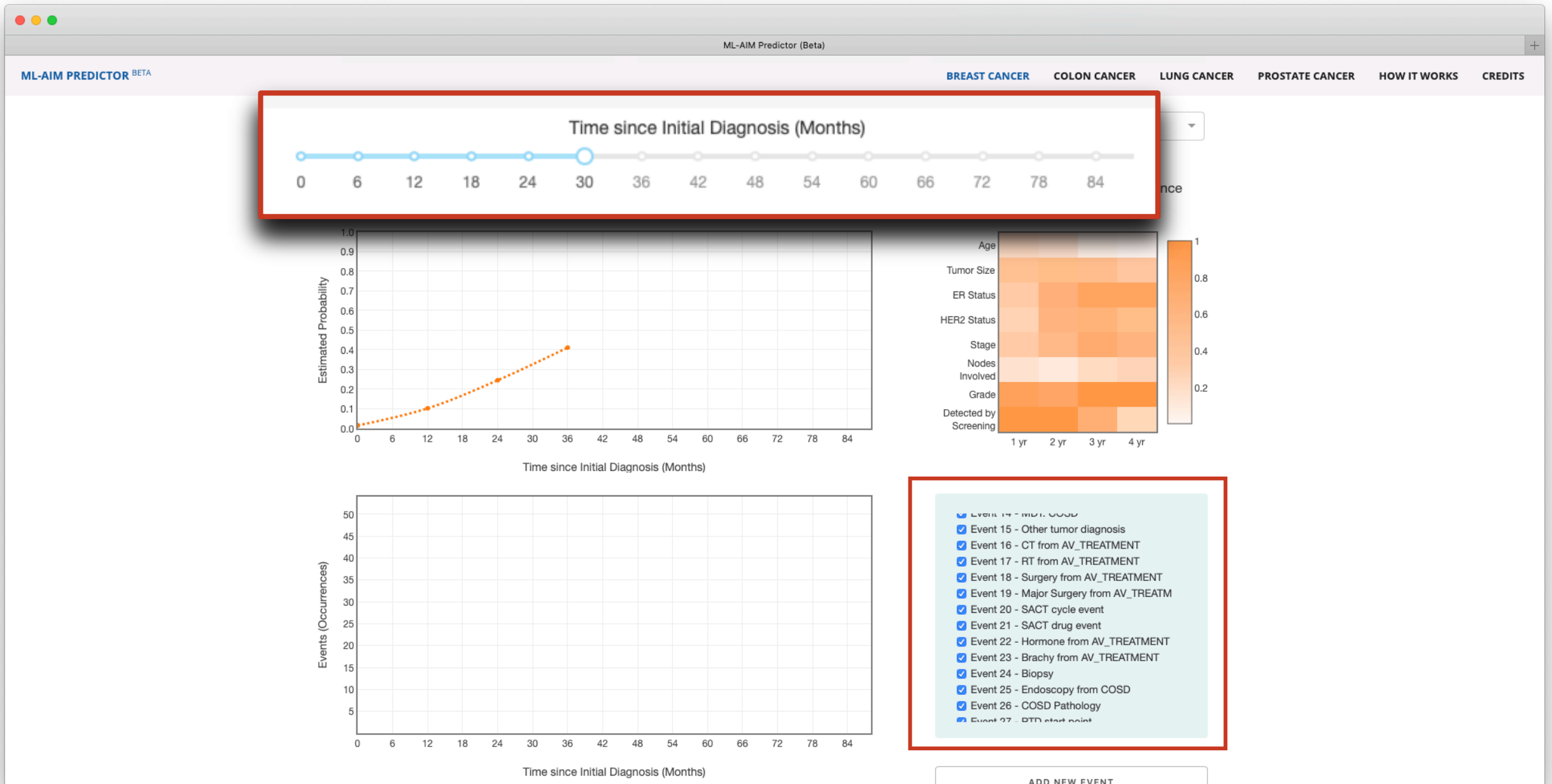


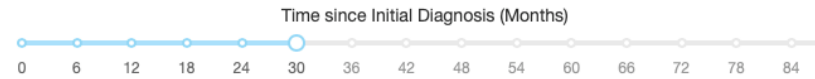
## Individualized Feature Importance

← Prediction Horizons →



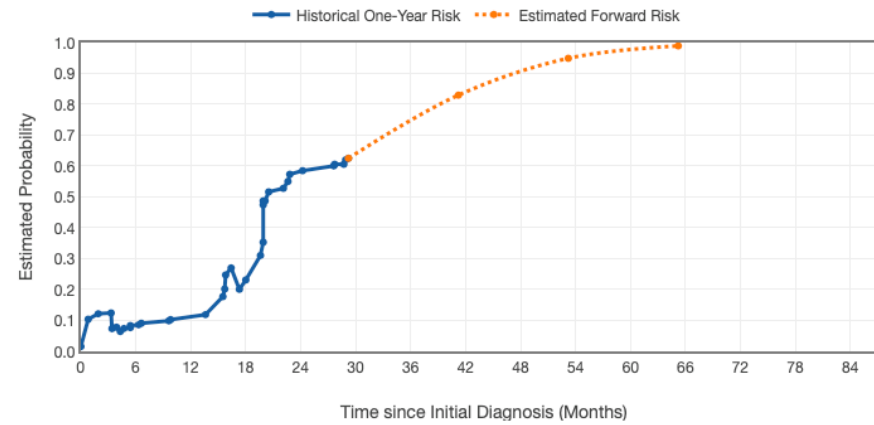






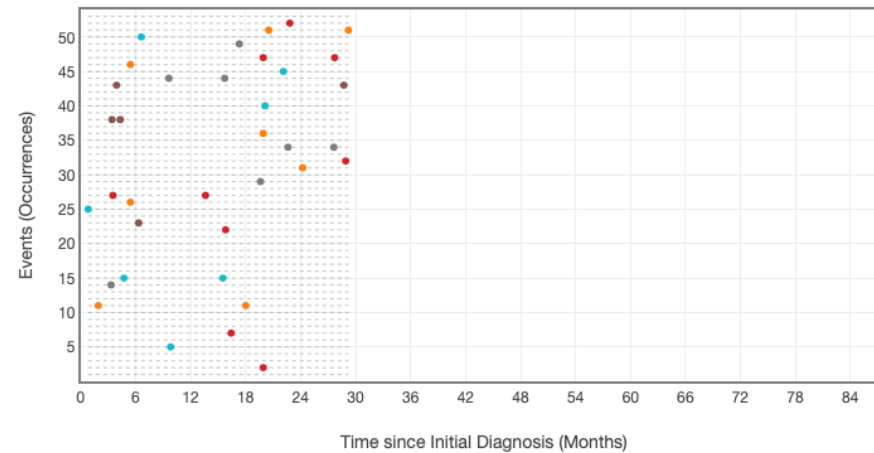
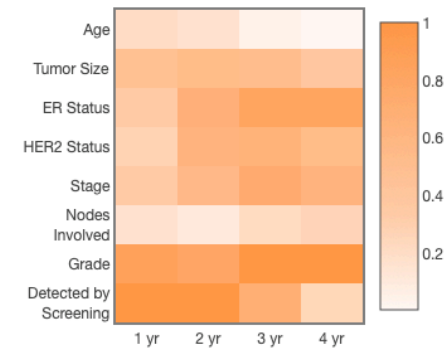
Patient 3

Mortality Risk over Time



Individualized Feature Importance

← Prediction Horizons →

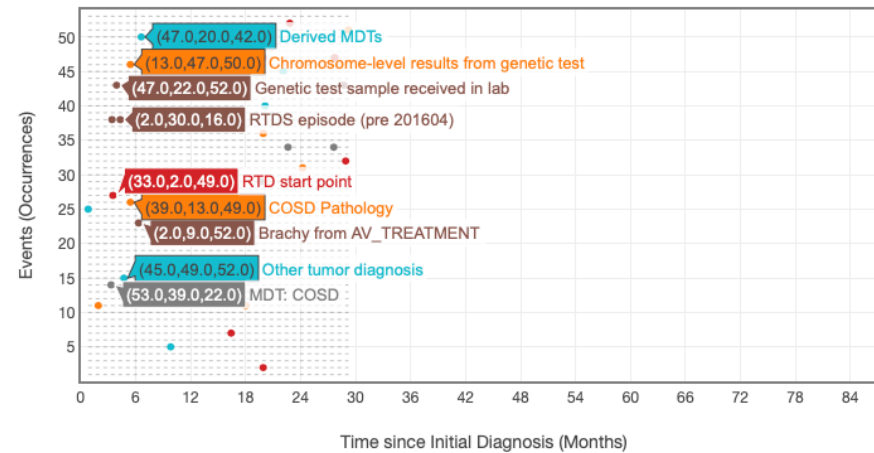
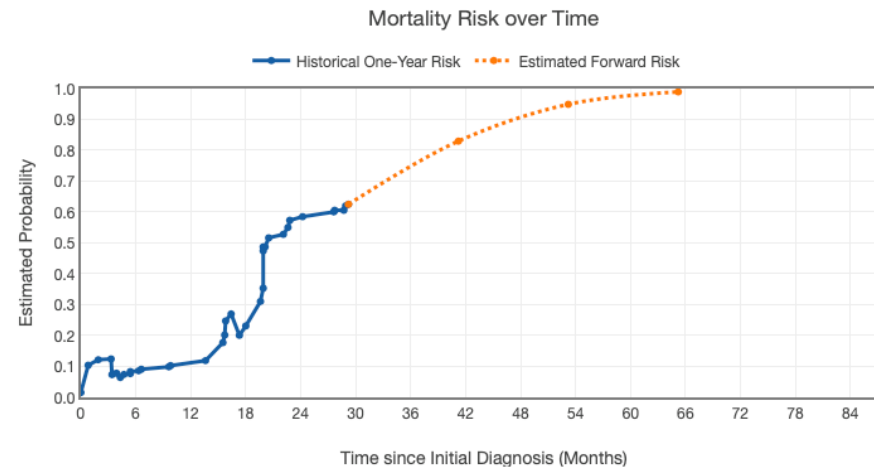
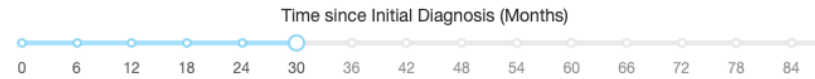


- ✓ Event 14 - MDT COSD
- ✓ Event 15 - Other tumor diagnosis
- ✓ Event 16 - CT from AV\_TREATMENT
- ✓ Event 17 - RT from AV\_TREATMENT
- ✓ Event 18 - Surgery from AV\_TREATMENT
- ✓ Event 19 - Major Surgery from AV\_TREATM
- ✓ Event 20 - SACT cycle event
- ✓ Event 21 - SACT drug event
- ✓ Event 22 - Hormone from AV\_TREATMENT
- ✓ Event 23 - Brachy from AV\_TREATMENT
- ✓ Event 24 - Biopsy
- ✓ Event 25 - Endoscopy from COSD
- ✓ Event 26 - COSD Pathology
- ✓ Event 27 - BTD start point

ADD NEW EVENT

PASS

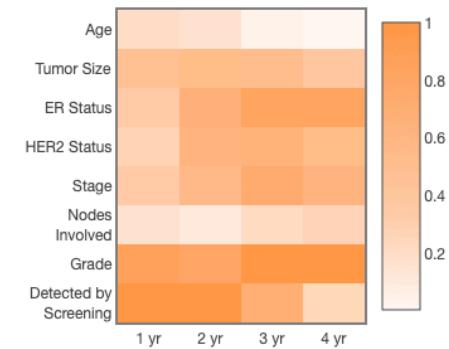




Patient 3

## Individualized Feature Importance

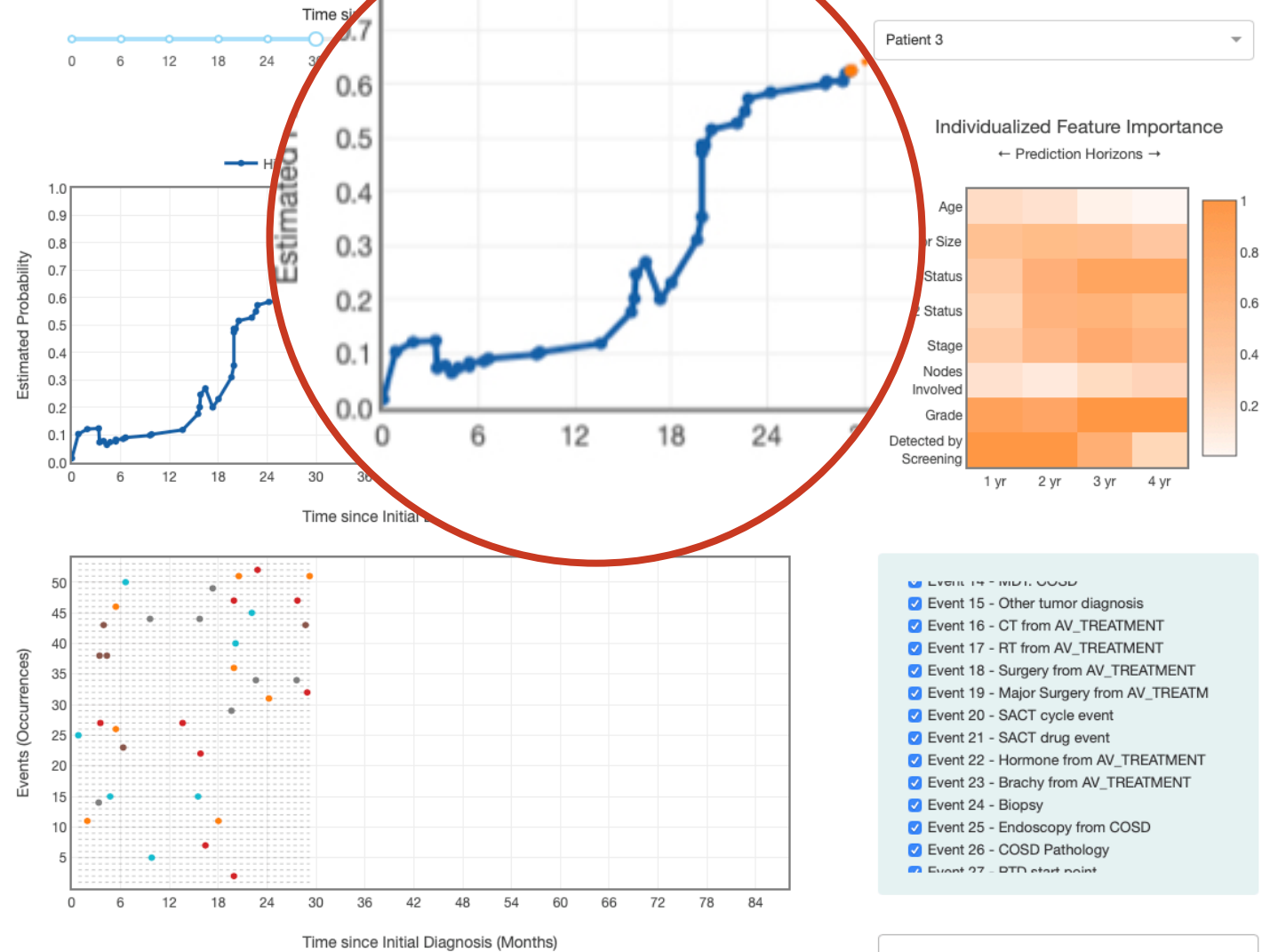
← Prediction Horizons →

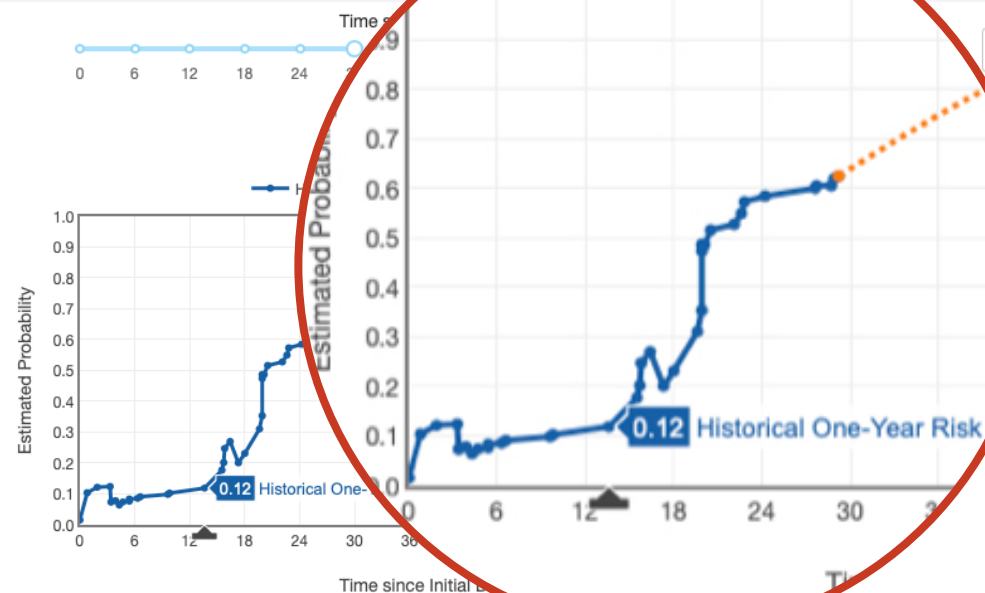


- ✓ Event 14 - MDT: COSD
- ✓ Event 15 - Other tumor diagnosis
- ✓ Event 16 - CT from AV\_TREATMENT
- ✓ Event 17 - RT from AV\_TREATMENT
- ✓ Event 18 - Surgery from AV\_TREATMENT
- ✓ Event 19 - Major Surgery from AV\_TREATM
- ✓ Event 20 - SACT cycle event
- ✓ Event 21 - SACT drug event
- ✓ Event 22 - Hormone from AV\_TREATMENT
- ✓ Event 23 - Brachy from AV\_TREATMENT
- ✓ Event 24 - Biopsy
- ✓ Event 25 - Endoscopy from COSD
- ✓ Event 26 - COSD Pathology
- ✓ Event 27 - RTD start point

ADD NEW EVENT

Patient 3

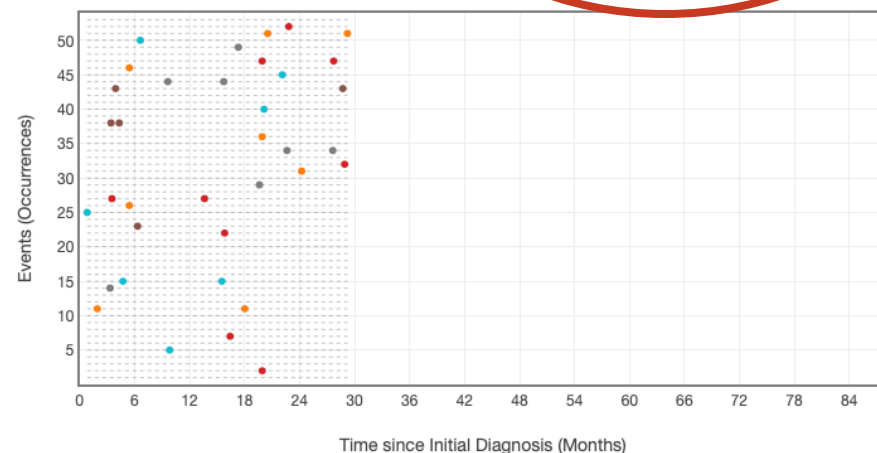
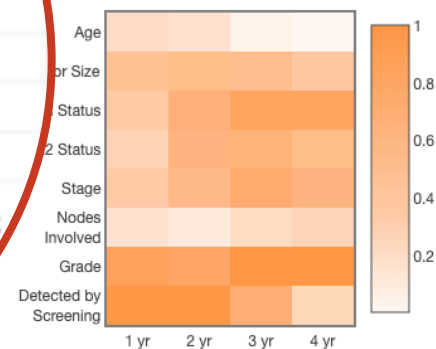




Patient 3

## Individualized Feature Importance

← Prediction Horizons →

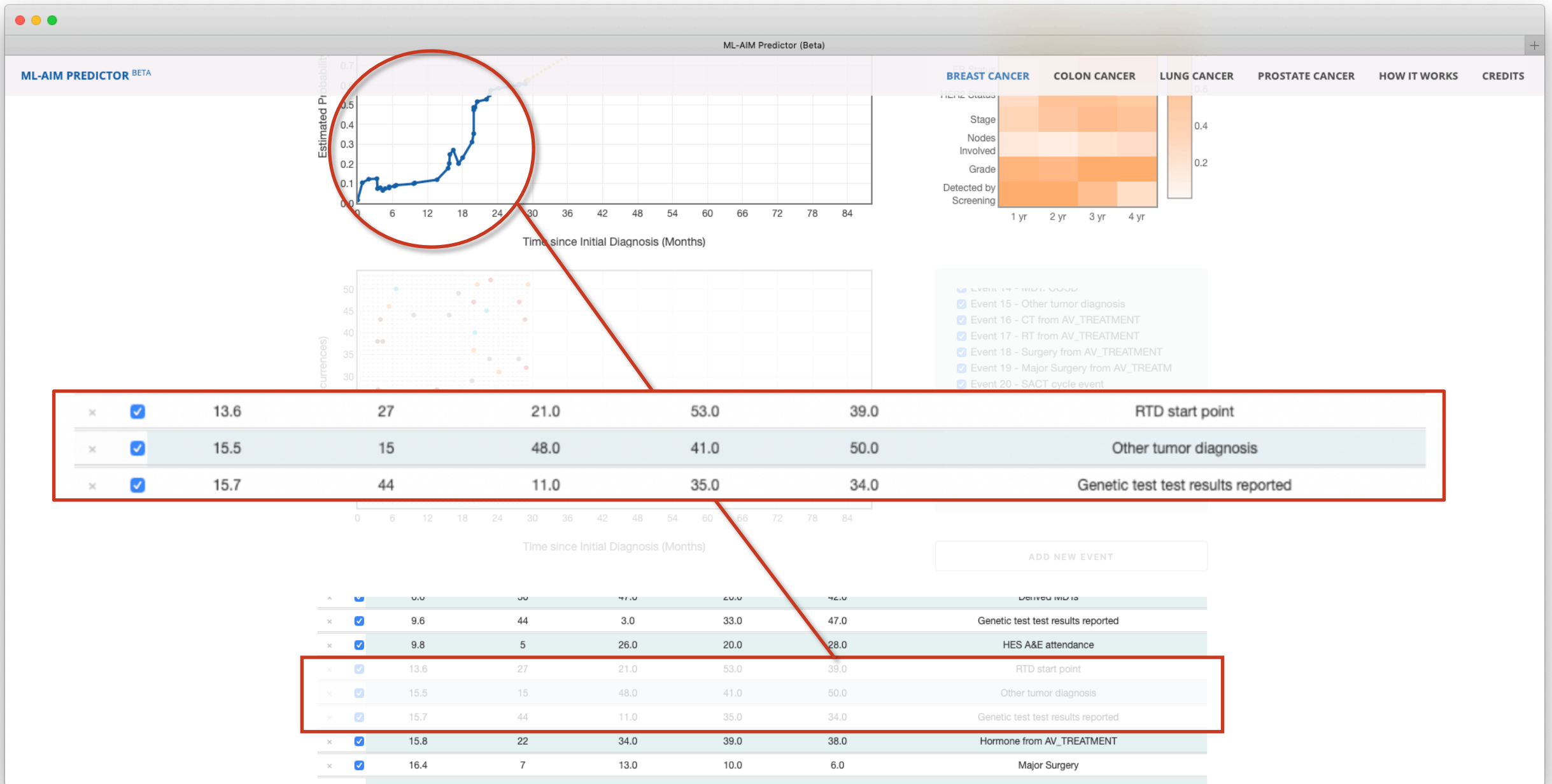


- ✓ Event 14 - IMRT, COSD
- ✓ Event 15 - Other tumor diagnosis
- ✓ Event 16 - CT from AV\_TREATMENT
- ✓ Event 17 - RT from AV\_TREATMENT
- ✓ Event 18 - Surgery from AV\_TREATMENT
- ✓ Event 19 - Major Surgery from AV\_TREATM
- ✓ Event 20 - SACT cycle event
- ✓ Event 21 - SACT drug event
- ✓ Event 22 - Hormone from AV\_TREATMENT
- ✓ Event 23 - Brachy from AV\_TREATMENT
- ✓ Event 24 - Biopsy
- ✓ Event 25 - Endoscopy from COSD
- ✓ Event 26 - COSD Pathology
- ✓ Event 27 - DTD start point

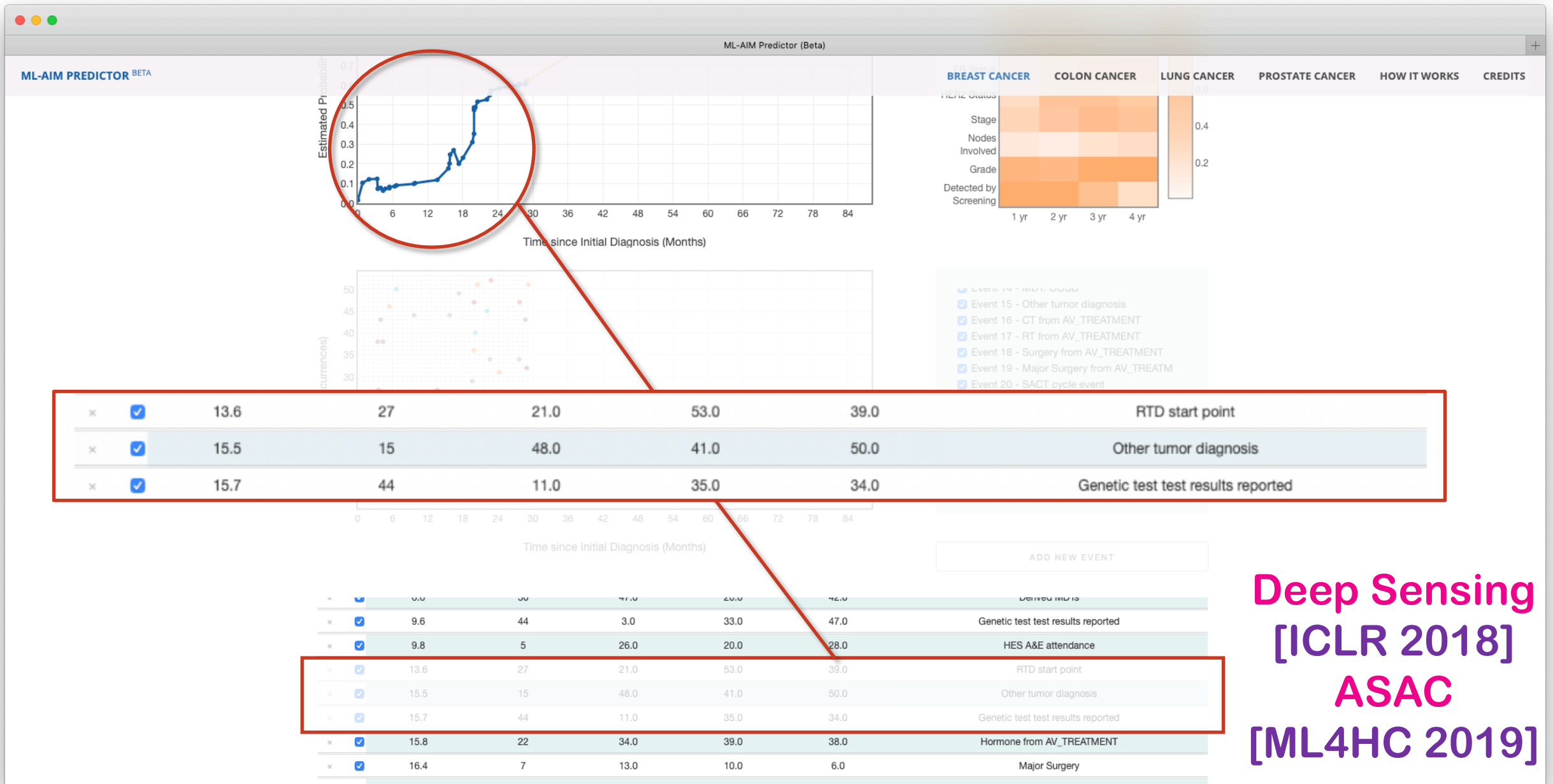
ADD NEW EVENT











Deep Sensing  
[ICLR 2018]  
ASAC  
[ML4HC 2019]

ML-AIM PREDICTOR BETA

ML-AIM Predictor (Beta)

BREAST CANCER

COLON CANCER

LUNG CANCER

PROSTATE CANCER

HOW IT WORKS

CREDITS

<input type="checkbox"/>	14.7	31	42.0	25.0	19.0	Genetic test sample analysis requested	
<input type="checkbox"/>	18.1	42	19.0	23.0	7.0		
<input checked="" type="checkbox"/>	18.6	42	1.0	23.0	17.0		
<input checked="" type="checkbox"/>	18.7	46	7.0	26.0	51.0		Chromosome-level results from genetic test
<input checked="" type="checkbox"/>	20.0	18	29.0	23.0	39.0		Surgery from AV_TREATMENT
<input checked="" type="checkbox"/>	21.0	45	29.0	40.0	35.0		Gene-level results from genetic test
<input checked="" type="checkbox"/>	21.1	33	14.0	11.0	24.0		Path sample taken

Risk of Recurrence vs. Treatment Options

Treatment Option	One-Year Risk (Population-based)	One-Year Risk (Individualized)	Treatment Propensity Score
No Treatment	48%	35%	35%
Radiotherapy	31%	21%	47%
Chemotherapy	26%	6%	13%
Chemo + Radiotherapy	21%	13%	31%

Top 3 Similar Patients

Patient ID	Age	Tumor Size	ER Status	HER2 Status	Stage 1	Stage 2	Stage 3	Stage 4	Nodes Involved	Grade 1	Grade 2	Grade 3	Detected by Screening
1	48	19	1	1	0	1	0	0	4	1	0	0	0
32	53	17	1	1	0	1	0	0	4	0	1	0	0
27	45	25	0	1	0	1	0	0	3	0	1	0	0

ML-AIM PREDICTOR BETA

ML-AIM Predictor (Beta)

BREAST CANCER

COLON CANCER

LUNG CANCER

PROSTATE CANCER

HOW IT WORKS

CREDITS

<input type="checkbox"/>	14.7	31	42.0	25.0	19.0	Genetic test sample analysis requested	
<input type="checkbox"/>	18.1	42	19.0	23.0	7.0		
<input checked="" type="checkbox"/>	18.6	42	1.0	23.0	17.0		
<input checked="" type="checkbox"/>	18.7	46	7.0	26.0	51.0		Chromosome-level results from genetic test
<input checked="" type="checkbox"/>	20.0	18	29.0	23.0	39.0		Surgery from AV_TREATMENT
<input checked="" type="checkbox"/>	21.0	45	29.0	40.0	35.0		Gene-level results from genetic test
<input checked="" type="checkbox"/>	21.1	33	14.0	11.0	24.0		Path sample taken

Risk of Recurrence vs. Treatment Options

Treatment Option	One-Year Risk (Population-based)	One-Year Risk (Individualized)	Treatment Propensity Score
No Treatment	49%	35%	35%
Radiotherapy	31%	21%	47%
Chemotherapy	26%	6%	13%
Chemo + Radiotherapy	21%	13%	31%

Top 3 Similar Patients

Patient ID	Age	Tumor Size	ER Status	HER2 Status	Stage 1	Stage 2	Stage 3	Stage 4	Nodes Involved	Grade 1	Grade 2	Grade 3	Detected by Screening
1	48	19	1	1	0	1	0	0	4	1	0	0	0
32	53	17	1	1	0	1	0	0	4	0	1	0	0
27	45	25	0	1	0	1	0	0	3	0	1	0	0



ML-AIM PREDICTOR BETA

ML-AIM Predictor (Beta)

BREAST CANCER

COLON CANCER

LUNG CANCER

PROSTATE CANCER

HOW IT WORKS

CREDITS

<input type="checkbox"/>	14.7	31	42.0	25.0	19.0	Genetic test sample analysis requested	
<input type="checkbox"/>	18.1	42	19.0	23.0	7.0		
<input checked="" type="checkbox"/>	18.6	42	1.0	23.0	17.0		
<input checked="" type="checkbox"/>	18.7	46	7.0	26.0	51.0		Chromosome-level results from genetic test
<input checked="" type="checkbox"/>	20.0	18	29.0	23.0	39.0		Surgery from AV_TREATMENT
<input checked="" type="checkbox"/>	21.0	45	29.0	40.0	35.0		Gene-level results from genetic test
<input checked="" type="checkbox"/>	21.1	33	14.0	11.0	24.0	Path sample taken	

Risk of Recurrence vs. Treatment Options

Treatment Option	One-Year Risk (Population-based)	One-Year Risk (Individualized)	Treatment Propensity Score
No Treatment	49%	35%	35%
Radiotherapy	31%	21%	47%
Chemotherapy	26%	6%	13%
Chemo + Radiotherapy	21%	13%	31%

Top 3 Similar Patients

Patient ID	Age	Tumor Size	ER Status	HER2 Status	Stage 1	Stage 2	Stage 3	Stage 4	Nodes Involved	Grade 1	Grade 2	Grade 3	Detected by Screening
1	48	19	1	1	0	1	0	0	4	1	0	0	0
32	53	17	1	1	0	1	0	0	4	0	1	0	0
27	45	25	0	1	0	1	0	0	3	0	1	0	0



NSGP [NIPS 2017]  
GANITE [ICLR 2018]  
CMGP [ICML 2018]  
Counterfactual  
Recurrent Nets  
[NIPS 2018]

# Personalized medicine needs to go beyond risk predictions- Individualized Treatment Recommendations

Bob



Diagnosed with  
Disease X

Which treatment is best for Bob?

- **Problem:**  
Estimate the effect of a **treatment/intervention** on an **individual**

# RCTs do **not** support Personalized Medicine

**Randomized Control Trials:  
Average Treatment Effects**

**Population-level**



**Non-representative patients**

**Small sample sizes**

**Time consuming**

**Enormous costs**

**Adaptive Clinical Trials**

**[Atan, Zame, vdS, AISTATS 2019]**

# Delivering Personalized (Individualized) Treatments

**Randomized Control Trials:  
Average Treatment Effects**

**Population-level**



**Non-representative patients  
Small sample sizes  
Time consuming  
Enormous costs**

**Machine Learning:  
Individualized Treatment Effects**

**Patient-centric**



**Real-world observational data  
Scalable & adaptive implementation  
Fast deployment  
Cost-effective**

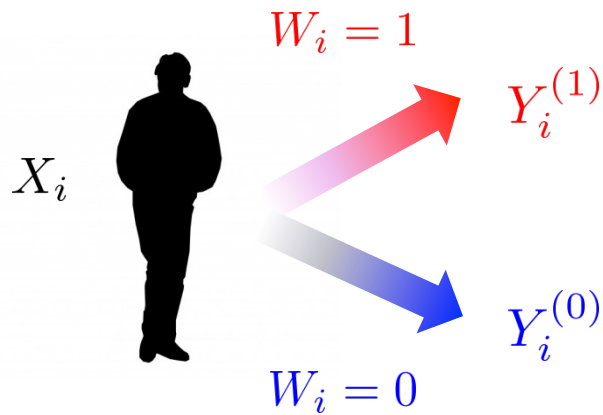
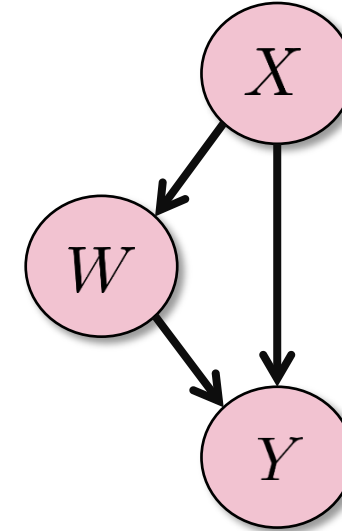
[Atan, vdS, 2015, 2018]  
[Alaa, vdS, 2017, 2018, 2019]  
[Yoon, Jordon, vdS, 2017]  
[Lim, Alaa, vdS, 2018]  
[Bica, Alaa, vdS, 2019]



# Potential outcomes framework [Neyman, 1923]

Observational data  $(X_i, W_i, Y_i)$

- Each patient  $i$  has **features**  $X_i \in \mathcal{X} \subset \mathbb{R}^d$
- Two **potential outcomes**  $Y_i^{(1)}, Y_i^{(0)} \in \mathbb{R}$
- Treatment **assignment**  $W_i \in \{0, 1\}$



Factual outcomes

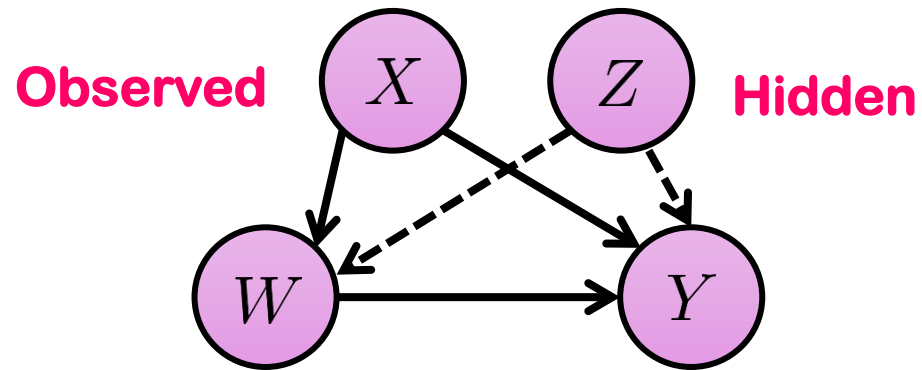
$$Y_i = W_i Y_i^{(1)} + (1 - W_i) Y_i^{(0)}$$

Causal effects

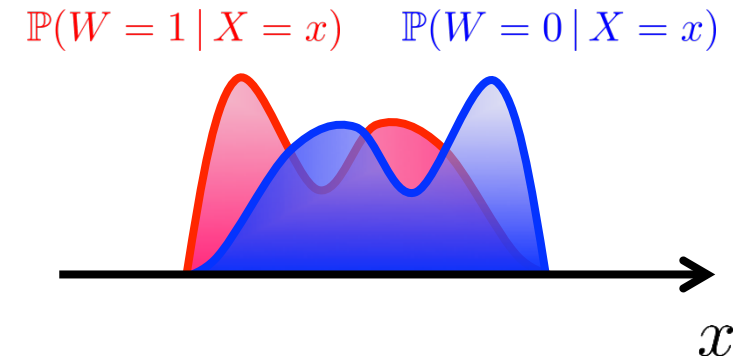
$$T(x) = \mathbb{E} \left[ Y_i^{(1)} - Y_i^{(0)} \mid X_i = x \right]$$

# Assumptions

No unmeasured confounders (Ignorability)

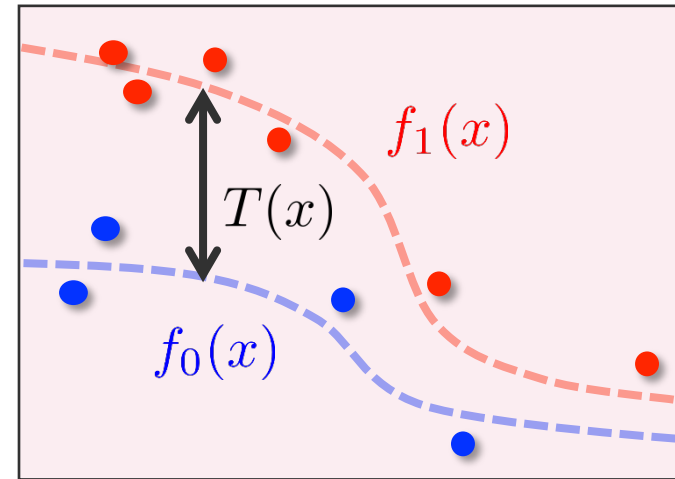
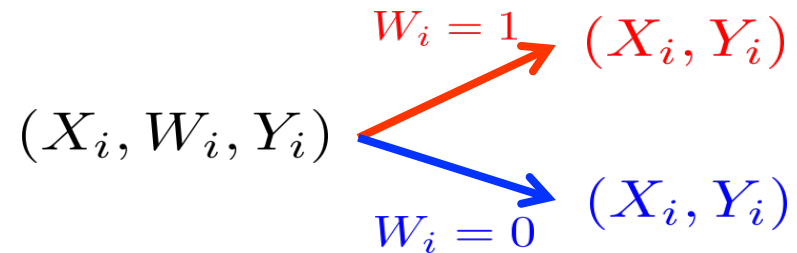


Common support



# Estimating individualized treatment effects

- **Observational data**



- **Treatment response surfaces**

$$f_1(x) = \mathbb{E}[Y^{(1)} \mid X = x]$$

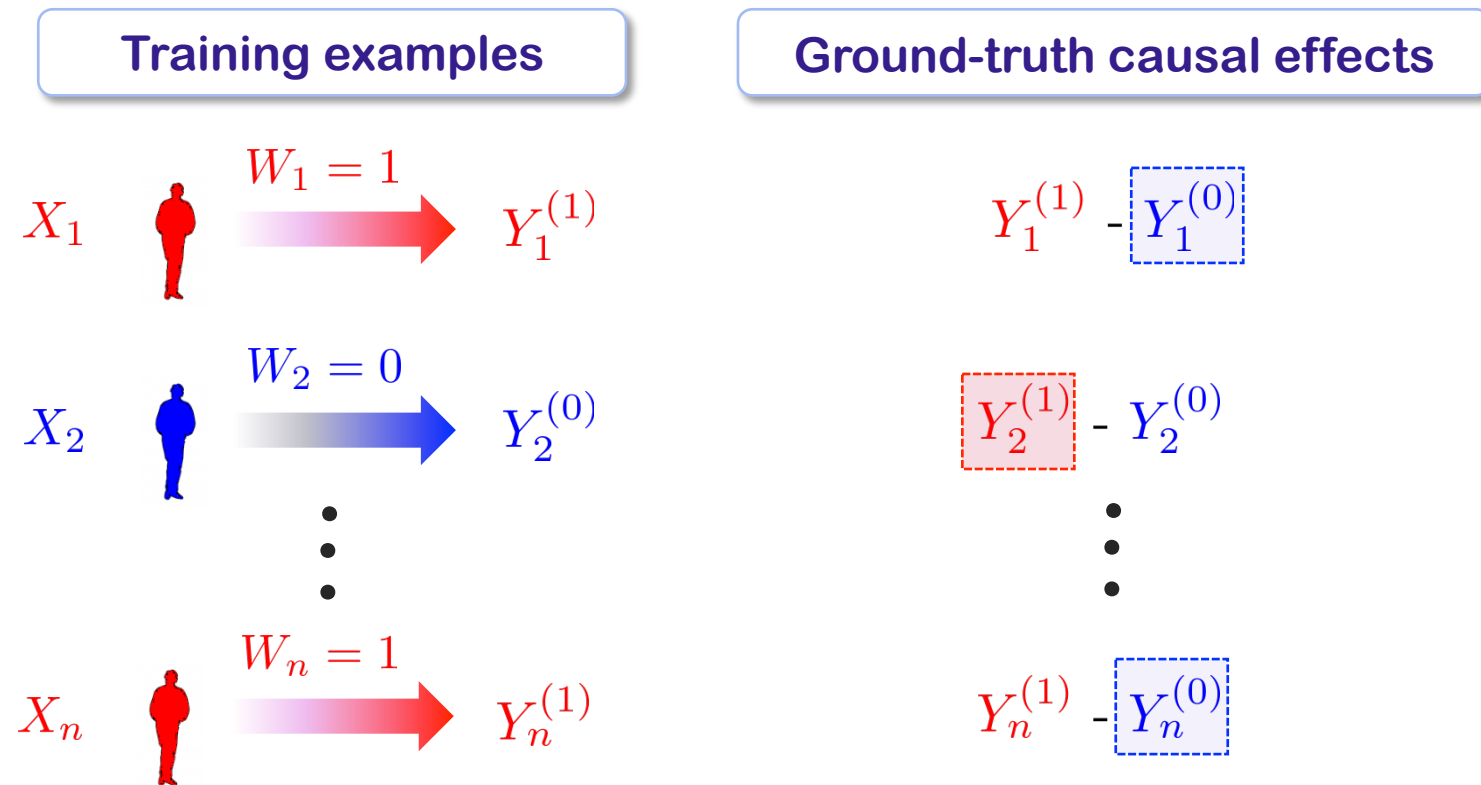
$$f_0(x) = \mathbb{E}[Y^{(0)} \mid X = x]$$

- **Estimate** causal effects: individualized treatment effects

$$T(x) = f_1(x) - f_0(x)$$

# Beyond supervised learning...

- Fundamental challenge of causal inference:  
we never observe **counterfactual** outcomes

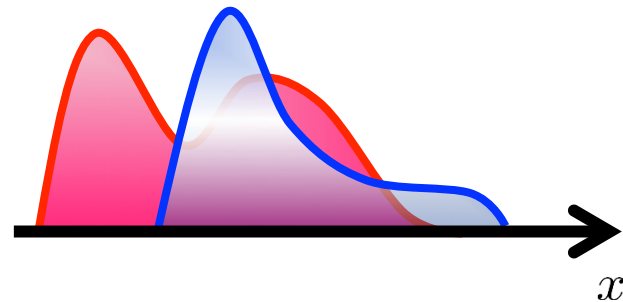


# Causal modeling $\neq$ predictive modeling

1- Need to model interventions  $(X_i, W_i, Y_i)$

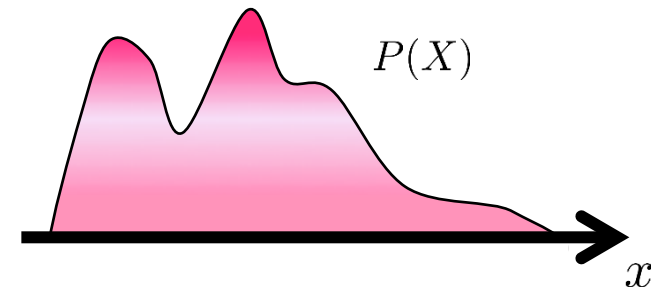
2- **Selection bias  $\rightarrow$  covariate shift:**  
training distribution  $\neq$  testing distribution

$$P(X | W = 1) \quad P(X | W = 0)$$



Training distribution

$\neq$



Testing distribution



# Many recent works on individualized treatment effects (ITEs)

- Bayesian Additive Regression Trees (BART) [Chipman et. al, 2010], [J. Hill, 2011]
- Causal Forests [Wager & Athey, 2016]
- Nearest Neighbor Matching (kNN) [Crump et al., 2008]
- Balancing Neural Networks [Johansson, Shalit and Sontag, 2016]
- Causal MARS [Powers, Qian, Jung, Schuler, N. Shah, T. Hastie, R. Tibshirani, 2017 ]
- Targeted Maximum Likelihood Estimator (TMLE) [Gruber & van der Laan, 2011]
- Counterfactual regression [Johansson, Shalit and Sontag, 2016]
- CMGP [Alaa & van der Schaar, 2017]
- GANITE [Yoon, Jordon & van der Schaar, 2018]

No theory, ad-hoc models

# A first theory for causal inference - individualized treatment effects

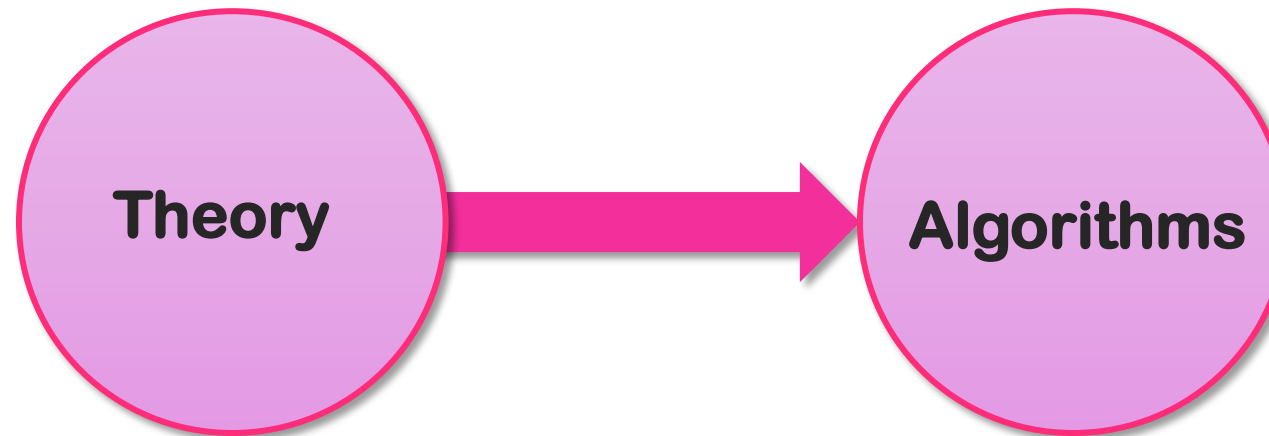
[Alaa, vdS, JSTSP 2017][ICML 2018]

**What is possible?**

(Fundamental limits)

**How can it be achieved?**

(Practical implementation)



# Bayesian nonparametric ITE estimation

- **True ITE model**

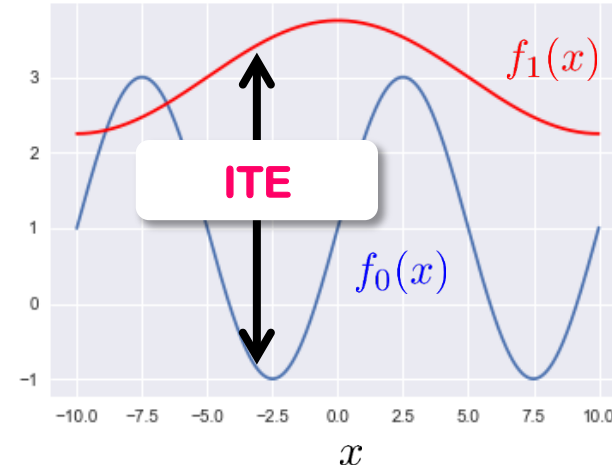
$$T(x) = f_1(x) - f_0(x)$$

- **ITE estimation**

- Prior over response functions:  $f_0, f_1 \sim \Pi$

- Point estimator  $\hat{T}(\cdot)$  induced by Bayesian posterior  $d\Pi_n(T \mid \mathcal{D})$

- Precision of estimating heterogeneous effects  $\text{PEHE}(\hat{T}) \triangleq \mathbb{E} \|\hat{T} - T\|_{L^2(\mathbb{P})}^2$



# Minimax Rate for ITE Estimation

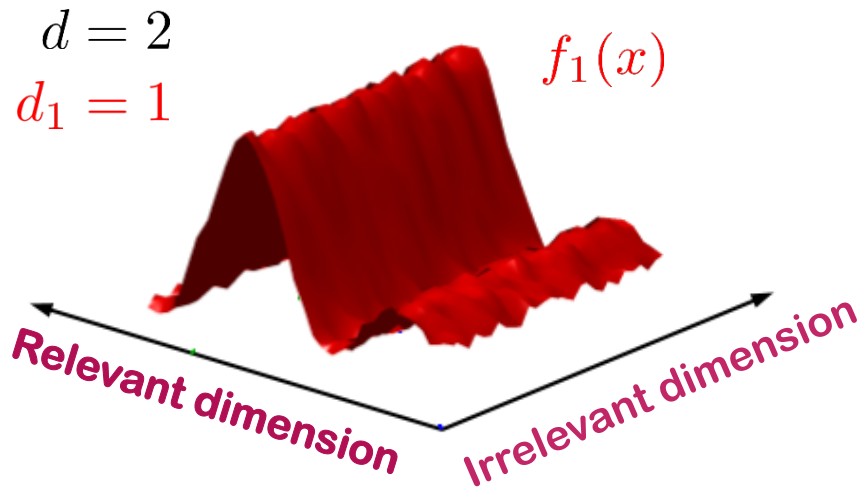
- Depends on the “complexity” of  $f_0(x)$  and  $f_1(x)$  ...

Sparsity  $d$

$f_0(x) \rightarrow d_0$  relevant dimensions

$f_1(x) \rightarrow d_1$  relevant dimensions

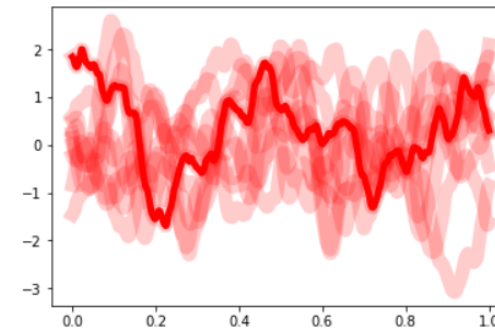
$$x \in [0, 1]^d, d_0, d_1 \leq d$$



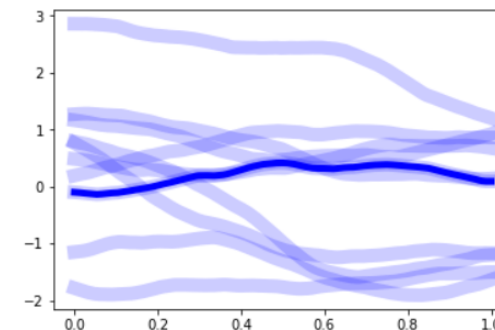
Smoothness  $\alpha$

$f_0(x) \rightarrow$  Hölder ball  $H^{\alpha_0}$

$f_1(x) \rightarrow$  Hölder ball  $H^{\alpha_1}$



$\alpha_1 \downarrow \downarrow$   
**Rough functions**



$\alpha_0 \uparrow \uparrow$   
**Smooth functions**

# Minimax Rate for ITE Estimation

## ● Theorem 1

The minimax rate for ITE estimation is given by:

$$\inf_{\hat{T}} \sup_{f_0, f_1} \text{PEHE}(\hat{T}) \asymp n^{-\left(1 + \frac{1}{2} \left( \frac{d_0}{\alpha_0} \vee \frac{d_1}{\alpha_1} \right)\right)^{-1}}$$



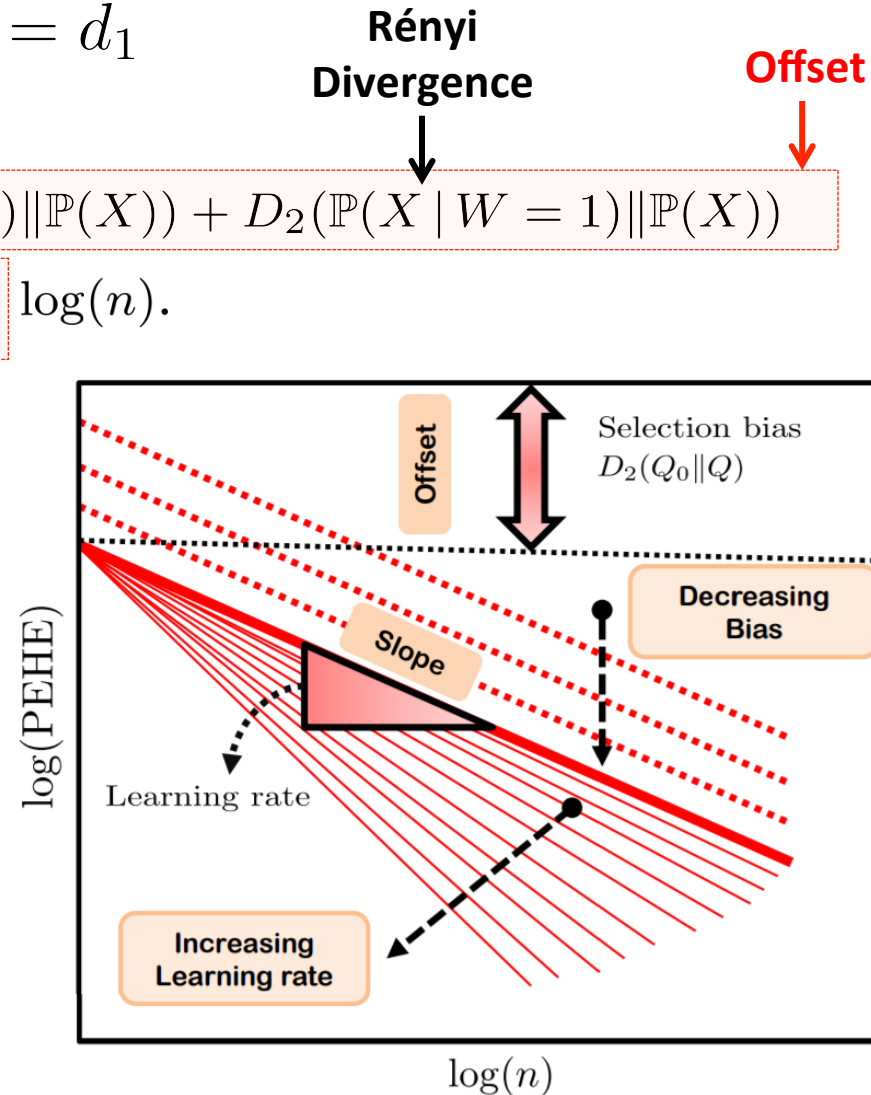
# Should we care about selection bias?

- Assume that  $\alpha_0 = \alpha_1$  and  $d_0 = d_1$

**Minimax-optimal estimator**

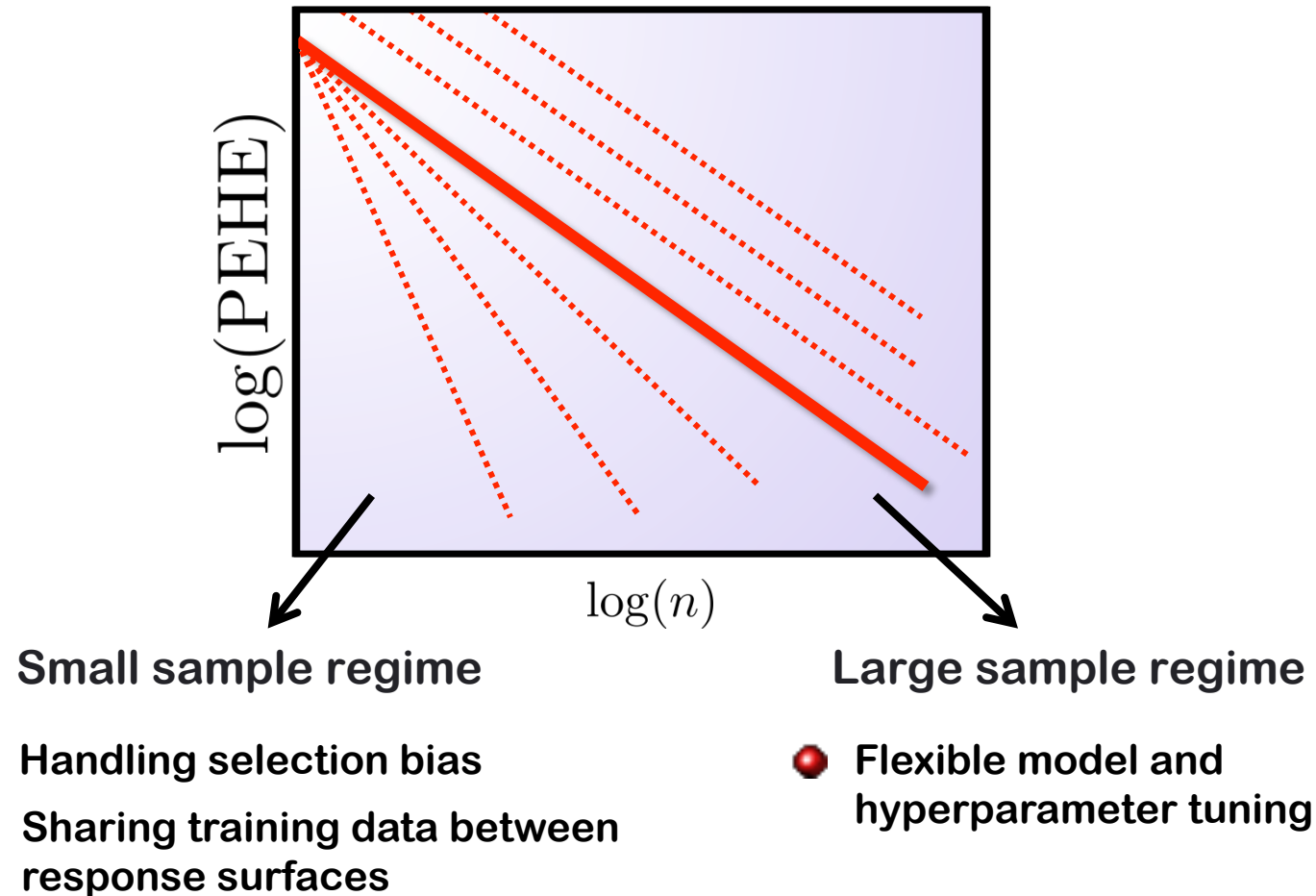
$$\log(\text{PEHE}(\hat{T})) \approx \boxed{D_2(\mathbb{P}(X | W = 0) \| \mathbb{P}(X)) + D_2(\mathbb{P}(X | W = 1) \| \mathbb{P}(X))} \\ + \log(C) - \boxed{\frac{2\alpha_0}{2\alpha_0 + d_0}} \log(n).$$

**Slope**



# Theory guides model design

- We want models that do well in both small and large sample regimes



# ITE Estimation using Multi-task Gaussian processes

[Alaa and vdS, NIPS 2017, ICML 2018]

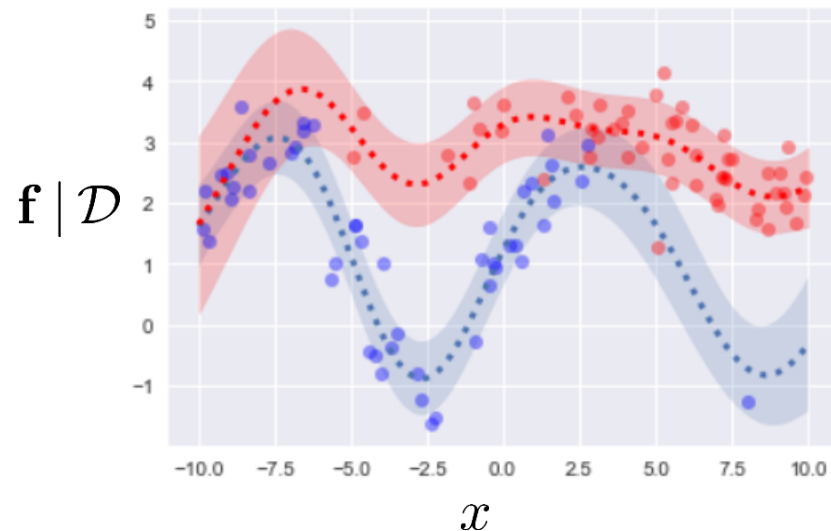
## ● Multi-task Gaussian Process [Bonilla et al., 2008].

$$f_0, f_1 \sim \mathcal{GP}(0, \mathbf{K}_{\beta_0, \beta_1}) \quad \text{Matern kernel = Prior over on vvRKHS } H^{\beta_0} \times H^{\beta_1}$$

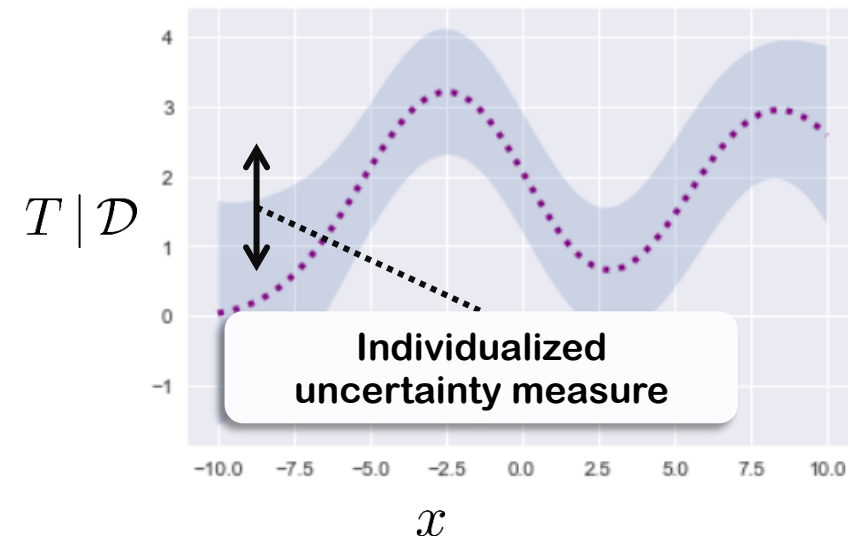
$$\mathbf{K}_{\theta}(x, x') = \mathbf{A}_0 k_{\beta_0}(x, x') + \mathbf{A}_1 k_{\beta_1}(x, x')$$

Shared representations!

Posterior potential outcomes distribution



Posterior ITE distribution

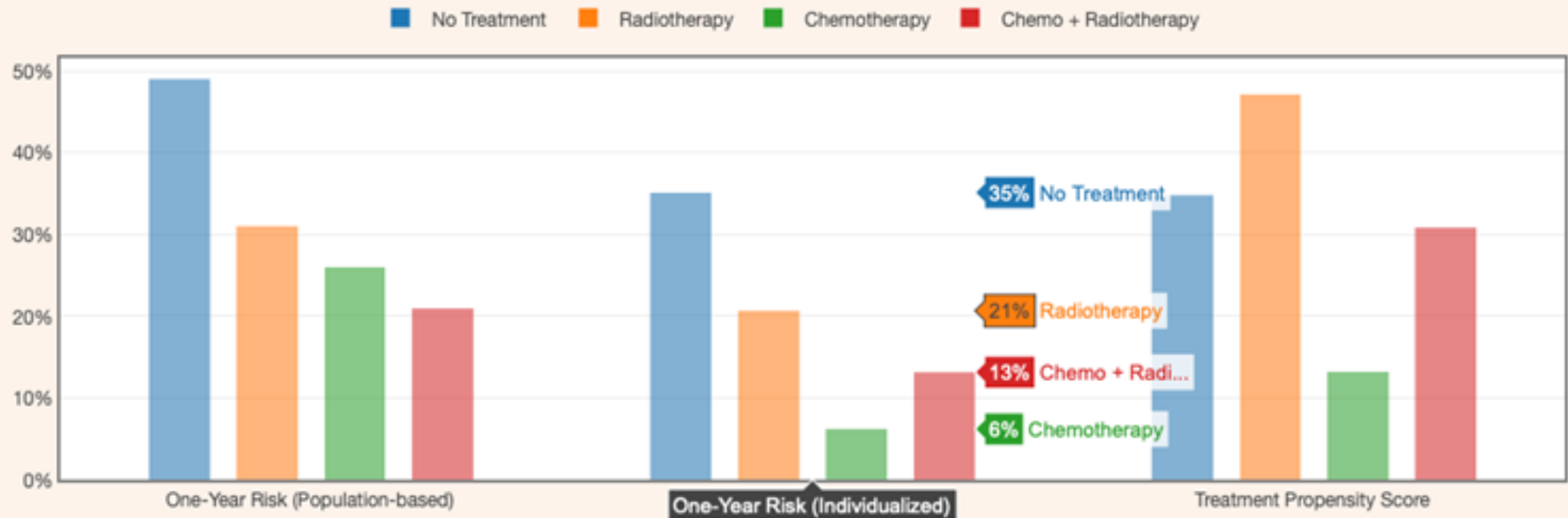


Automated Feature Relevance Determination !

# Multiple Treatments: GANITE [Yoon, Jordon, vdS, ICLR 2018]

## Estimation of Individualized Treatment Effects using Generative Adversarial Nets

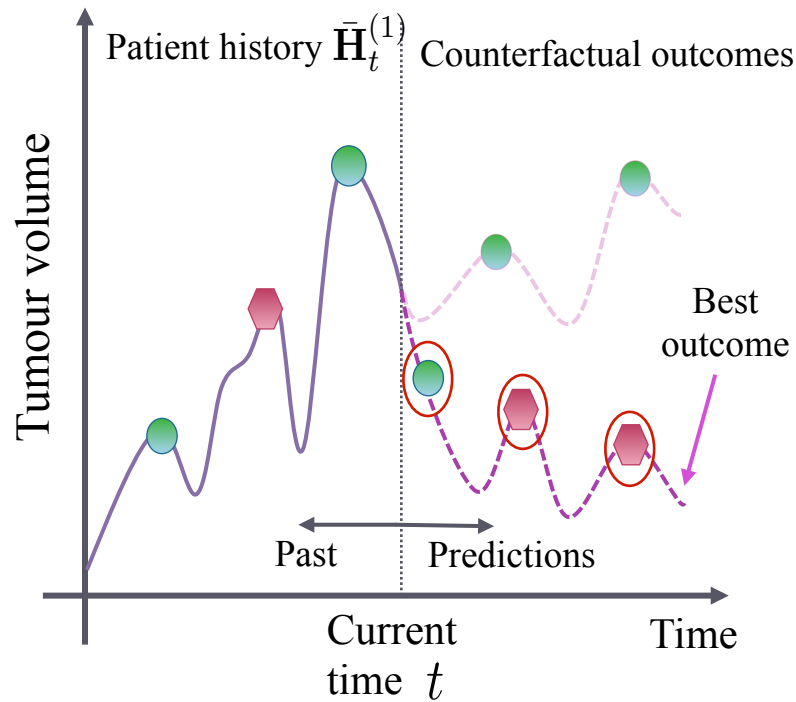
Risk of Recurrence vs. Treatment Options



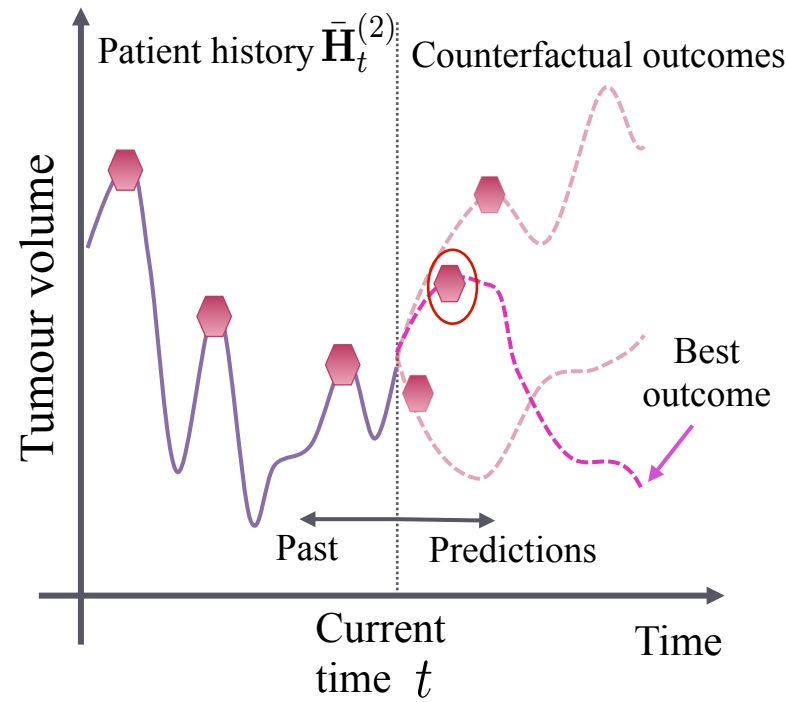
# Individualized Treatment Effects over Time

[Lim, Alaa, vdS, NeurIPS 2018][Bica, Alaa, vdS, 2019]

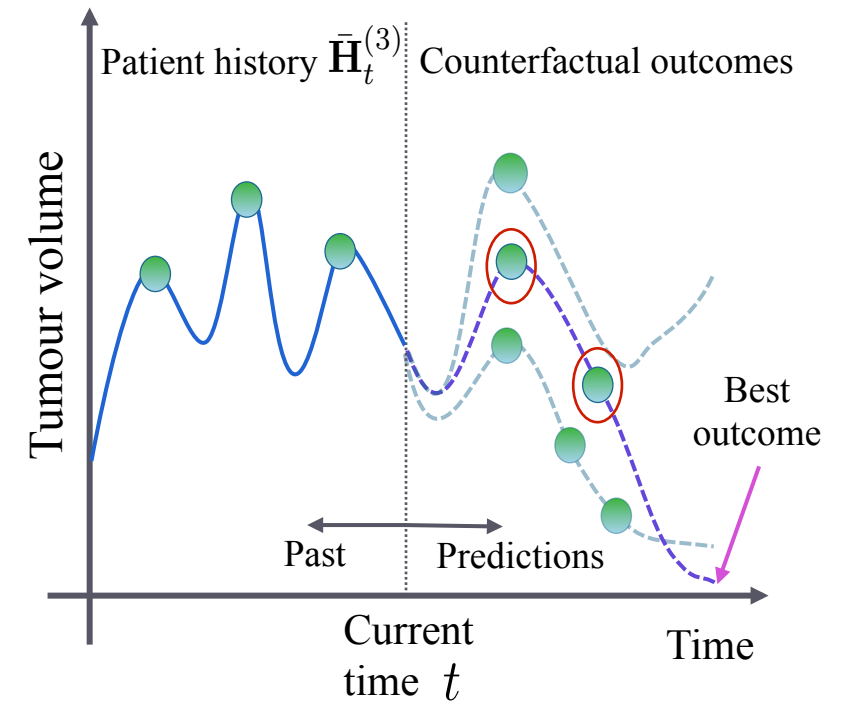
## When to treat? How to treat? When to stop?



(a) Decide treatment plan



(b) Decide optimal time of treatment



(c) Decide when to stop treatment

● Chemotherapy      ● Radiotherapy



**ML-AIM**

Machine Learning and Artificial Intelligence for Medicine

Research Laboratory led by Prof. Mihaela van der Schaar

Details about our algorithms:

<http://www.vanderschaar-lab.com>

Details about our software:

<http://www.vanderschaar-lab.com>

# MATHEMATICAL FRONTIERS

## Machine Learning in Medicine



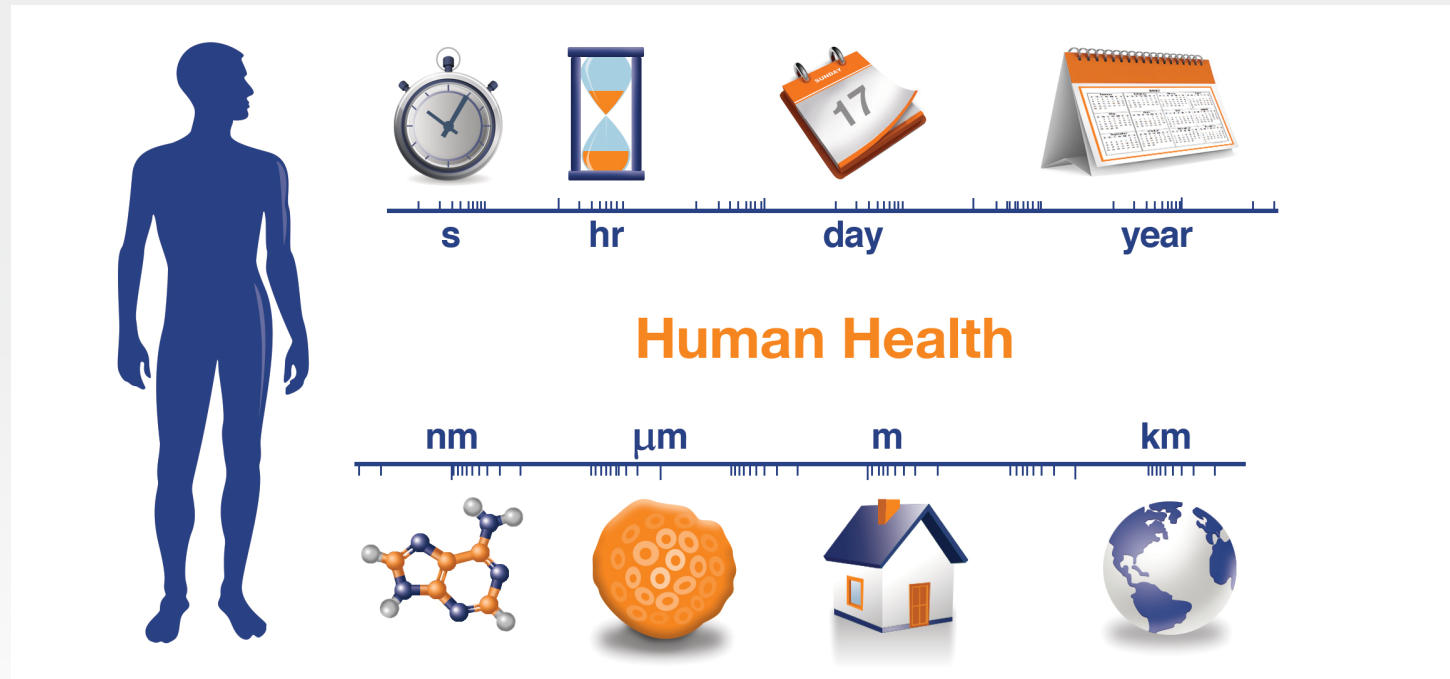
**Juan Gutierrez,  
University of Texas  
at San Antonio**

*Professor and Chair of Mathematics*

## **Machine Learning in Biomedical Sciences**

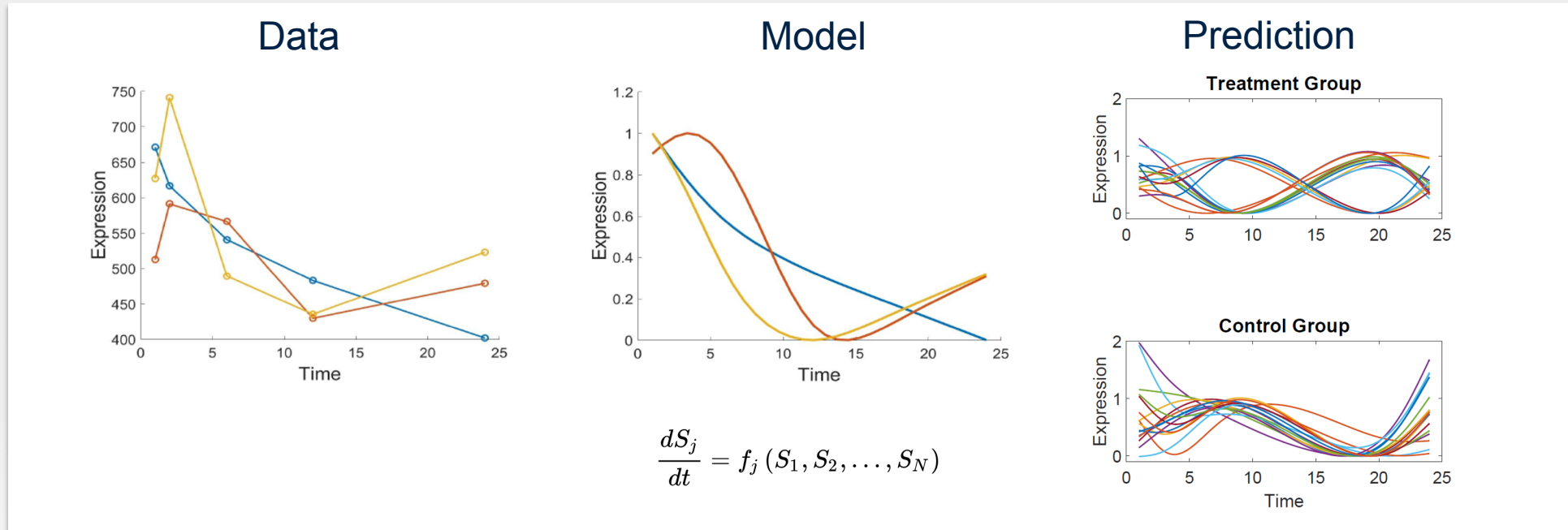


# Human Health Spans Multiple Temporal and Spatial Scales



The increased availability of data is changing how we approach this comprehensive understanding.

# Data → Model → Prediction

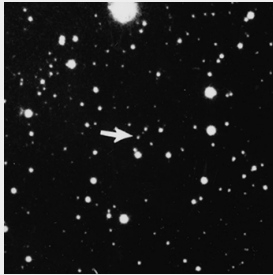


The canon in mathematical biology is to progress iteratively through data, models and predictions (not necessarily in that order).

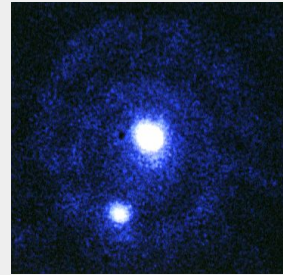
This paradigm does not always work.

# The questions have evolved in mathematical biology

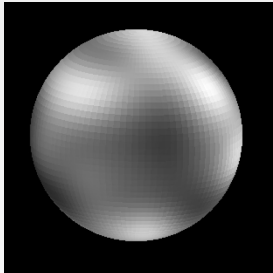
## Pluto: An analogy



18 Feb 1930  
4.7 billion miles



1994, HST/FOC

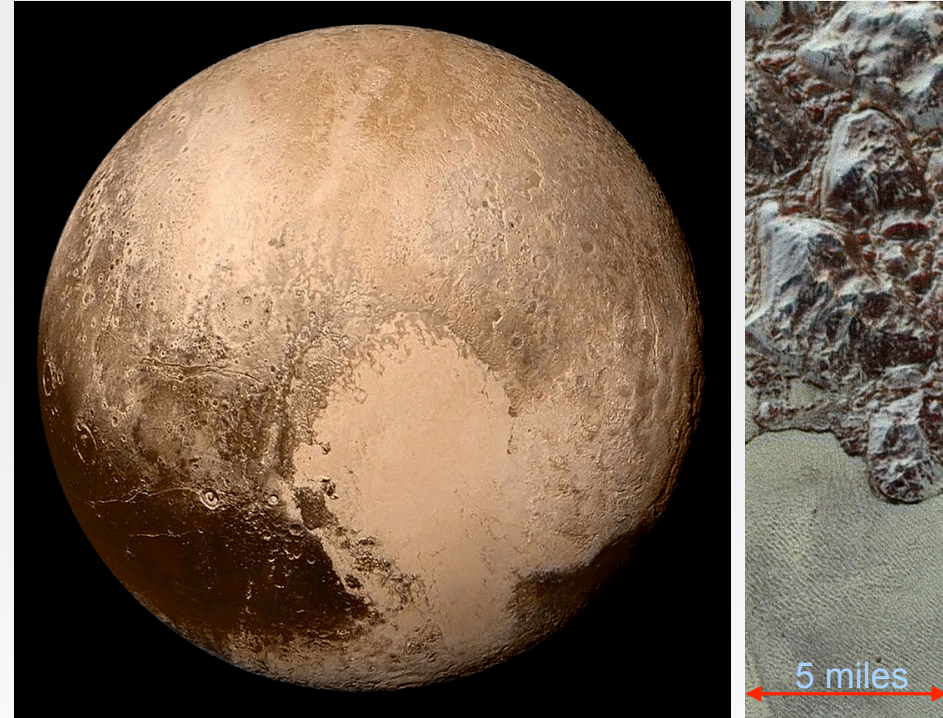


1996, HST/FOC

HST: Hubble Space Telescope  
FOC: Faint Object Camera  
NHS: New Horizons Spacecraft



July 1, 2015 NHS



July 14, 2015, New Horizons Spacecraft

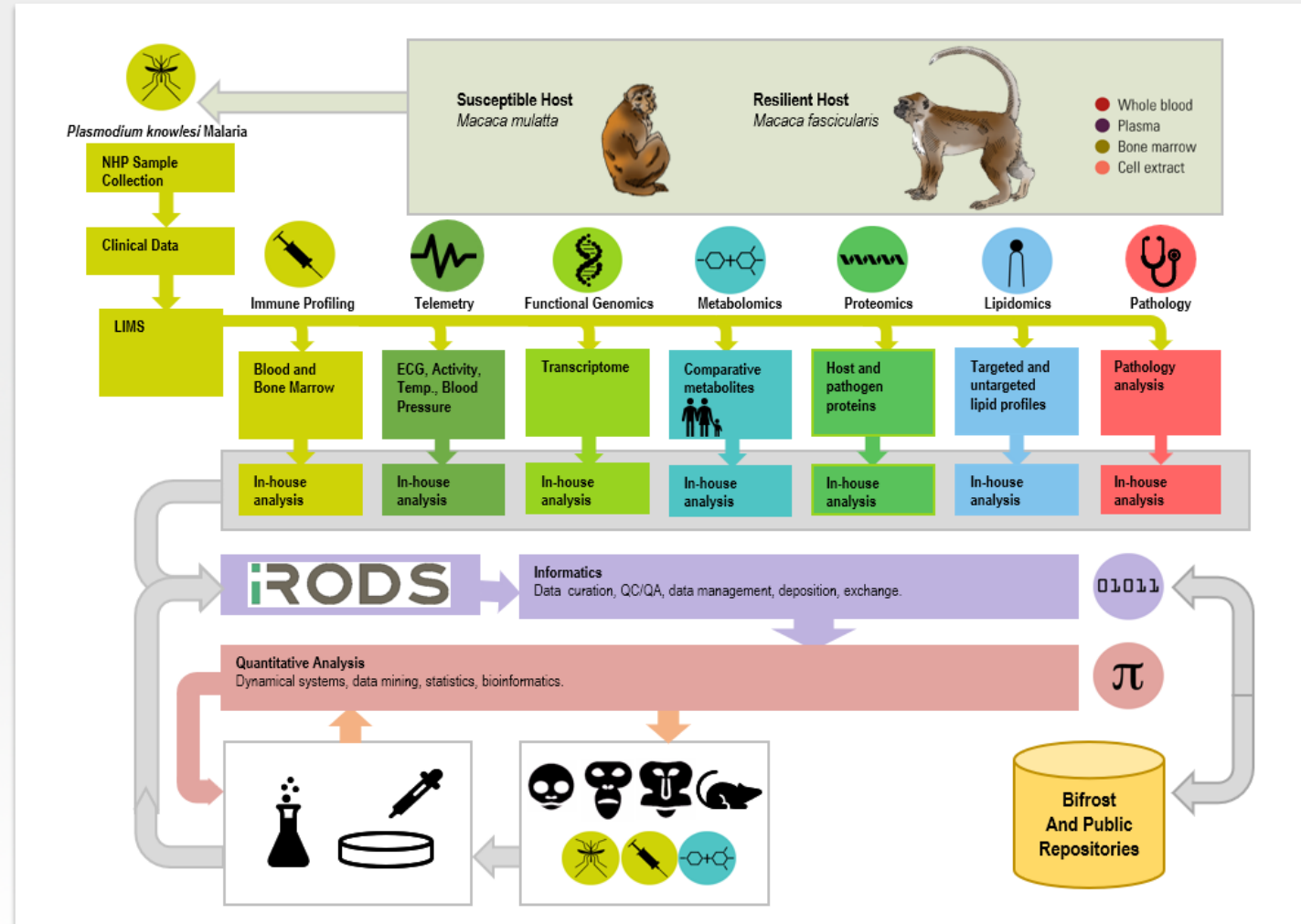
We went from “*where in the sky is this planet*” to “*name this mountain*”.  
The difference is **availability of data**.

Given the brevity of this presentation, no technical details are discussed. Only the high-order organization of a case study are presented next.

# **AN EXAMPLE OF THE NEED OF MACHINE LEARNING: EARLY DETECTION OF DISEASE**



## A “New Horizons” for Biomedical Research: MaHPIC/HAMMER



US National Institute of Allergy and Infectious Diseases, National Institutes of Health, Department of Health and Human Services contract #HHSN272201200031C, 2012-2017, which supported the *Malaria Host-Pathogen Interaction Center (MaHPIC)*.

Defense Advanced Research Projects Agency (DARPA) and the US Army Research Office through the program *Technologies for Host Resilience - Host Acute Models of Malaria to study Experimental Resilience (THoR's HAMMER)*, DARPA contract #W911NF-16-C-0008, 2016-2019

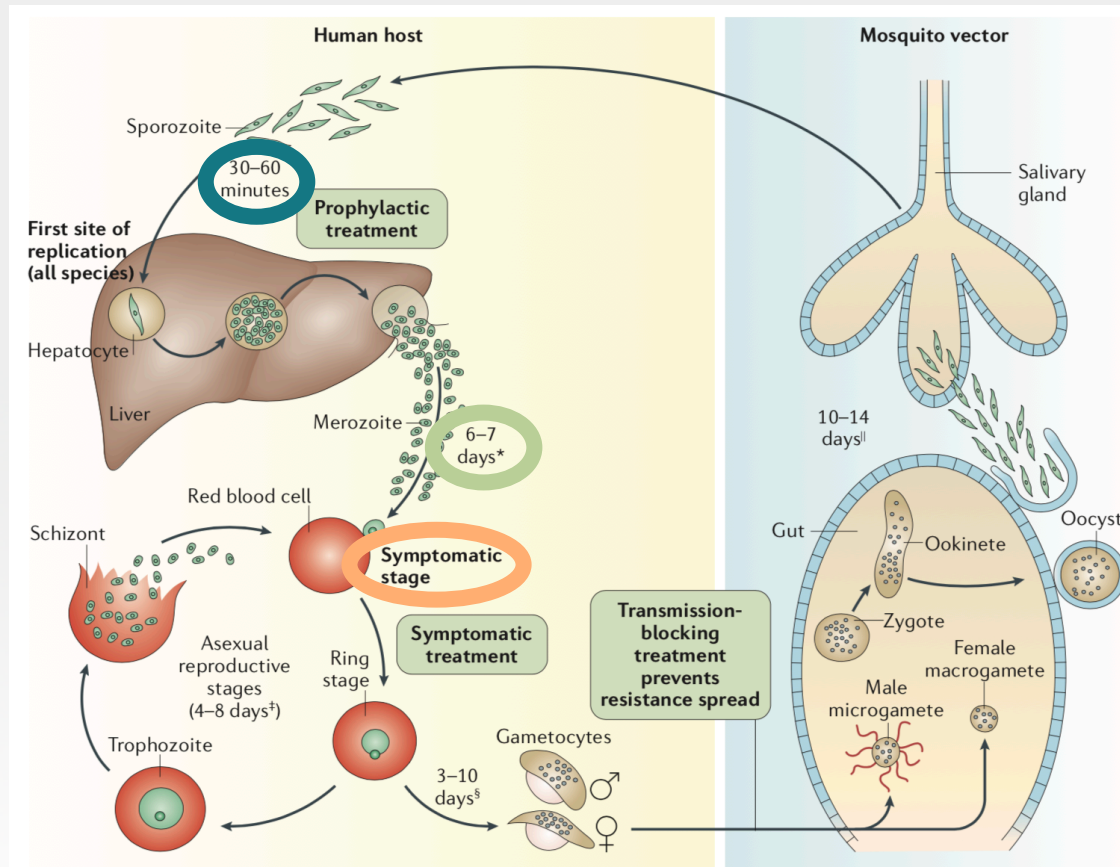
*Terabytes of heterogenous biomedical data!!!*

## Two interesting questions can be addressed now that we have more data

- What causes severity of disease in some individuals, and mild or manageable disease in others?
  - Some individuals affected with malaria show no symptoms.
- Is it possible to detect disease before the onset of symptoms?
  - Once symptoms develop, severity might be impossible to stop.
  - Within 24 hours of the onset of symptoms, a severe malaria patient could die.

Can mathematics help answer these questions?

## Malaria Parasite Life Cycle



Margaret A. Phillips<sup>1</sup>, Jeremy N. Burrows<sup>2</sup>, Christine Manyando<sup>3</sup>,  
Rob Hooft van Huijsduijnen<sup>2</sup>, Wesley C. Van Voorhis<sup>4</sup> and Timothy N. C. Wells<sup>2</sup>, *Malaria Primer*

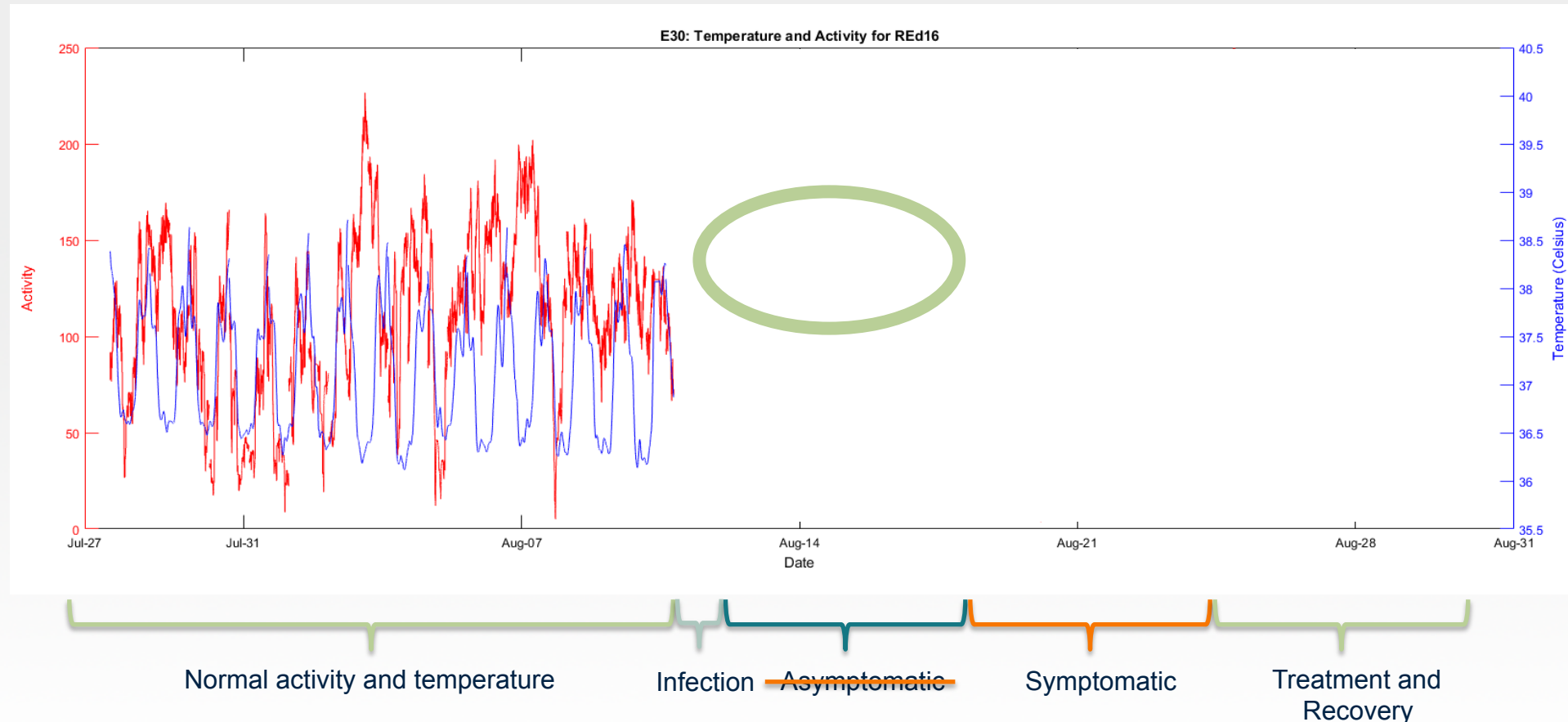
Malaria killed 435,000 people worldwide in 2017, mostly kids under the age of 5 in developing countries. 219 million reported cases.

Currently, there is no early diagnostic test to confirm the presence of *Plasmodium* parasites in the liver.

Once symptoms erupt, complications can occur within 24 hours.



# Focus on question 2: Early Detection of Disease



# Early Detection of Disease



- With the entire time series, we could easily identify the different stages using: wavelets, Fourier analysis, etc.
- But in practice the entire time series is **not** available.
- The goal: detect infection as early as possible with as little data as possible.
- Hefty goal: Detect disease with 10 seconds of ECG data



Apple Watch Series 4  
(Not an endorsement. Shown as an example)

# The heart is a pump made of muscle and regulated by electricity

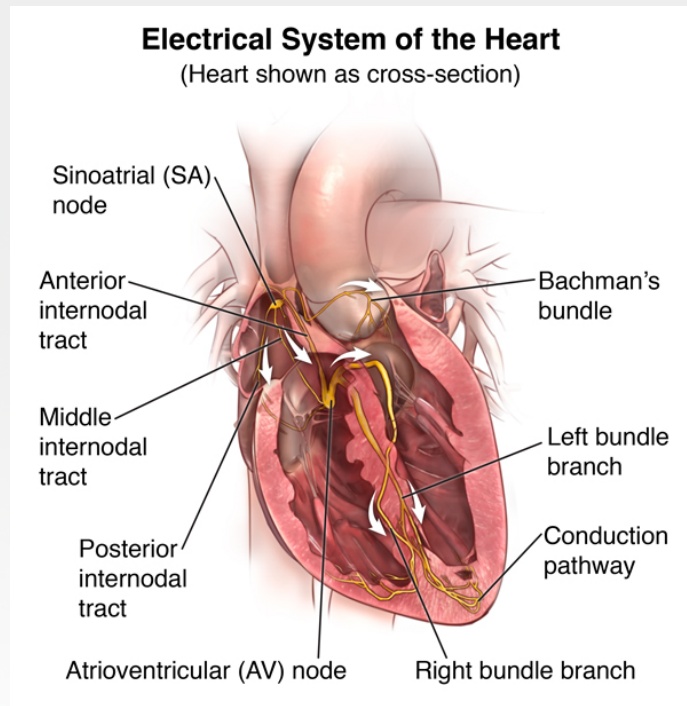


Image source: [http://www.hopkinsmedicine.org/healthlibrary/test\\_procedures/cardiovascular/signal-averaged\\_electrocardiogram\\_92\\_P07984/](http://www.hopkinsmedicine.org/healthlibrary/test_procedures/cardiovascular/signal-averaged_electrocardiogram_92_P07984/)  
Accessed on 1/31/2016

- An electrical impulse is generated in the **SA**.
- It travels to the **AV**, where signal is slowed down briefly, then continue via the bundle of His into the ventricles.
- The right and left atria (upper chambers) contract first for a short time before the left and right ventricles (lower chambers)

# The sequence of depolarization results in a characteristic electrical pattern

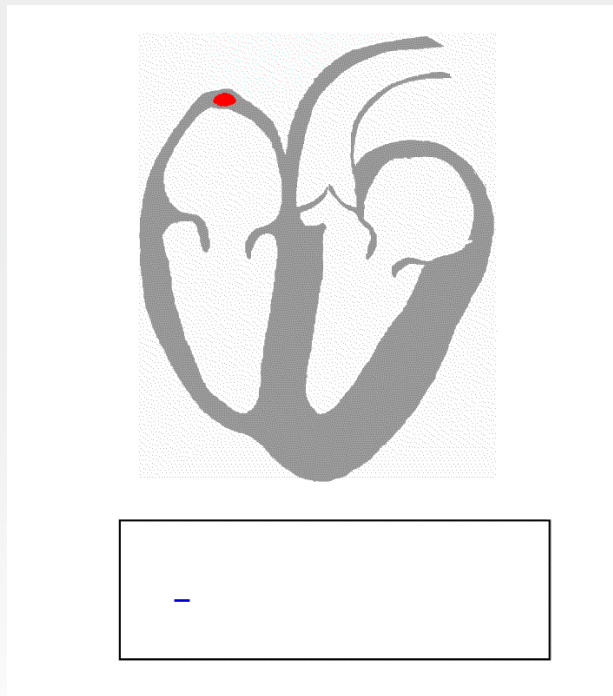
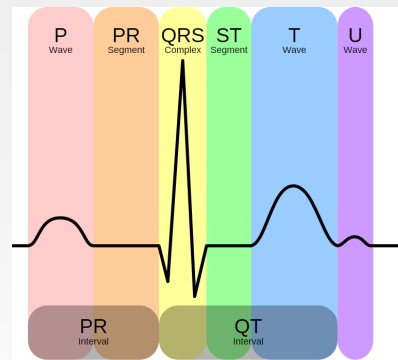


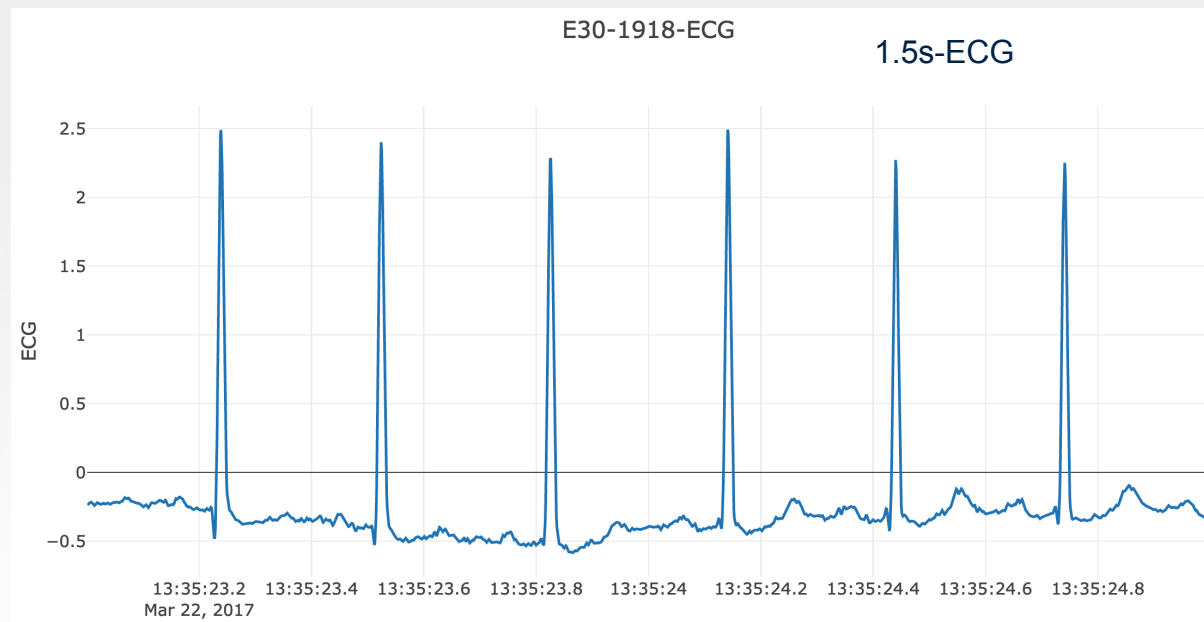
Image source: [https://commons.wikimedia.org/wiki/File:ECG\\_Principle\\_fast.gif](https://commons.wikimedia.org/wiki/File:ECG_Principle_fast.gif)  
Accessed on 1/31/2016



- Depolarization begins in the **right atrium** at the sinoatrial node (SA).
- It propagates to the **left atrium** first via the Bachman's bundle, and then interatrial septum (IS), anterior IS, and the coronary sinus.
- Then it propagates to the **atrioventricular node**, resulting in a large electrical discharge.
- It follows the path of the **Bundle of His**, and into the **Purkenje fibers**.

## ECG Pre-processing

- Four days before inoculation and four days after inoculation.
- Each day was segmented into hourly intervals of data.
- Hour intervals were segmented into 10-second intervals.
- 13 subjects \* 8 days \* 24 hours \* 60 minutes \* 6 10-second segments  
= 898,560 observations. Each observation is a time series with 10,000 points



Tao Sheng's dissertation

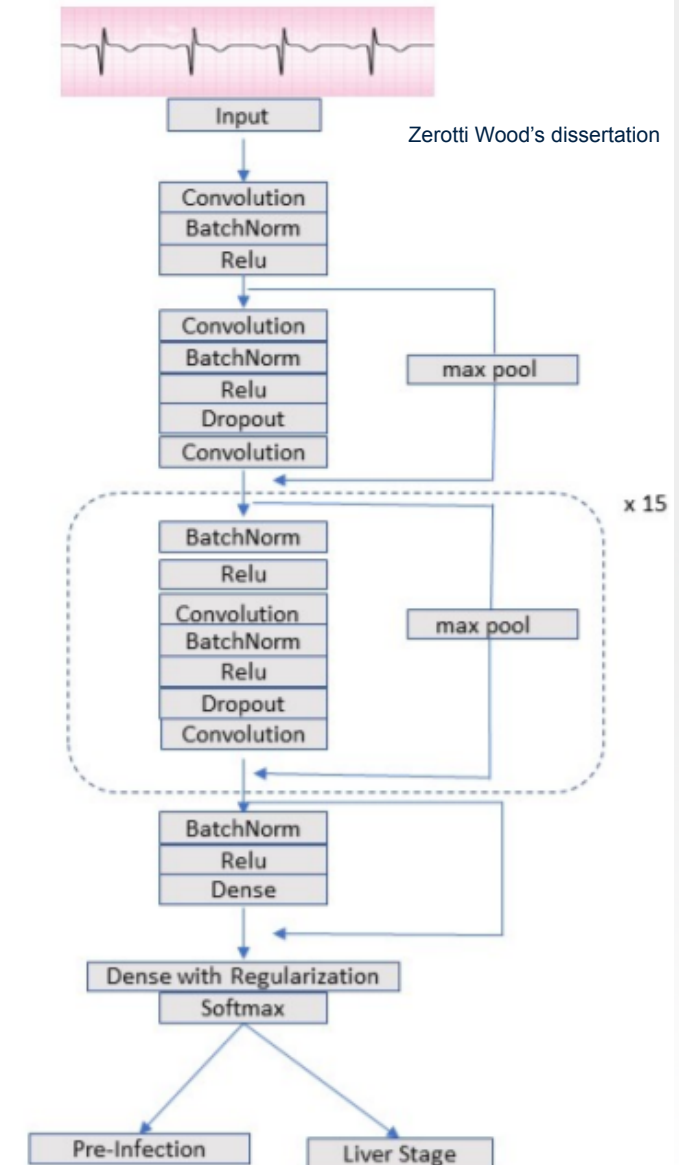
# The Canonical Methods Fail

- In trying to identify what 10-second segments of ECG data correspond to pre-infection of liver-stage, traditional methods were unable to surpass 70% accuracy (COSINOR models, wavelets, Fourier analysis).
- This opened the door to explore machine learning. Could a neural network detect these states with greater accuracy?



## ECG Processing

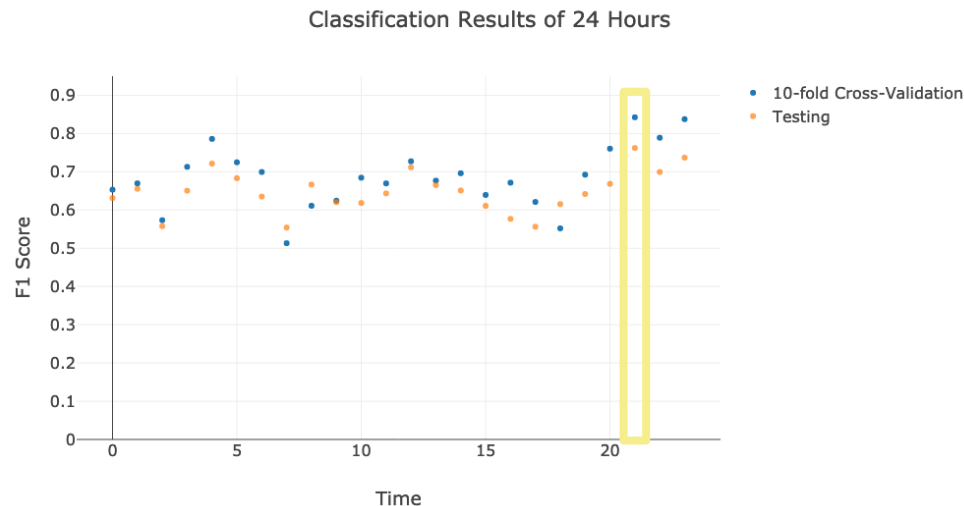
- A random 90% of these observations were used to train a neural network.
- A random 10% was used as the development.
- Each hour was analyzed. Hours with lower activity (as measured with accelerometers) had better predictive power, as expected.
- 13 subjects \* 8 days \* 60 minutes \* 6 10-second segments  
= 18,720 observations. Each observation is a time series with 10,000 points





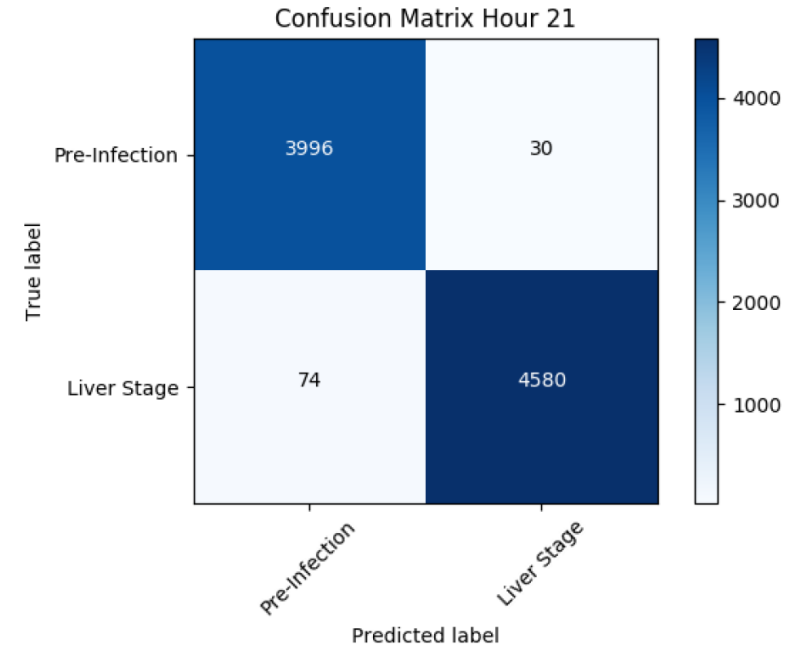
# Early Detection of Disease via Telemetry

Using machine learning, we detected *Plasmodium* infection based on electrocardiogram (ECG) signals with over 98% accuracy during the liver stage of the disease, importantly, before the onset of symptoms that are caused by the blood-stage of the disease that is characteristic of malaria.



The later hours with less activity yield the best classification

Tao Sheng's dissertation



	Precision	Recall	$F_1$ score	Support
Pre-Infection	.982	.993	.987	4026
Liver Stage	.993	.984	.989	4654

Zerotti Wood's dissertation

# Machine Learning: Improved Cognition for Humans

- ML allows detection of phenomena that remains undetectable through other methods.
- It requires large data sets.
- ML present challenges that open opportunities for foundational mathematical work.

# Challenges

- We looked at a particular study in a specific context, but there are traits that seem to be universal when we consider machine learning applied to medicine.
- Data collection and management is an often overlooked and a deep source of complications.
- There are foundational questions that deserve attention:
  - What are (necessary and sufficient) conditions for consistency of a learning process?
  - How to accelerate the rate of convergence of the learning process?
  - Why does it work

# Challenges

- Machine learning adds value to quantitative studies, particularly when we understand poorly a phenomenon, or when a well understood phenomenon becomes too complex to model.
- There is a delicate balance between knowledge and understanding. In this case, a neural network detected a phenomenon we poorly understand. It opens opportunities for basic research.
- The expertise required to undertake such studies is broad and takes a long time to develop. But this poses a conundrum: How to empower the next generation of scientists to execute multi-scale studies?

# FUTURE DIRECTION: Early Detection of Disease

## Early Detection of Disease



The ability to detect disease before symptoms occur could revolutionize health care and public health.

**Malarial liver-stage infections could be detected with only 10 seconds of ECG data.**

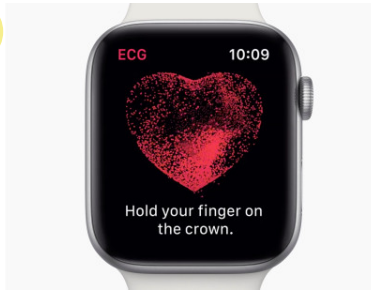
Other diseases may have unique signatures as well.



ED2 could be the next big thing. It would be a historical win, comparable to the Internet and GPS.

# FUTURE DIRECTION: Early Detection of Disease

1



Apple Watch Series 4

ECG, accelerometers, and other telemetry measures, have reached the consumer market. There is a complex ecosystem of capabilities distributed across many manufacturers.

2



The roadblock for broad adoption of these findings is the inability to reconcile telemetry data of hundreds of thousands of subjects with medical records to train artificial intelligence classifiers.

3



In the US, *only the US Armed Forces* have the capability to create this market (large personnel + VA).

The outcome would be a low-cost mechanism to detect physiological changes and promote early interventions.

JUAN.GUTIERREZ3@UTSA.EDU

**THANKS FOR YOUR ATTENTION!**



# MATHEMATICAL FRONTIERS

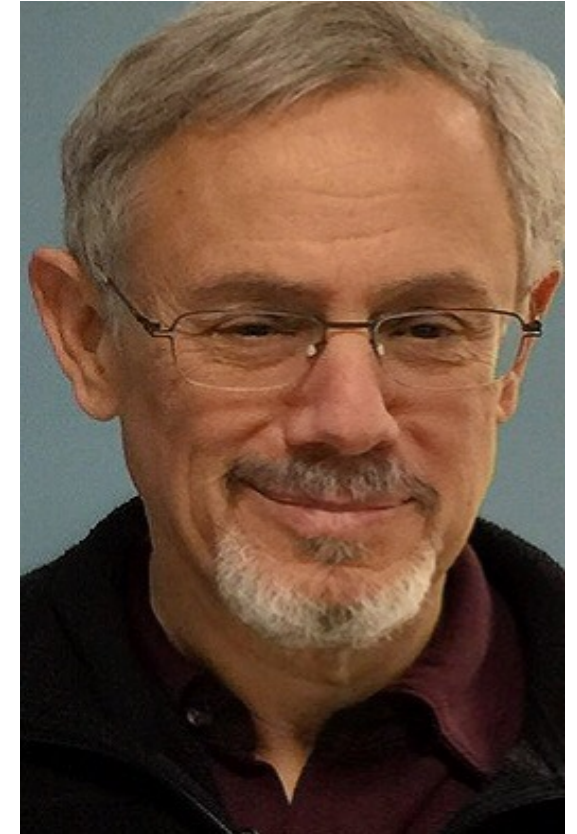
## Machine Learning in Medicine



**Mihaela van der Schaar,  
University of Cambridge,  
Alan Turing Institute, and UCLA**



**Juan Gutierrez,  
University of Georgia**



**Mark Green,  
UCLA (moderator)**

# MATHEMATICAL FRONTIERS

## 2019 Monthly Webinar Series, 2-3pm ET

**February 12:** *Machine Learning for Materials Science\**

**March 12:** *Mathematics of Privacy\**

**April 9:** *Mathematics of Gravitational Waves\**

**May 14:** *Algebraic Geometry\**

**June 11:** *Mathematics of Transportation\**

**July 9:** *Cryptography & Cybersecurity\**

**August 13:** *Machine Learning in Medicine*

**September 10:** *Logic and Foundations*

**October 8:** *Mathematics of Quantum Physics*

**November 12:** *Quantum Encryption*

**December 10:** *Machine Learning for Text*

*Made possible by support for BMSA from the  
**National Science Foundation**  
**Division of Mathematical Sciences**  
and the  
**Department of Energy**  
**Advanced Scientific Computing Research***

*\* Webinar posted*