Keynote 1: Explainable AI in Precision Medicine

- Su-In Lee is an Associate Professor in the Paul G. Allen School of Computer Science & Engineering, and an Adjunct Associate Professor in the Genome Sciences Department, the Department of Electrical Engineering and the Department of Biomedical Informatics and Medical Education at the University of Washington. She has received the National Science Foundation CAREER Award and been named an American Cancer Society Research Scholar.

Explainable Artificial Intelligence in Precision Medicine

Su-In Lee

Paul G. Allen School of Computer Science & Engineering

University of Washington, Seattle

What current machine learning (ML) *can* do for precision medicine

Patient

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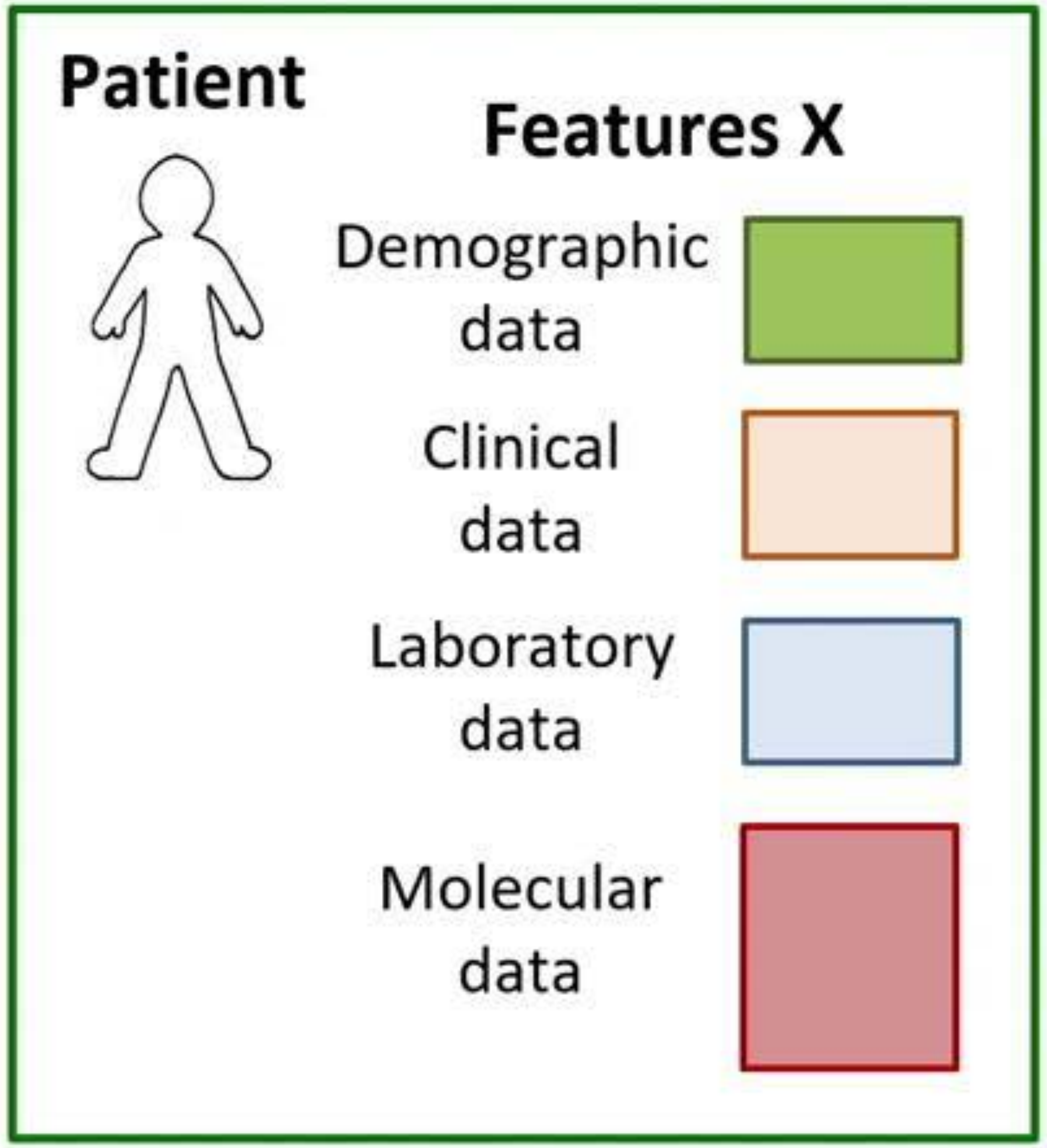

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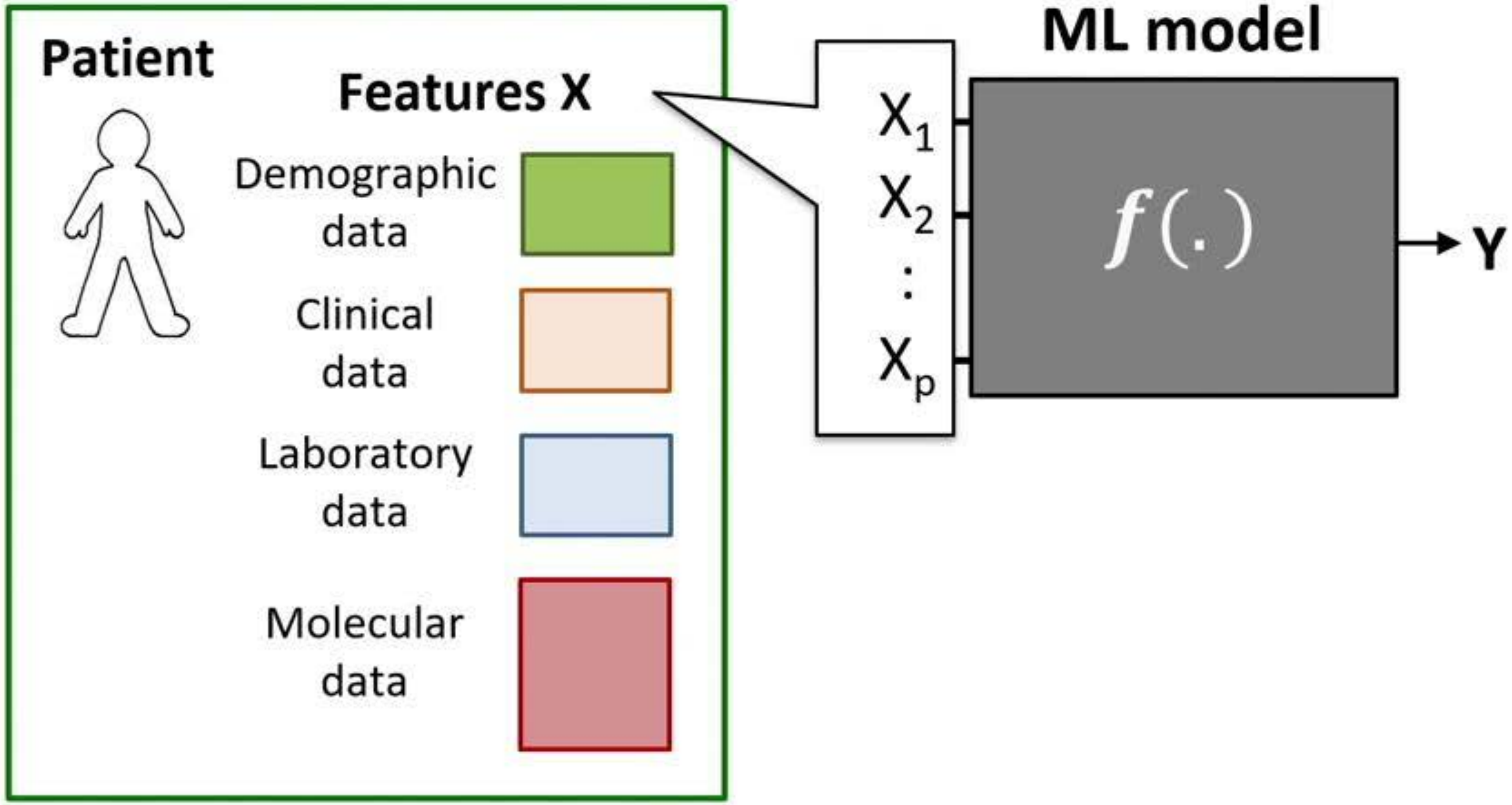

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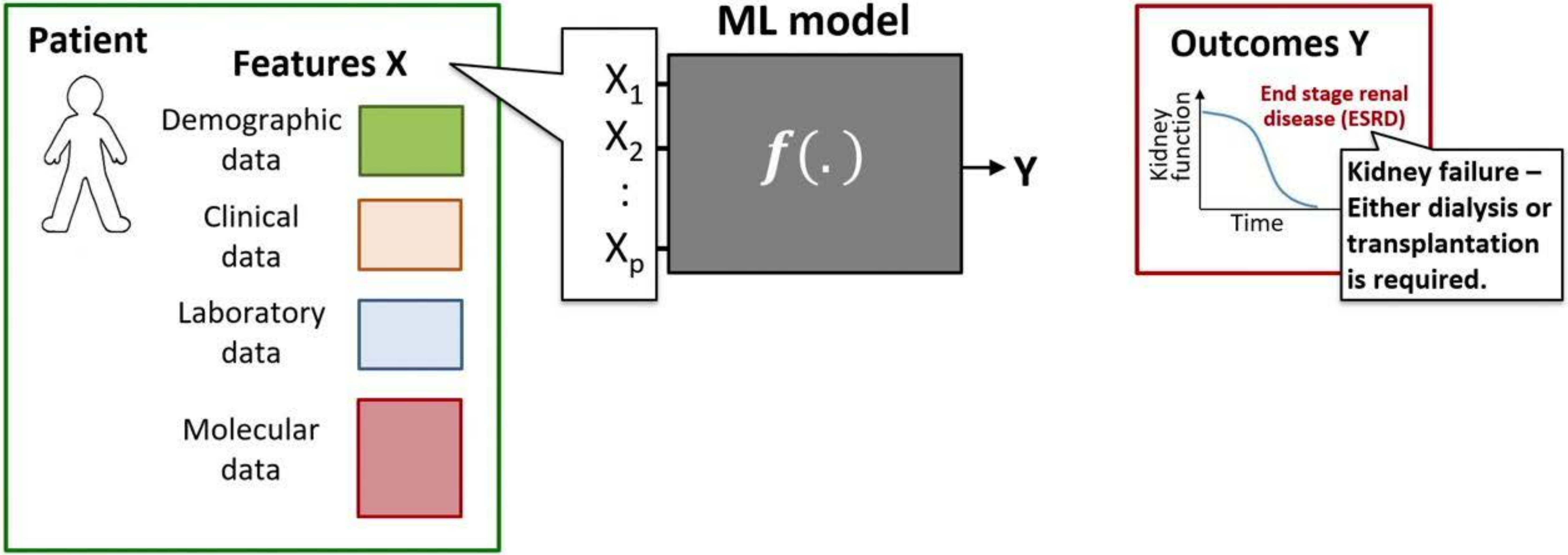

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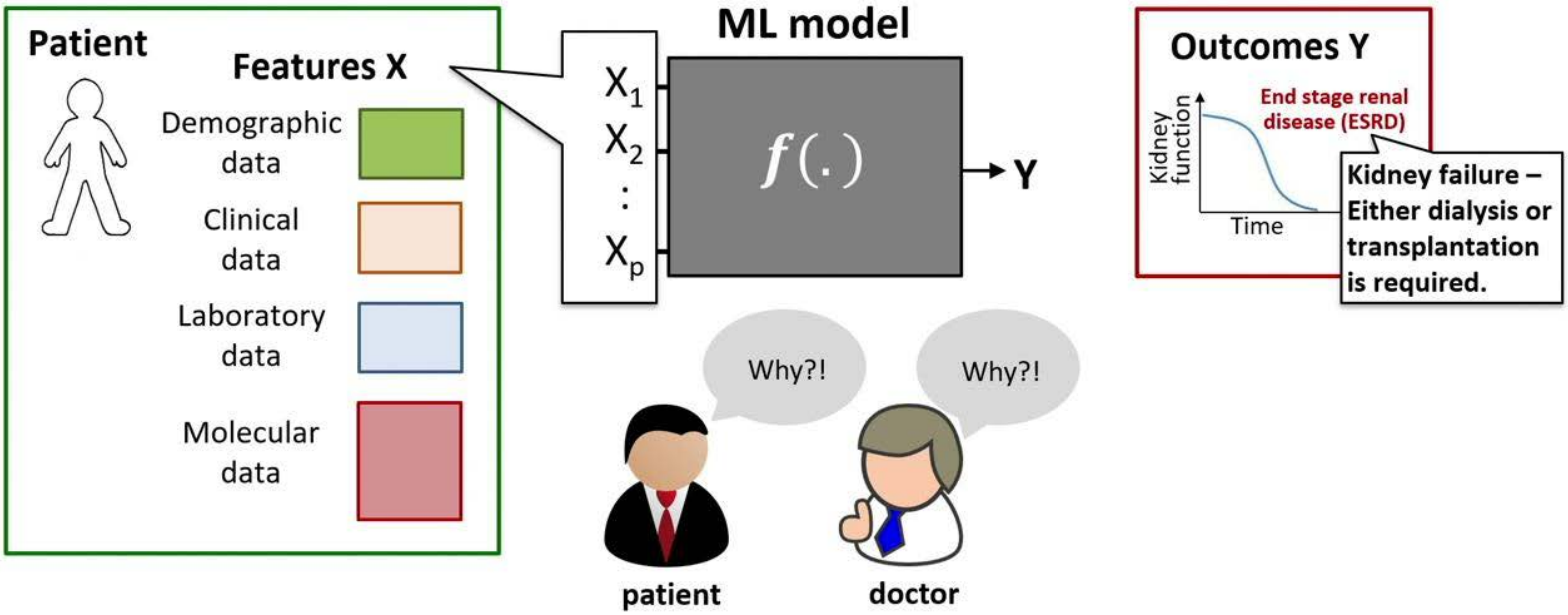

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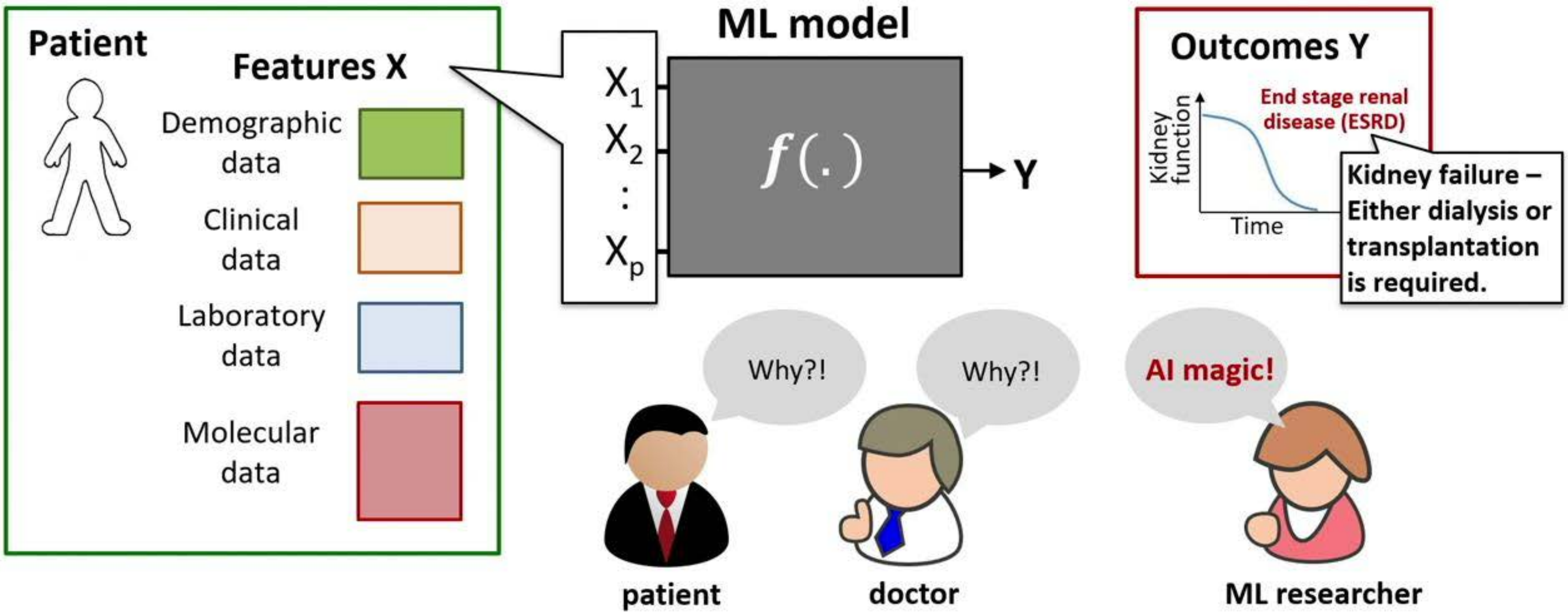

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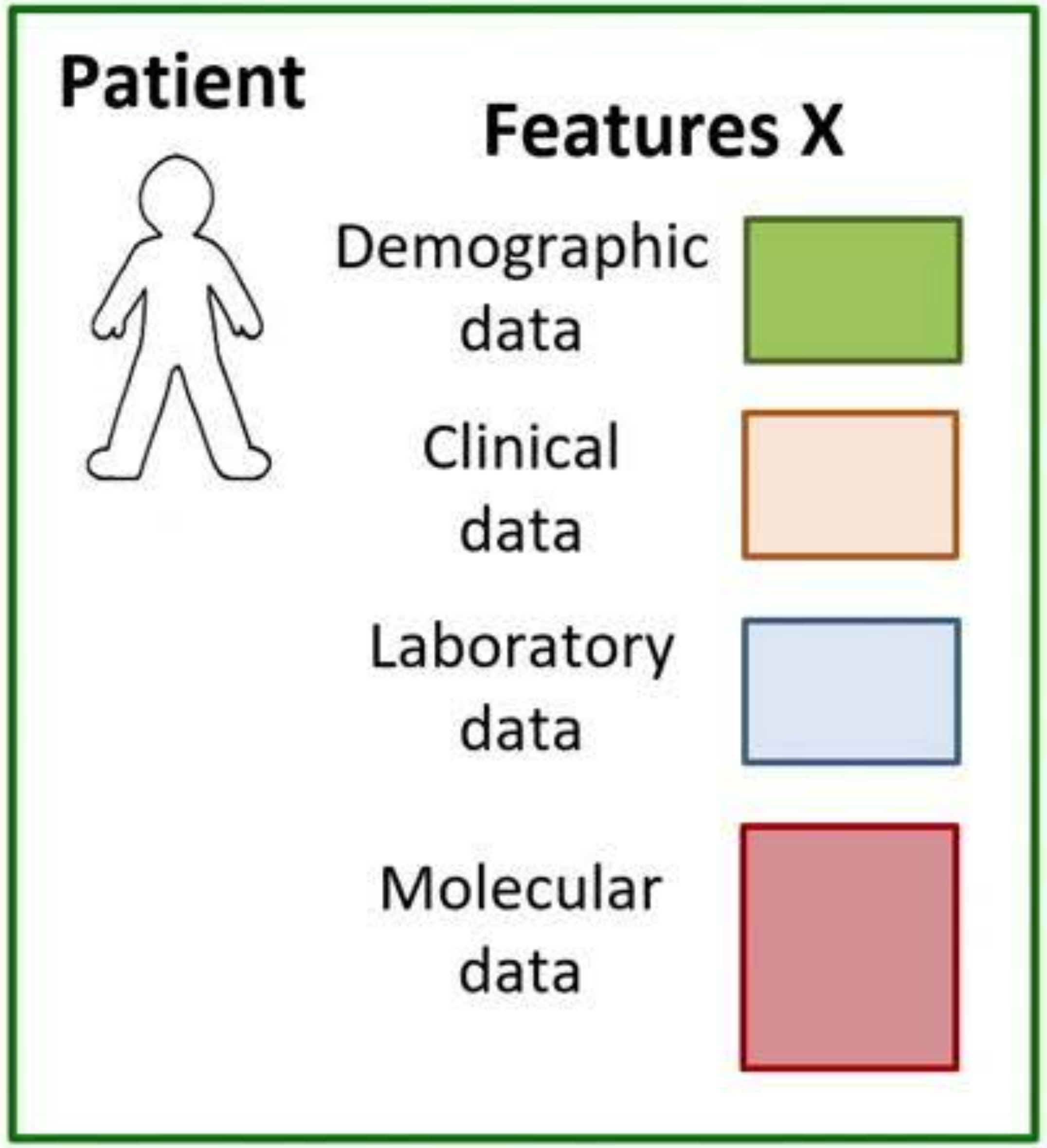

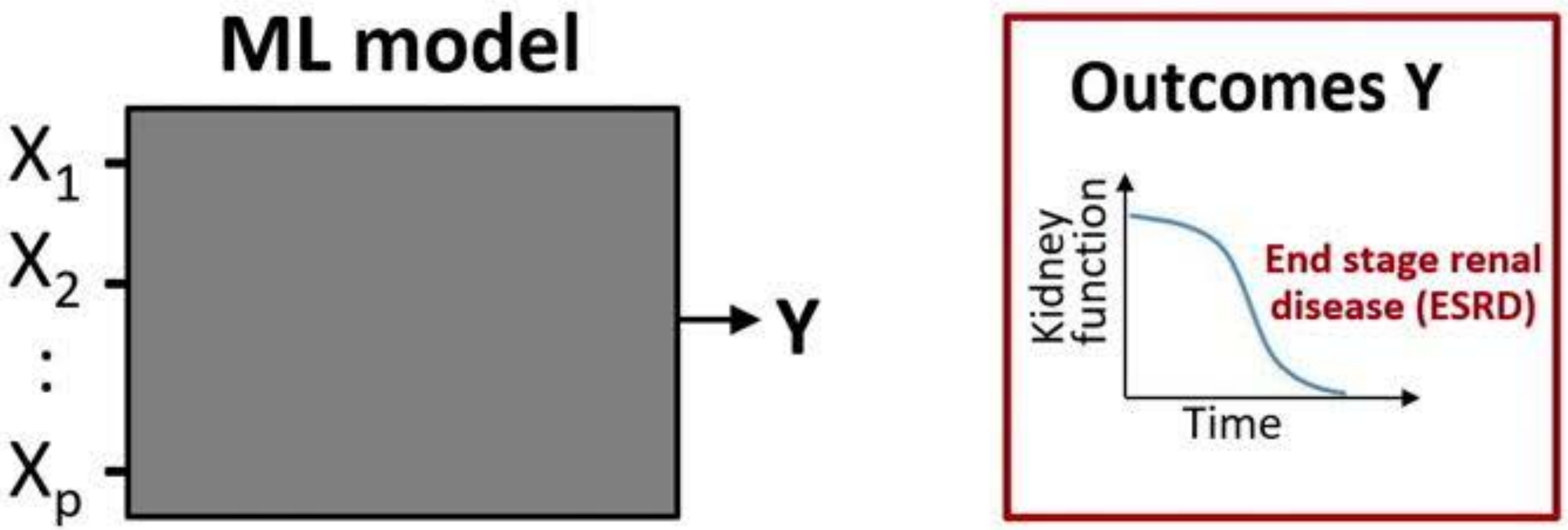

- **Interpretability** is sometimes more important than accuracy.
  - Why selected features make sense?
  - Which features contributed to the prediction and how?

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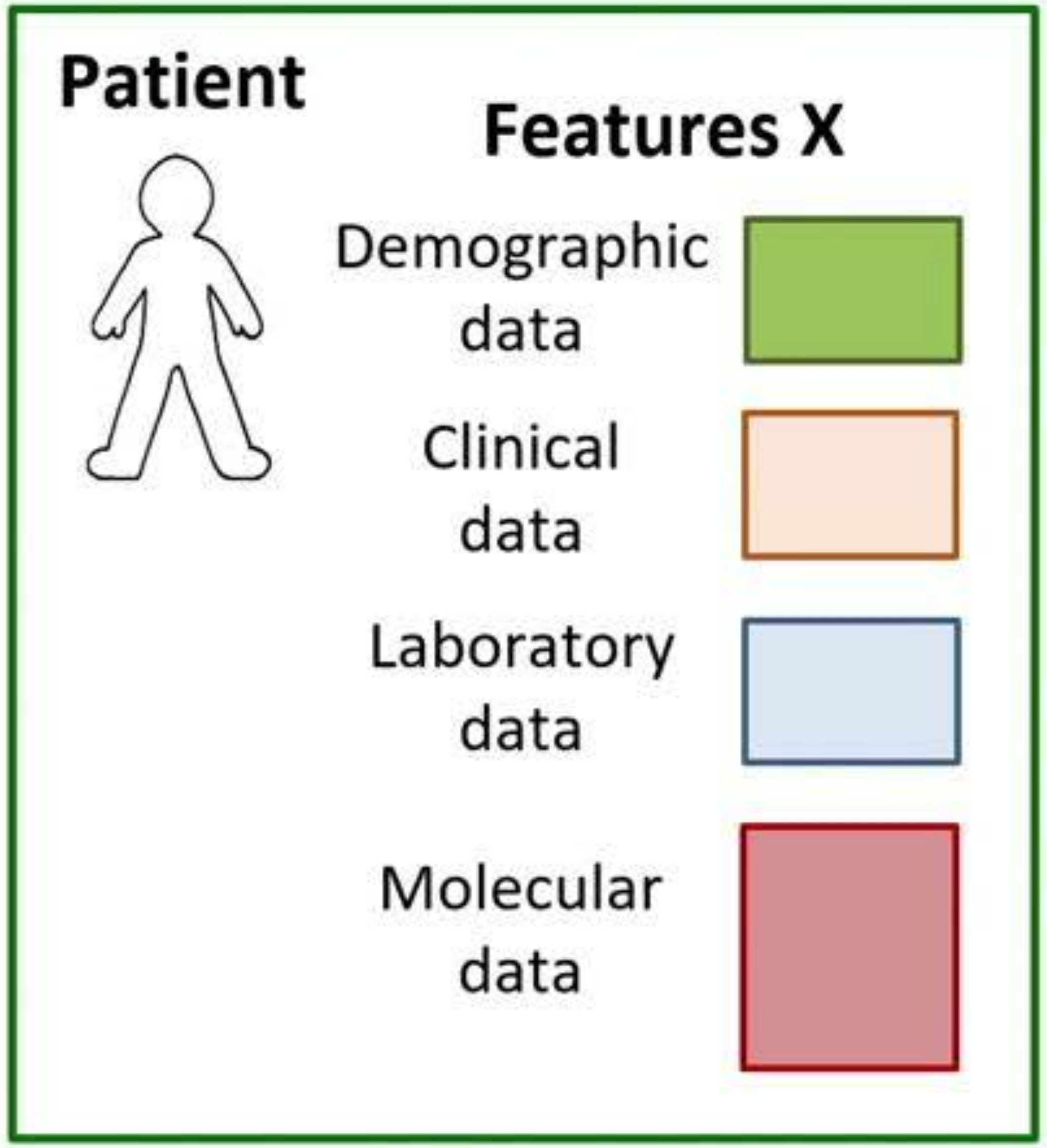

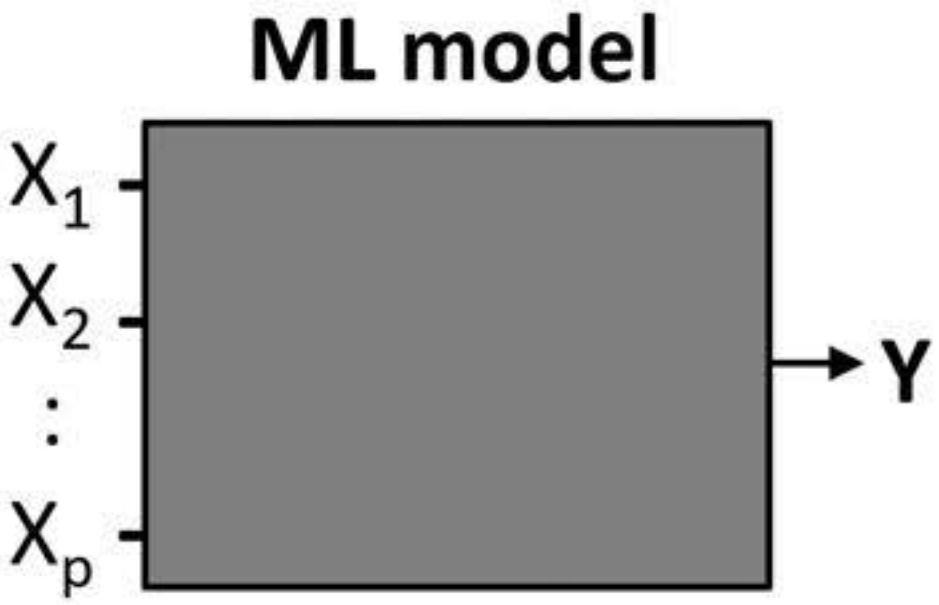

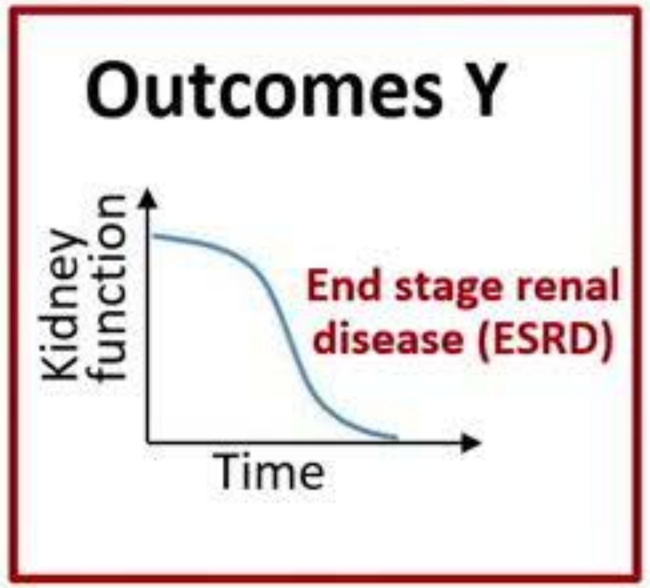

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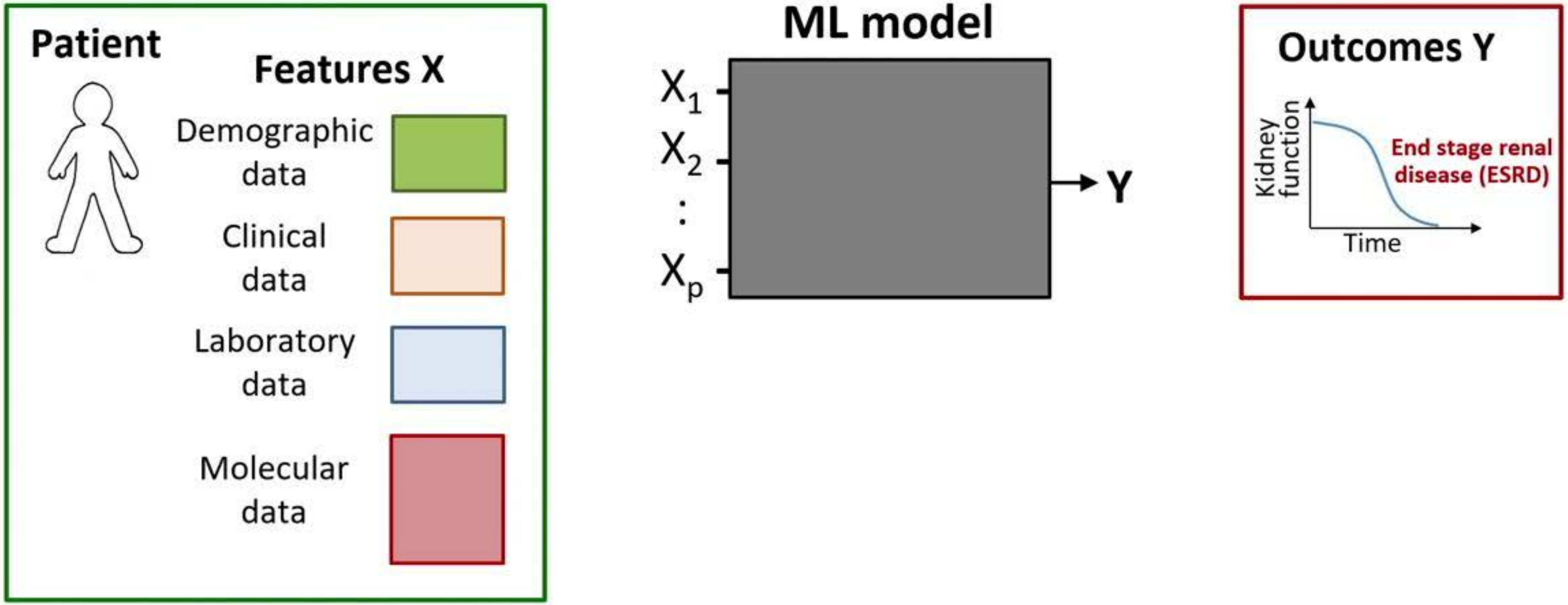
Interpretable ML for precision medicine



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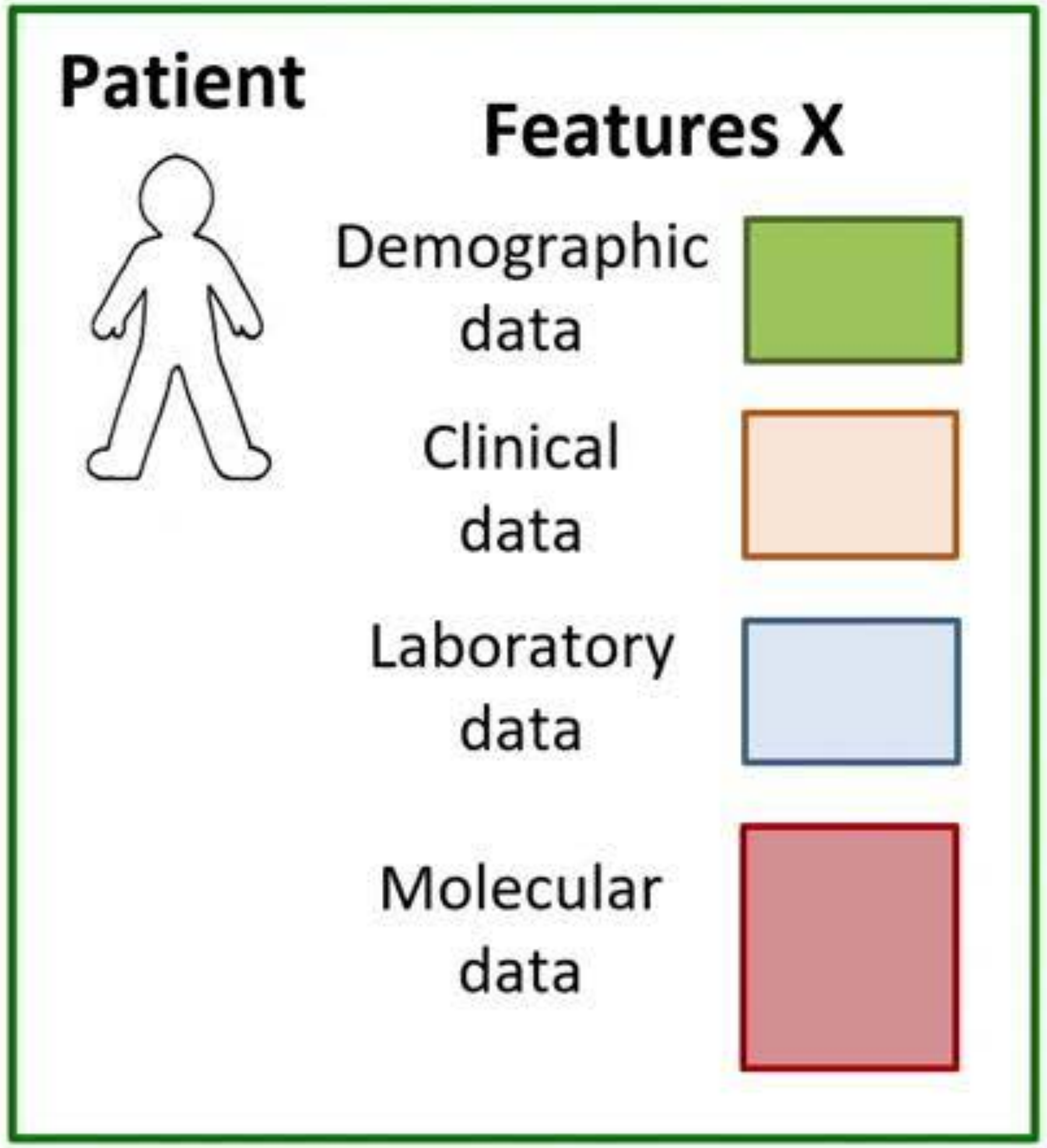
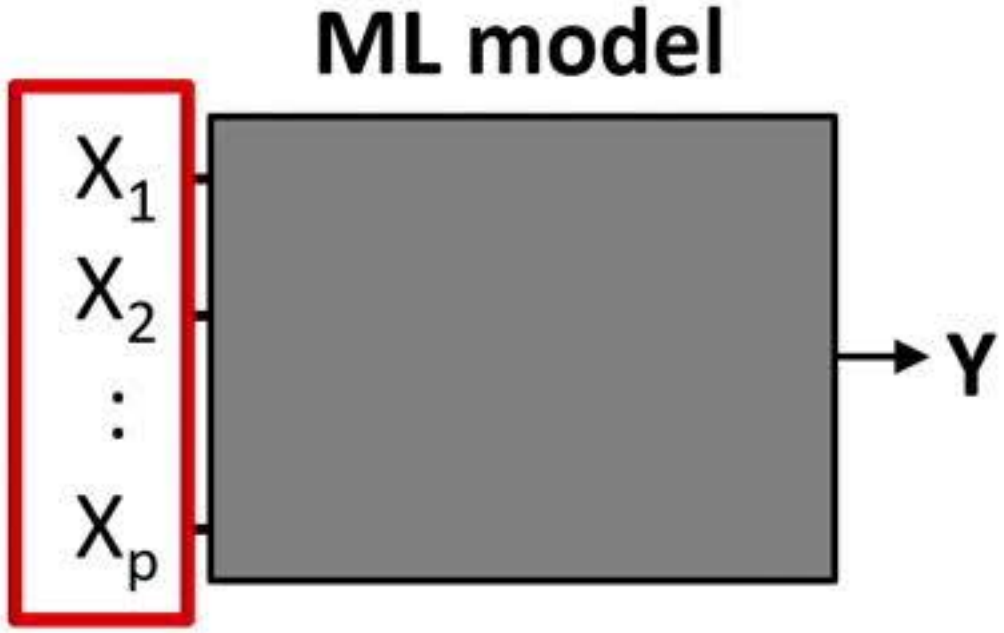
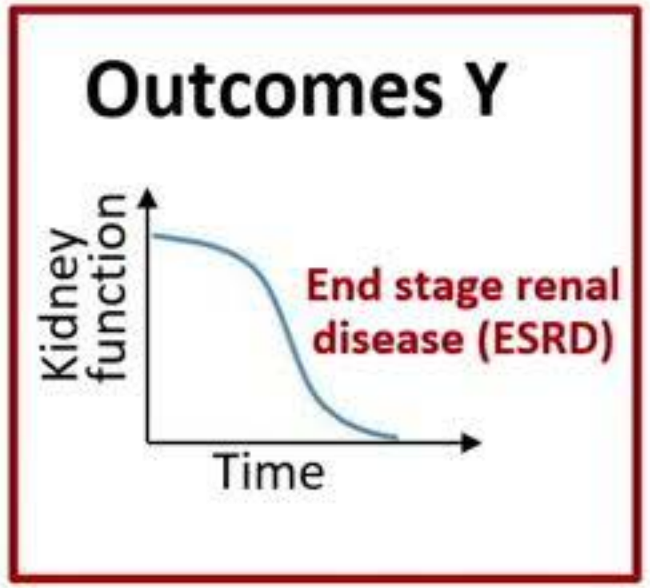


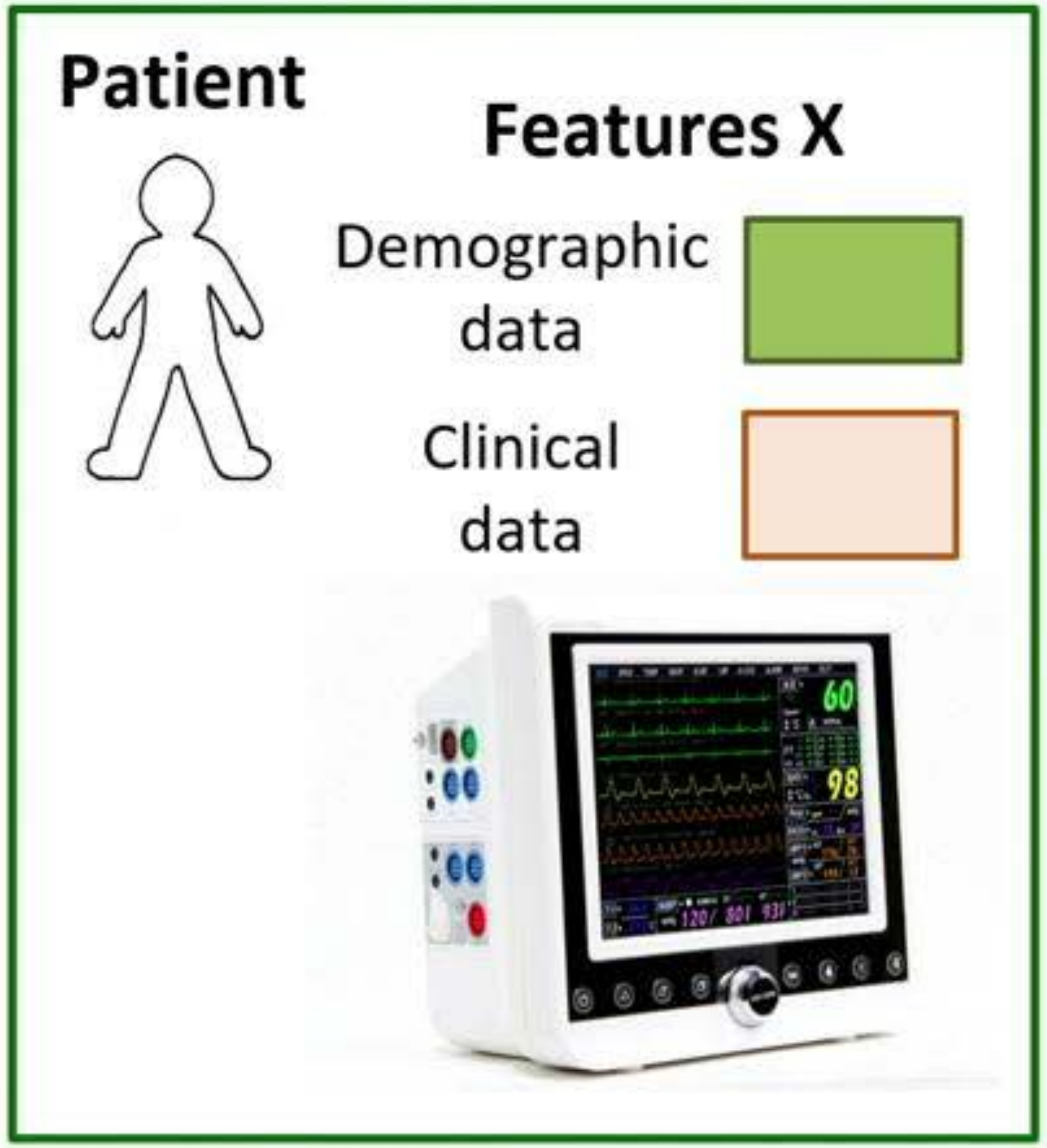


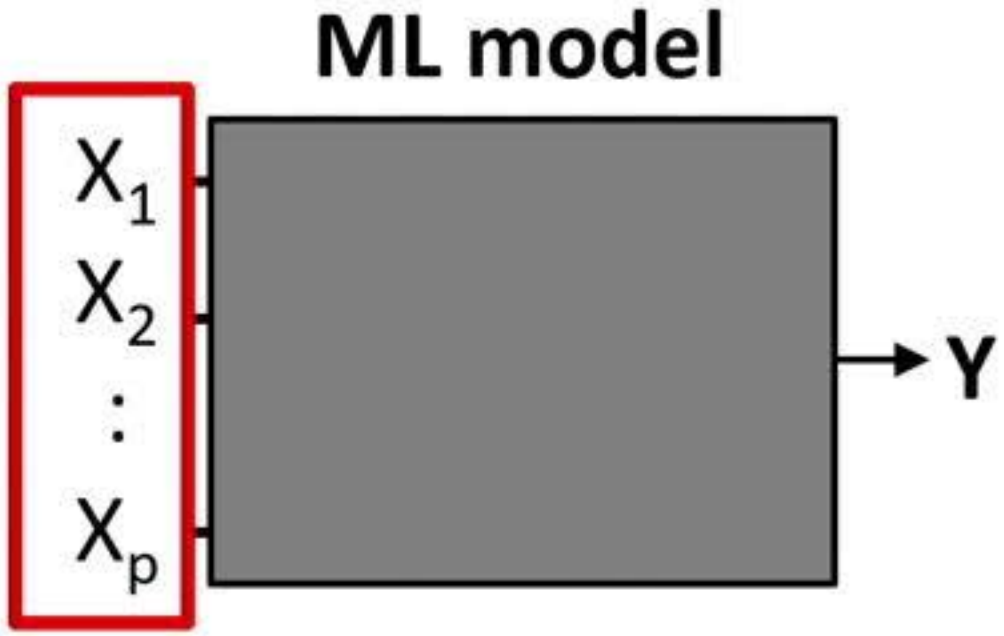


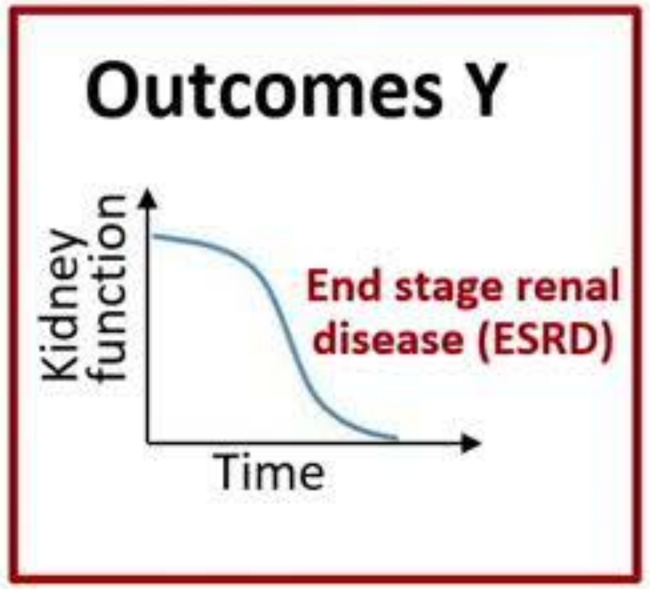
- **1. Learn interpretable feature representation.**
  - Pre-select or learn features likely relevant to Y.

Lee*, Celik*, et al. (2018)
Nature Communications

Interpretable ML for precision medicine







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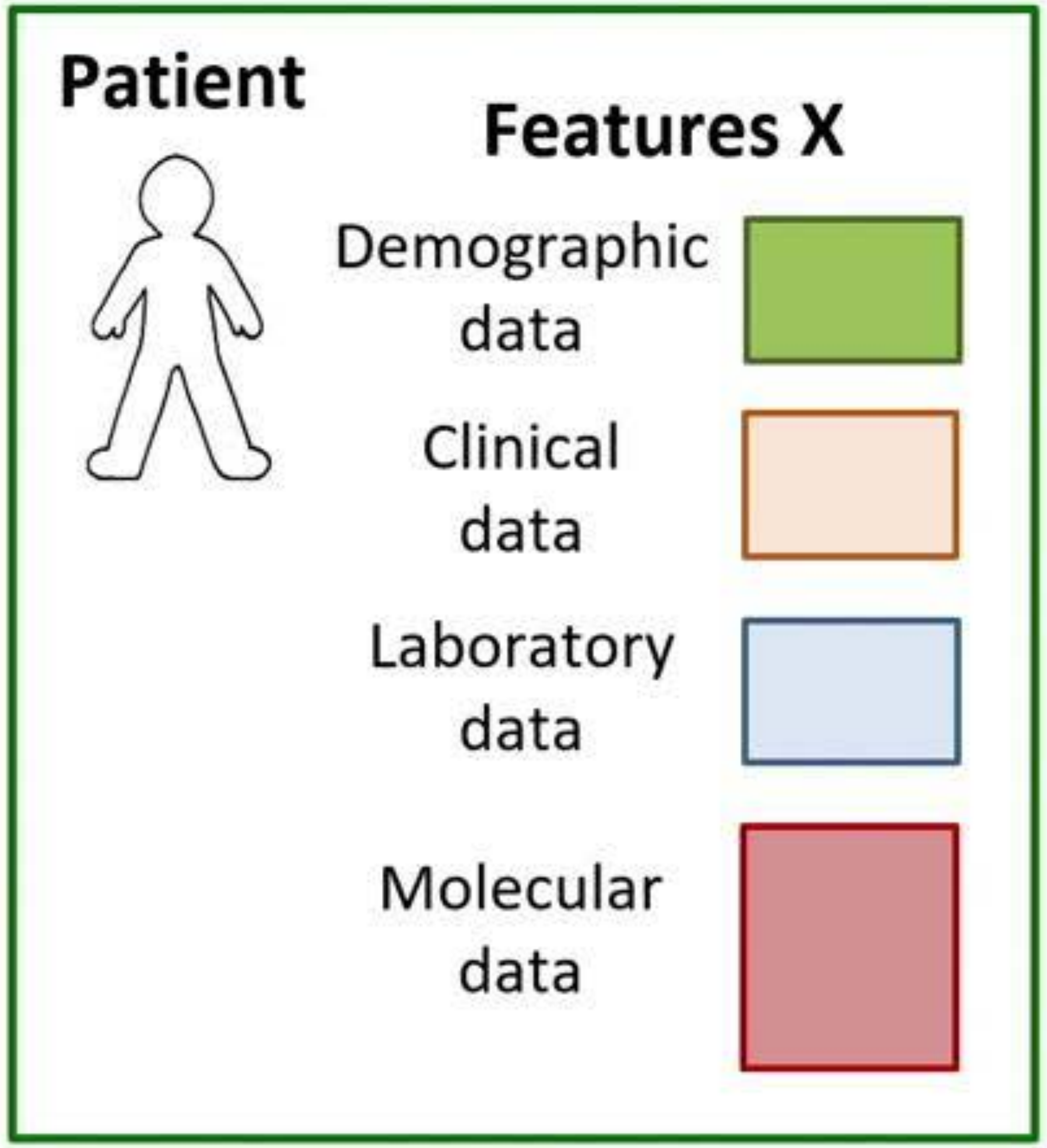

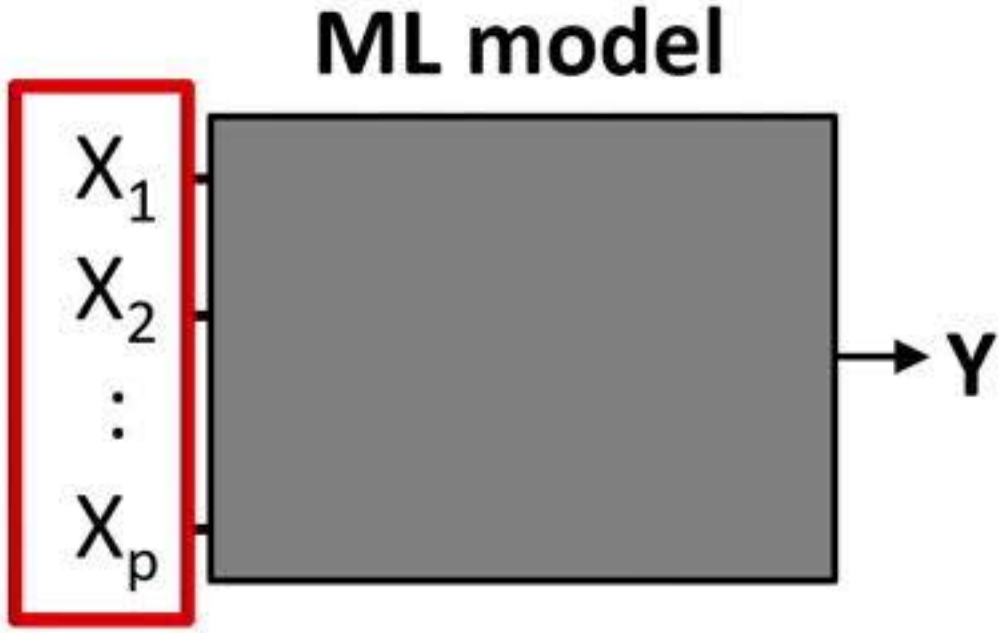

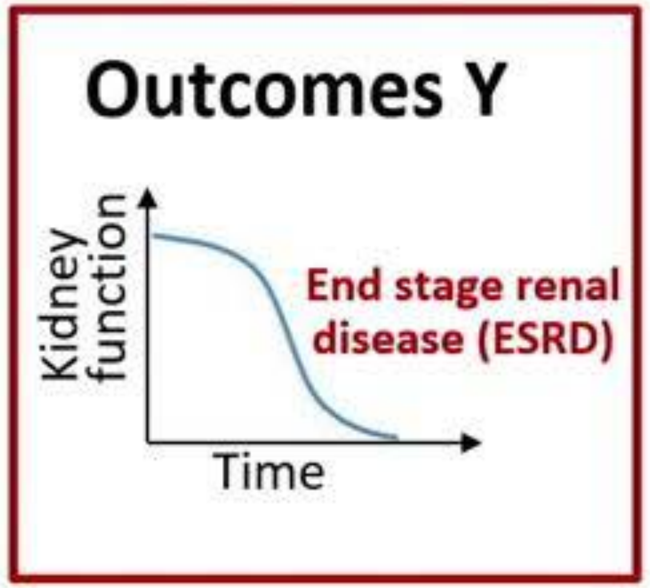

- **1. Learn interpretable feature representation.**
  - Pre-select or learn features likely relevant to Y.
  - Extract meaningful patterns from physiological signals.
  - Enable interactive prediction for time-sensitive diagnosis.

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Interpretable ML can transform important areas of medicine

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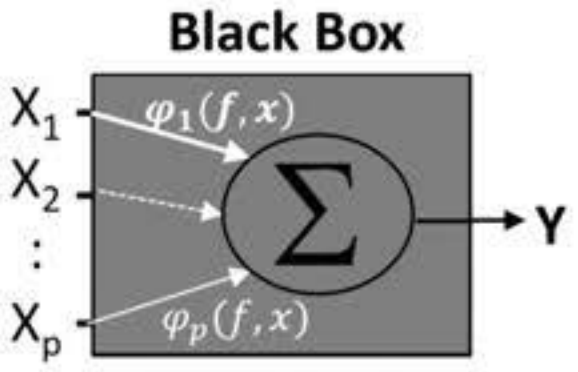
Prediction & decision support systems in hospitals

- Make interpretable predictions from complex models.



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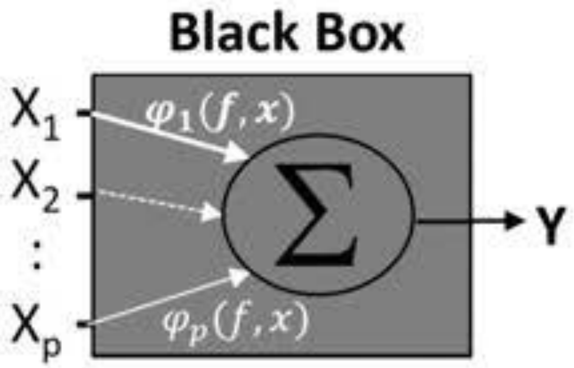
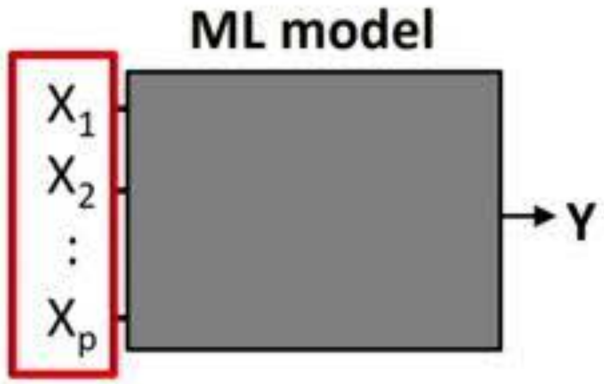


Cancer precision medicine

- Learn interpretable feature representations.



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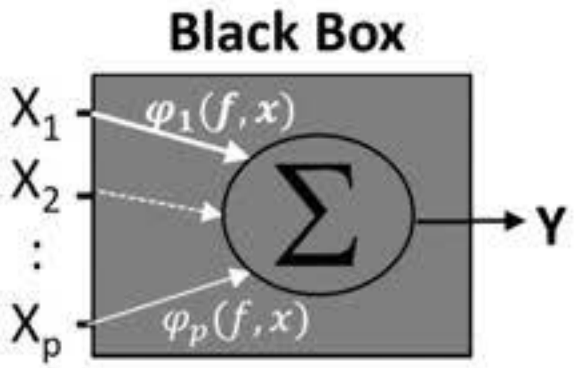

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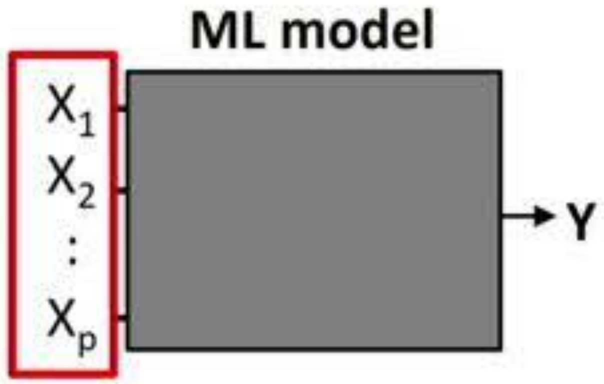

Alzheimer's disease therapeutic target discovery

- Integrate data sets for statistical power and interpretability.

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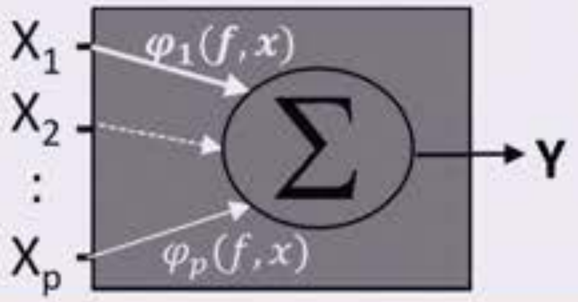
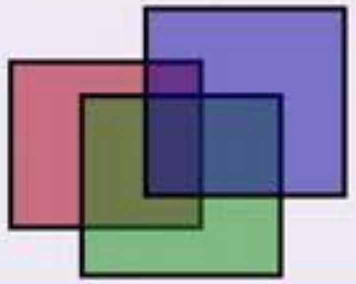
General ML techniques

Black Box



ML model

Data integration



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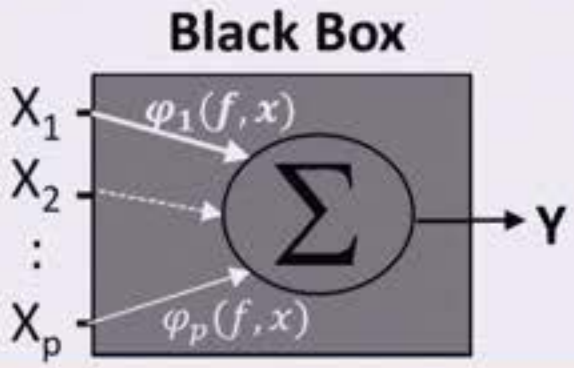

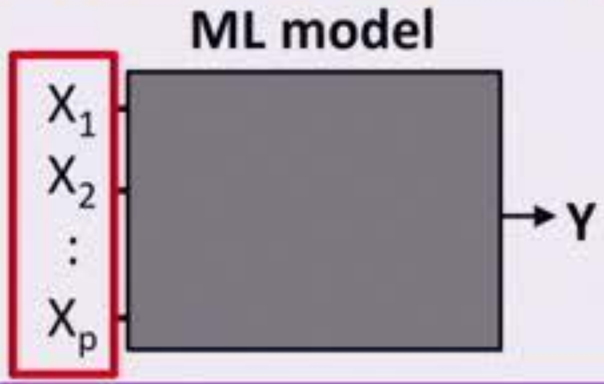

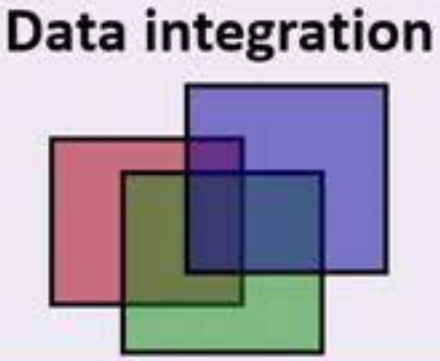

Bedside applications ← Basic science

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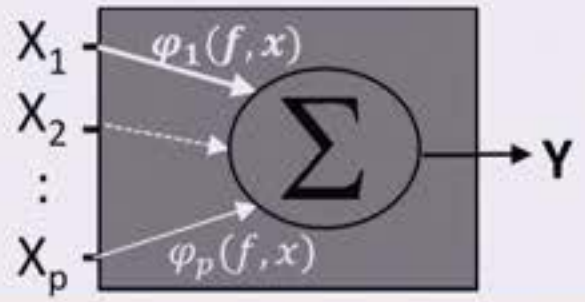
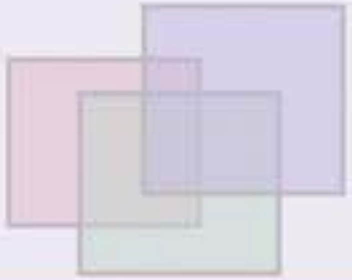
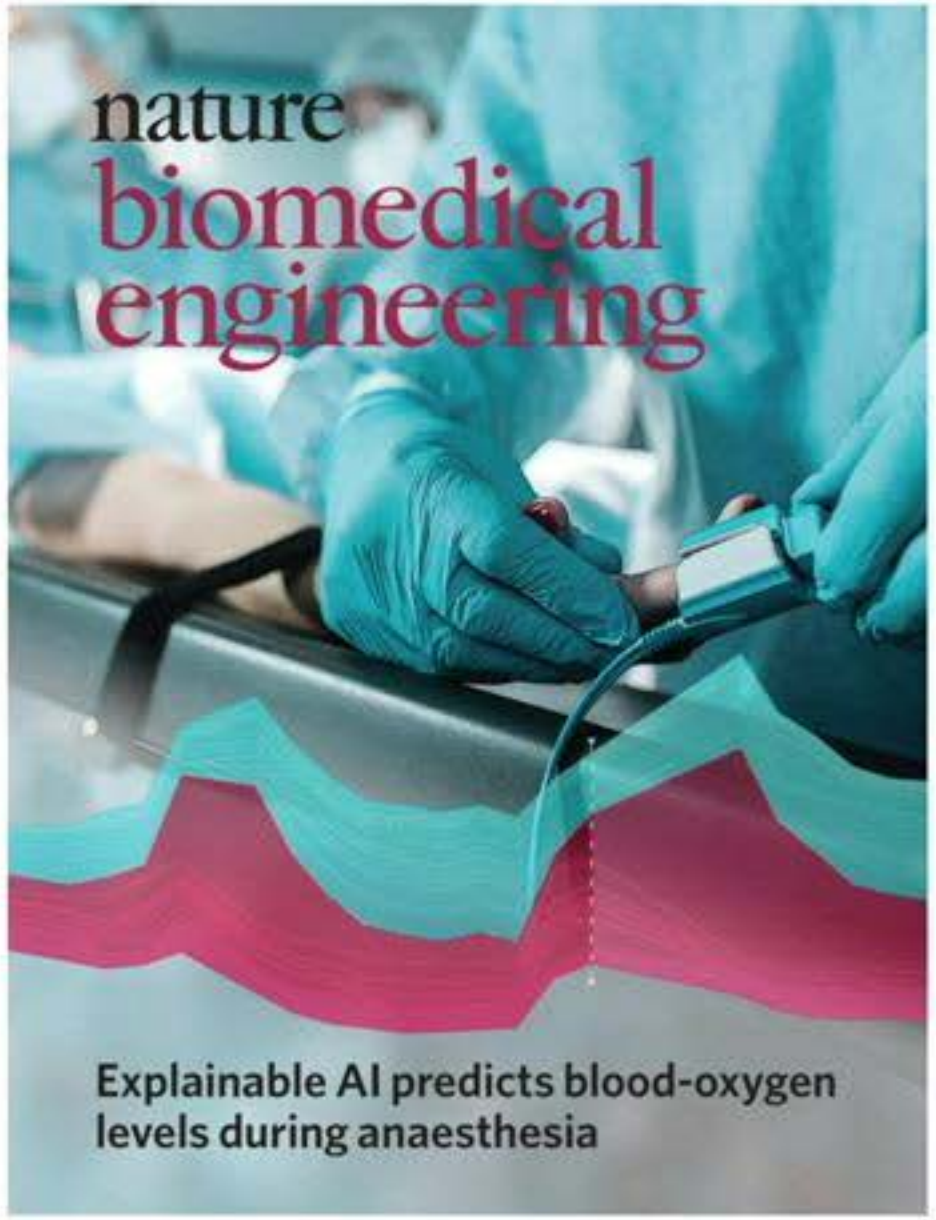




Bedside applications — **Basic science**

The operating room is a data-rich environment

- Over 200 million surgeries every year



Scott M. Lundberg, Bala Nair, Monica S. Vavilala, Mayumi Horibe, Michael J. Eisses, Trevor Adams, David E. Liston, Daniel King-Wai Low, Shu-Fang Newman, Jerry Kim, and Su-In Lee. **Explainable machine-learning predictions for the prevention of hypoxaemia during surgery.** *Nature BME* 2, 749–760 (2018) - **Featured on the Cover**

The operating room is a data-rich environment

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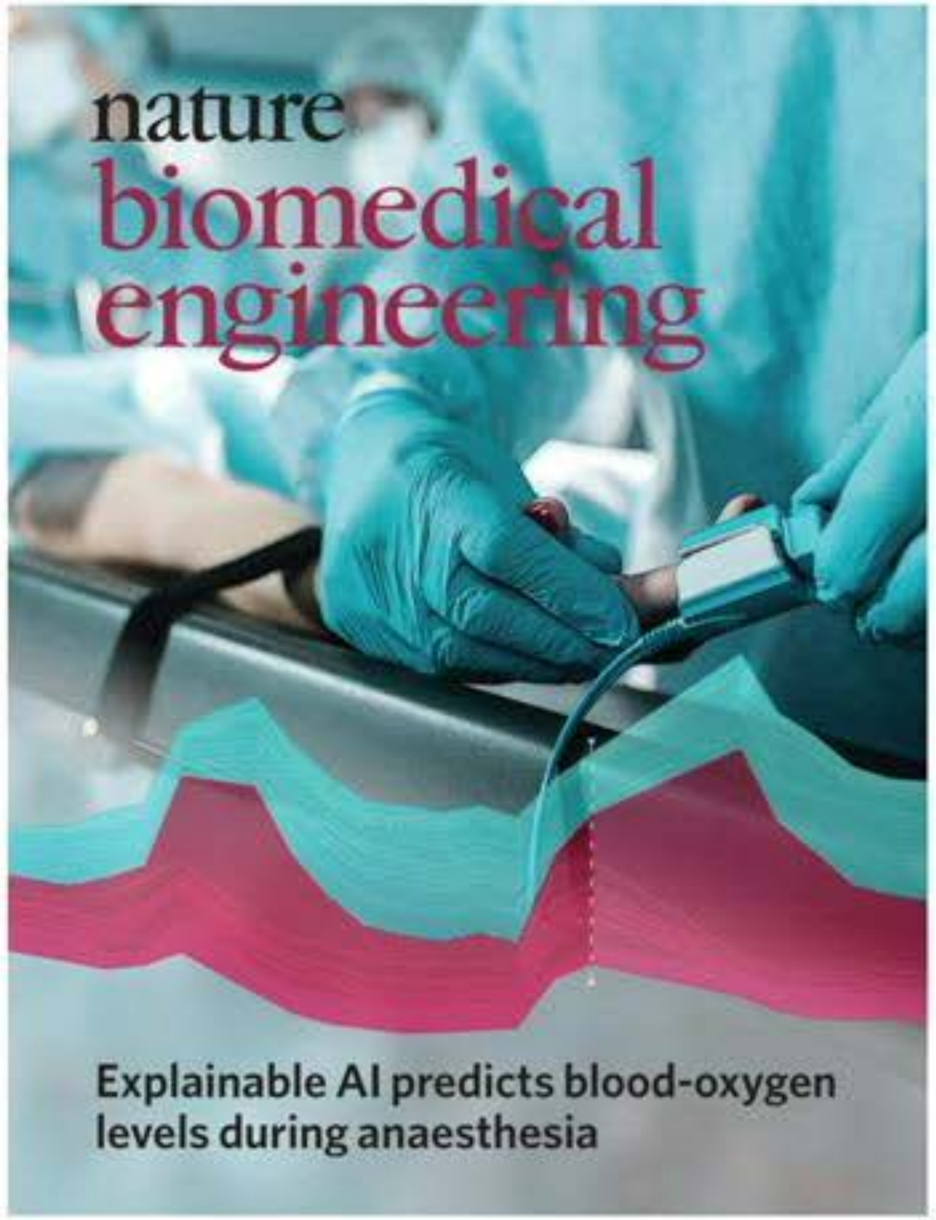
- Hypoxemia (i.e., low arterial blood oxygen tension)
  - The drop in SpO_2, i.e., arterial blood oxygen saturation as measured by pulse oximetry, to 92% or lower



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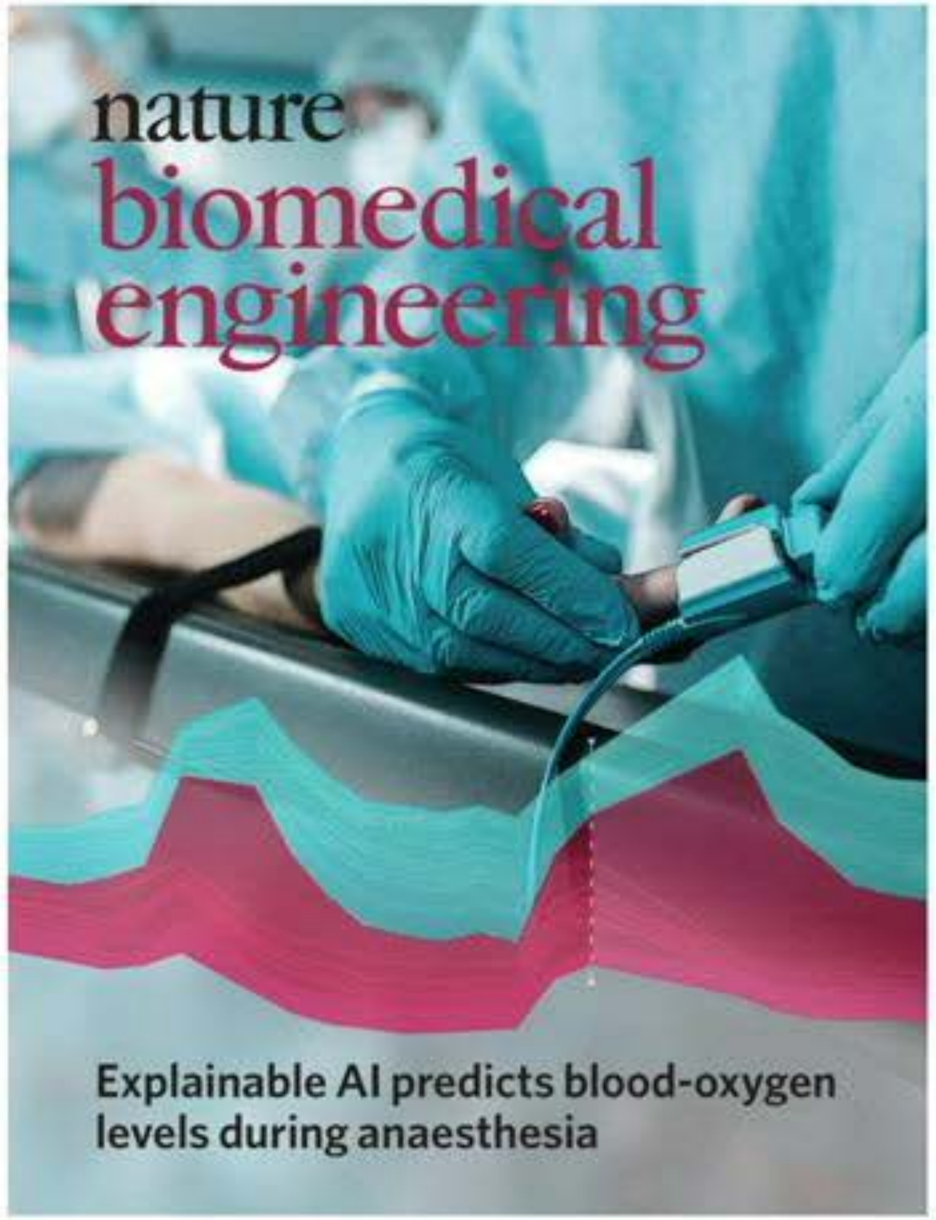

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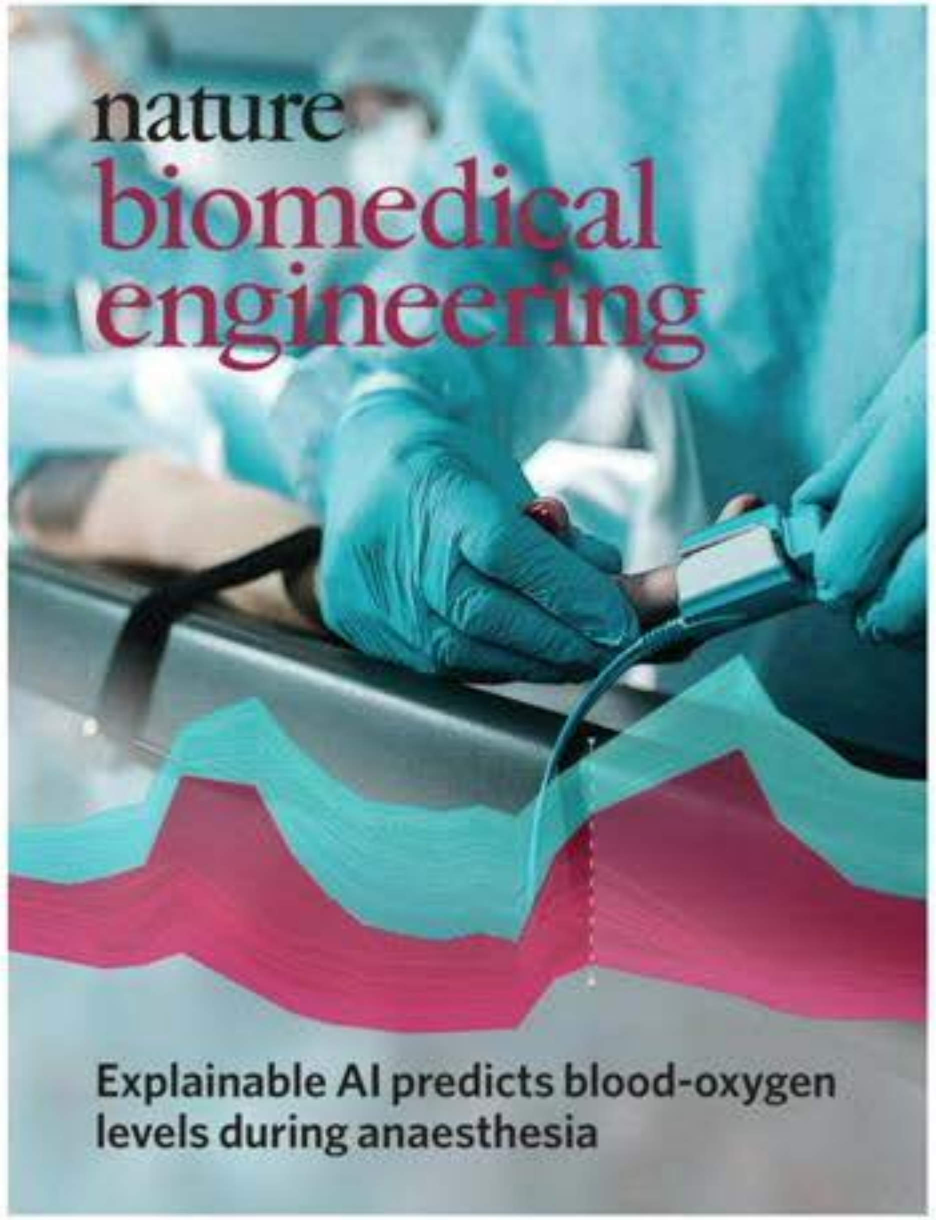
- Predicting hypoxemia events in advance would allow proactive intervention.
- We developed the *Prescience* system that can predict hypoxemia in the next 5 minutes in real time.



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Prescience predicts hypoxemia and explains why

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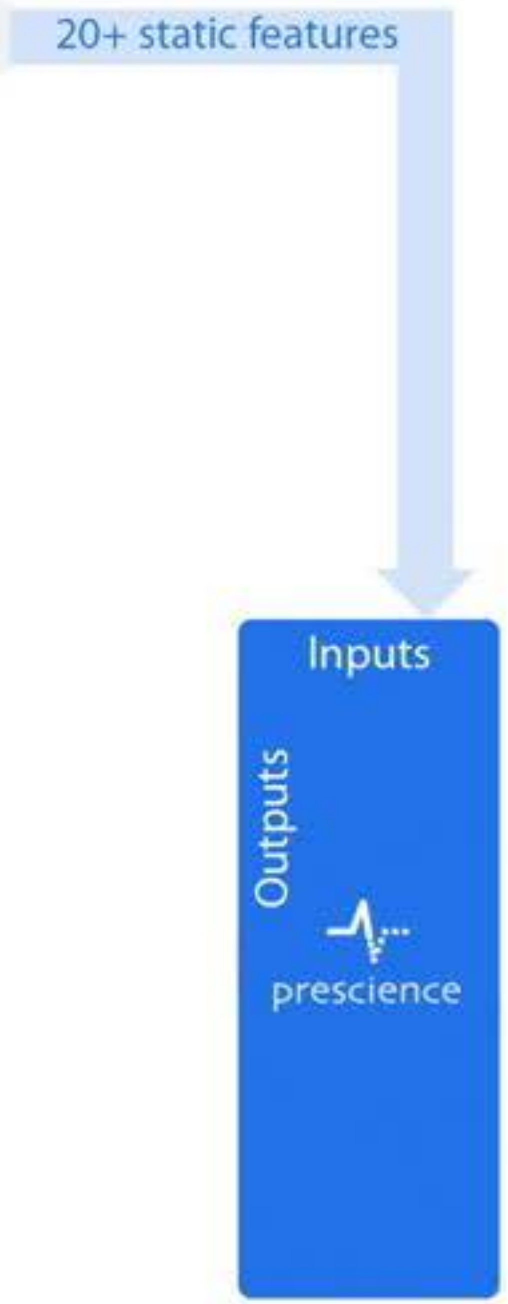
Liver cancer patient with hepatitis C   Age: 57   BMI: 34   ASA Code: III   15+ other attributes



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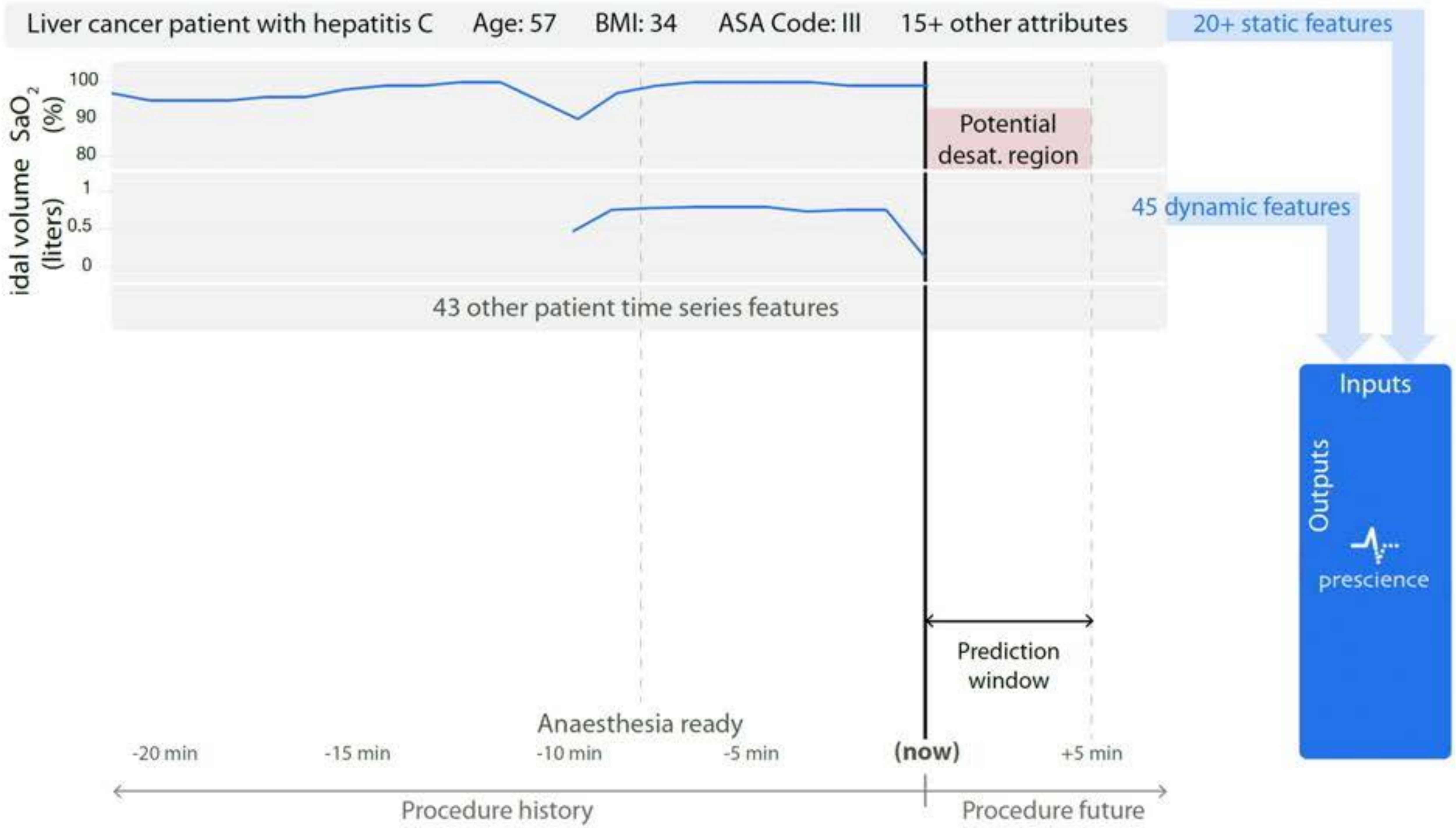

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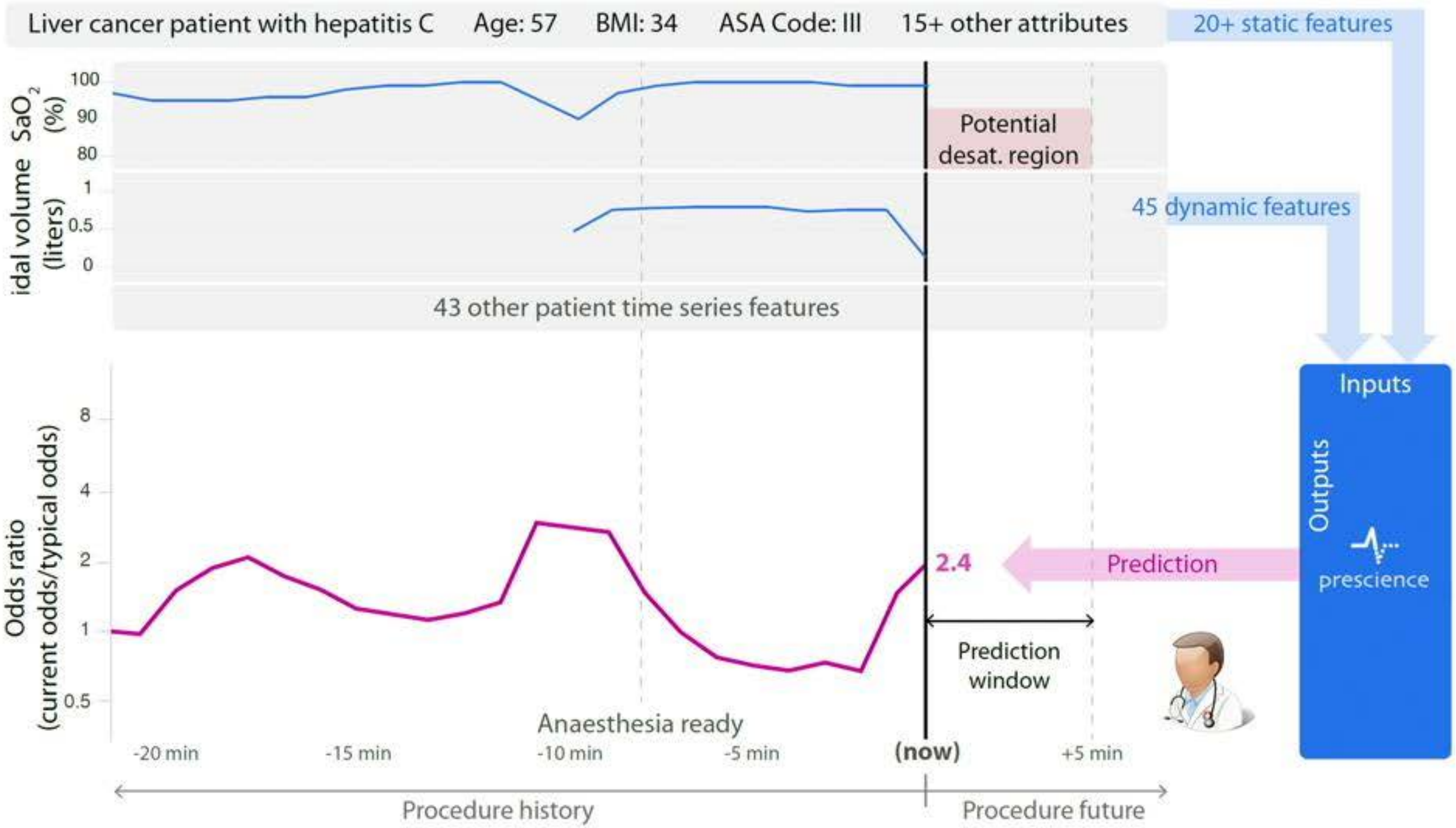

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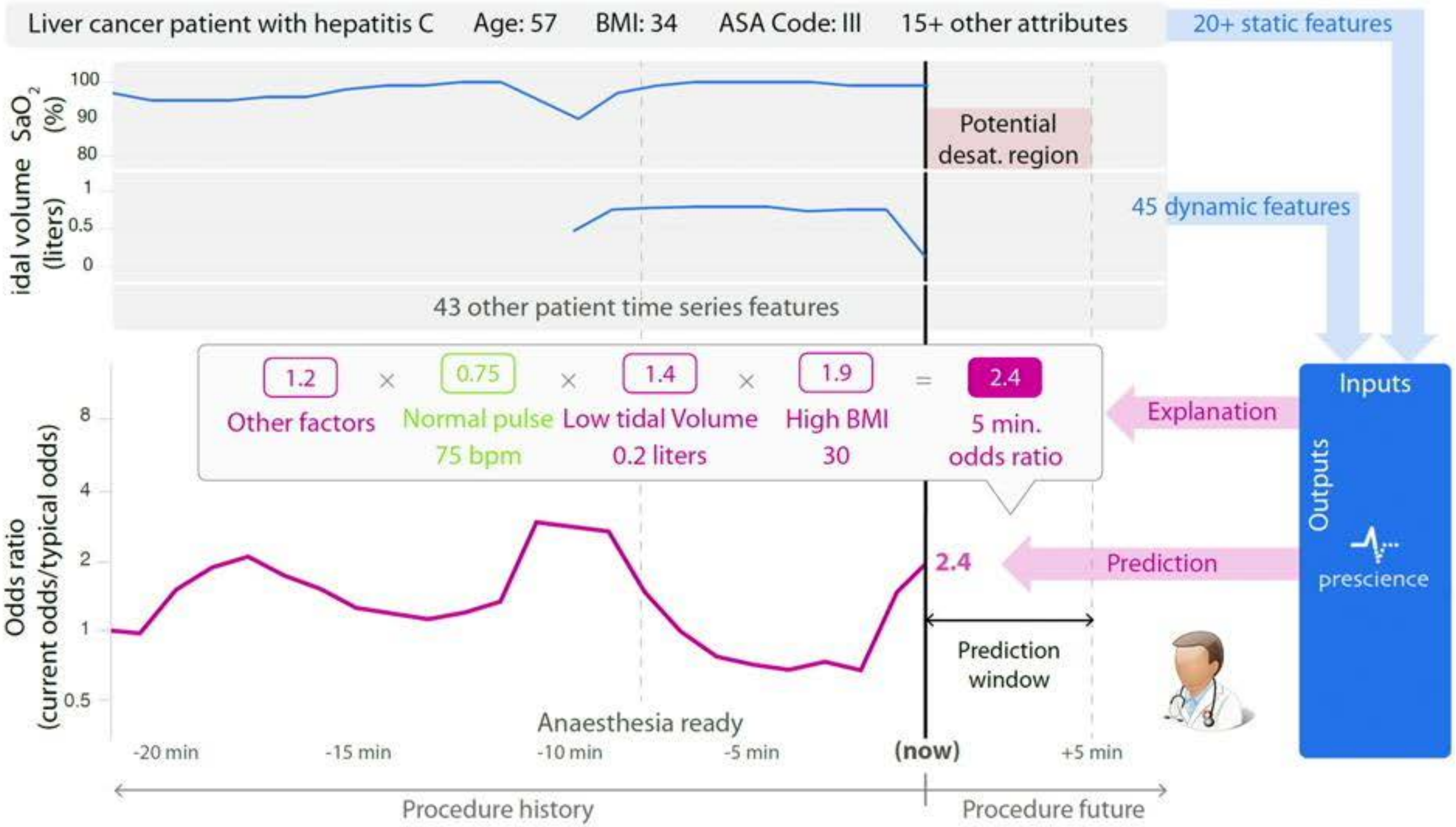

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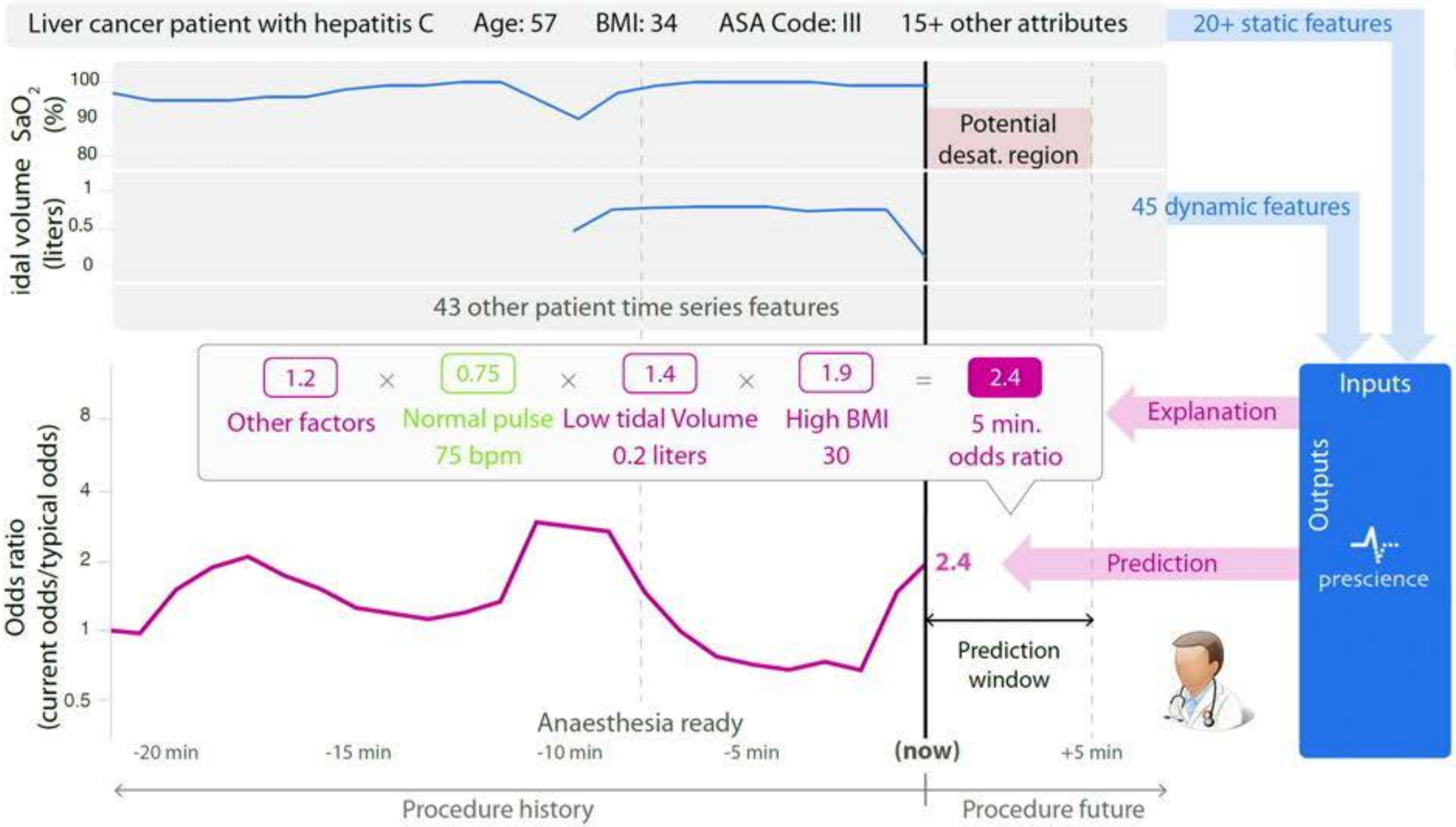


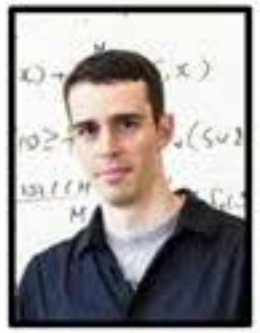
- Training data
  - Anesthesia Information Management System (AIMS) data
  - 50,000 surgeries from UW Medical Center and Harborview Medical Center

Anesthesiology & Pain Medicine

Bala Nair

Jerry Kim

Different prediction models result in different prediction performance



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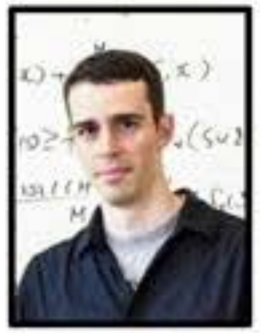

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- Receiver operating characteristic (ROC) curve from 10-fold cross validation tests.

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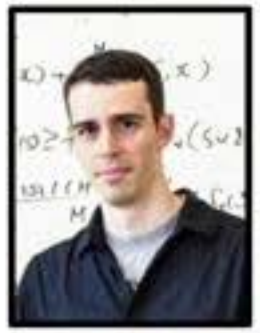

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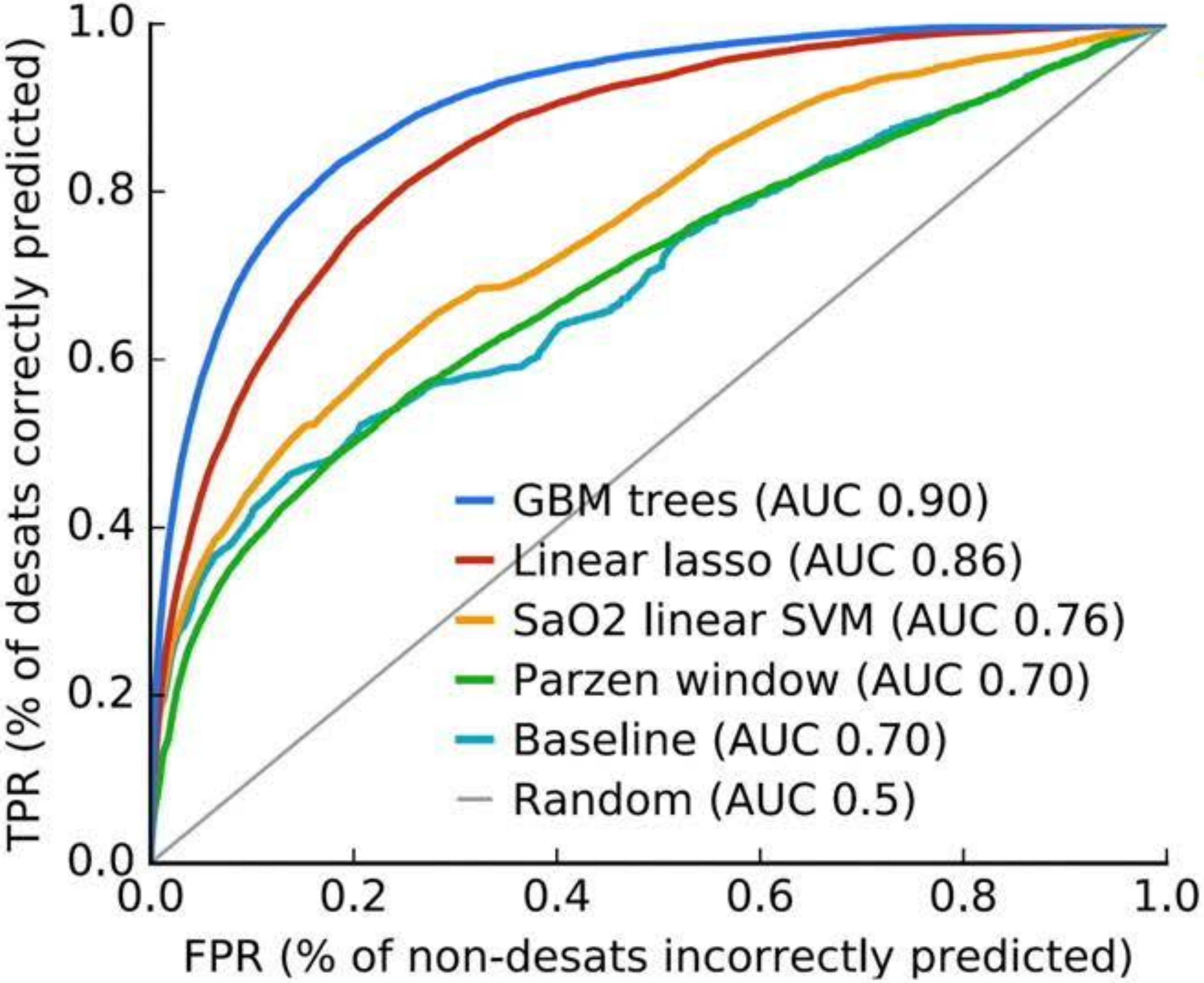

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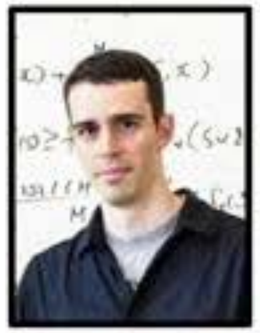
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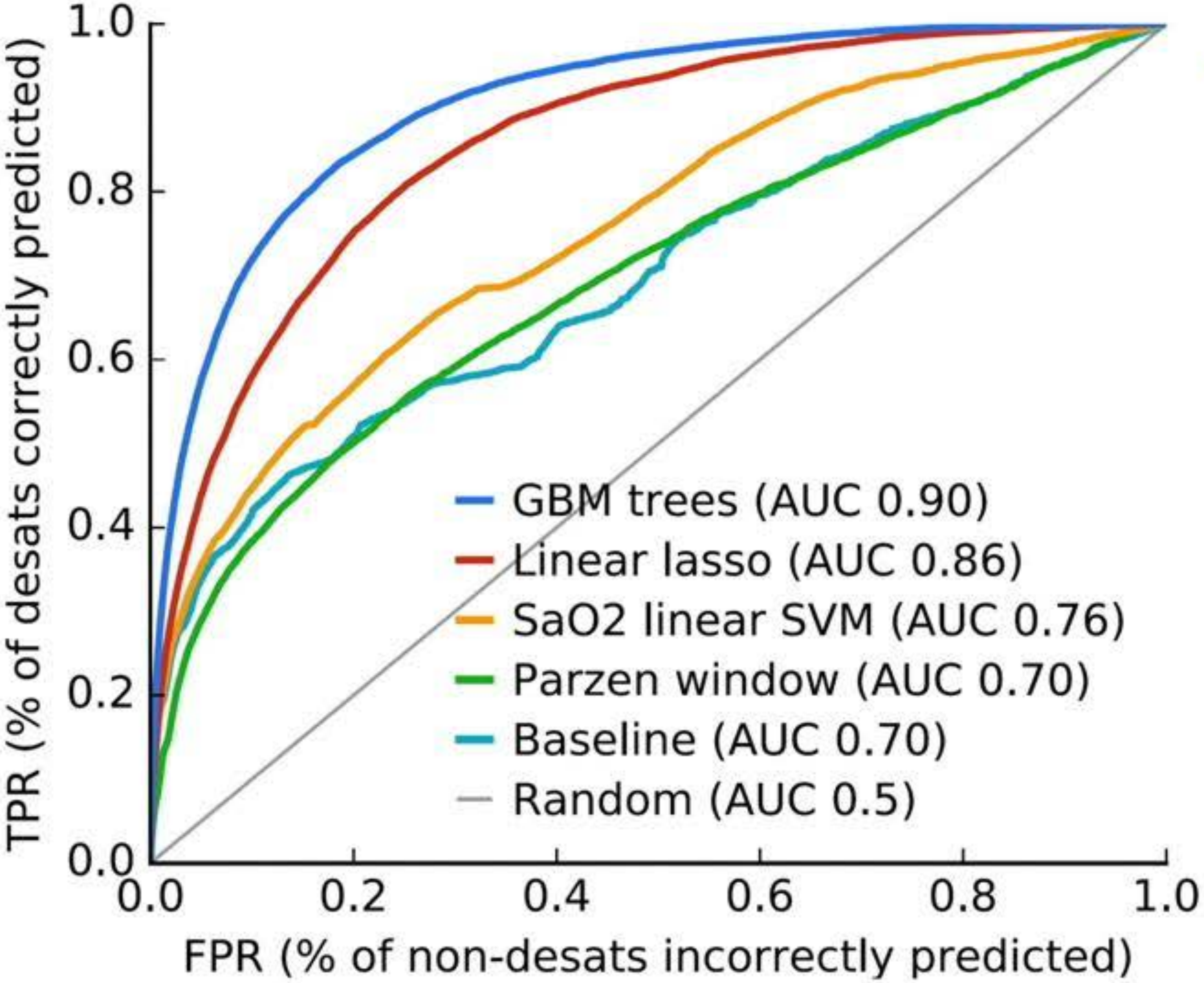

- Receiver operating characteristic (ROC) curve from 10-fold cross validation tests.
  - Simple vs. complex models

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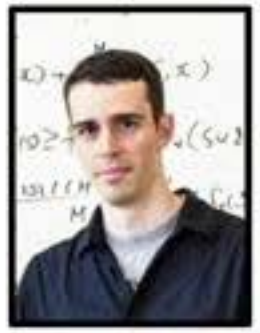

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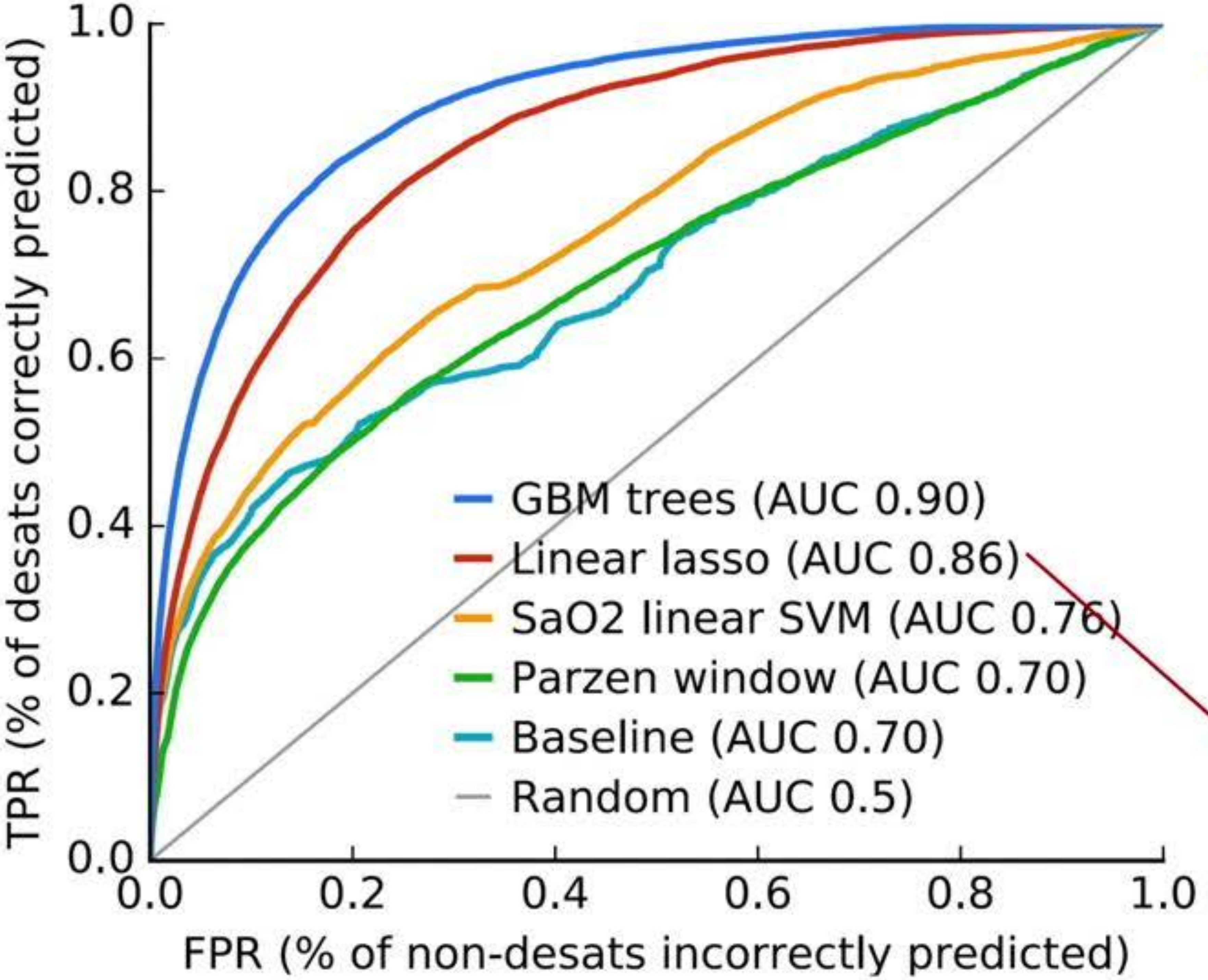

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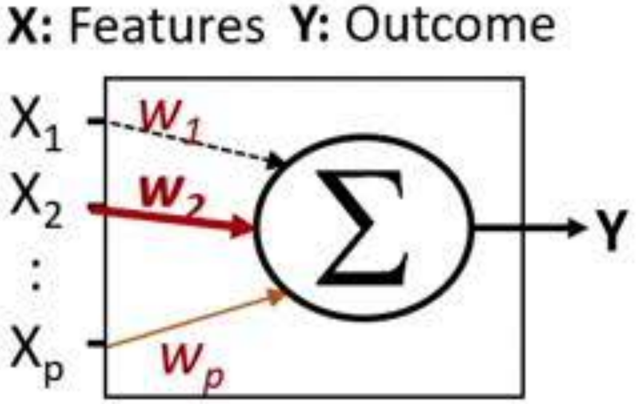
Generalized linear model



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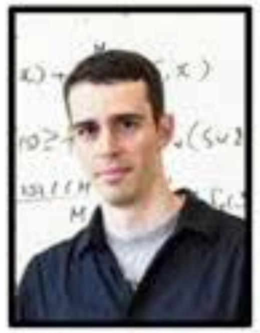

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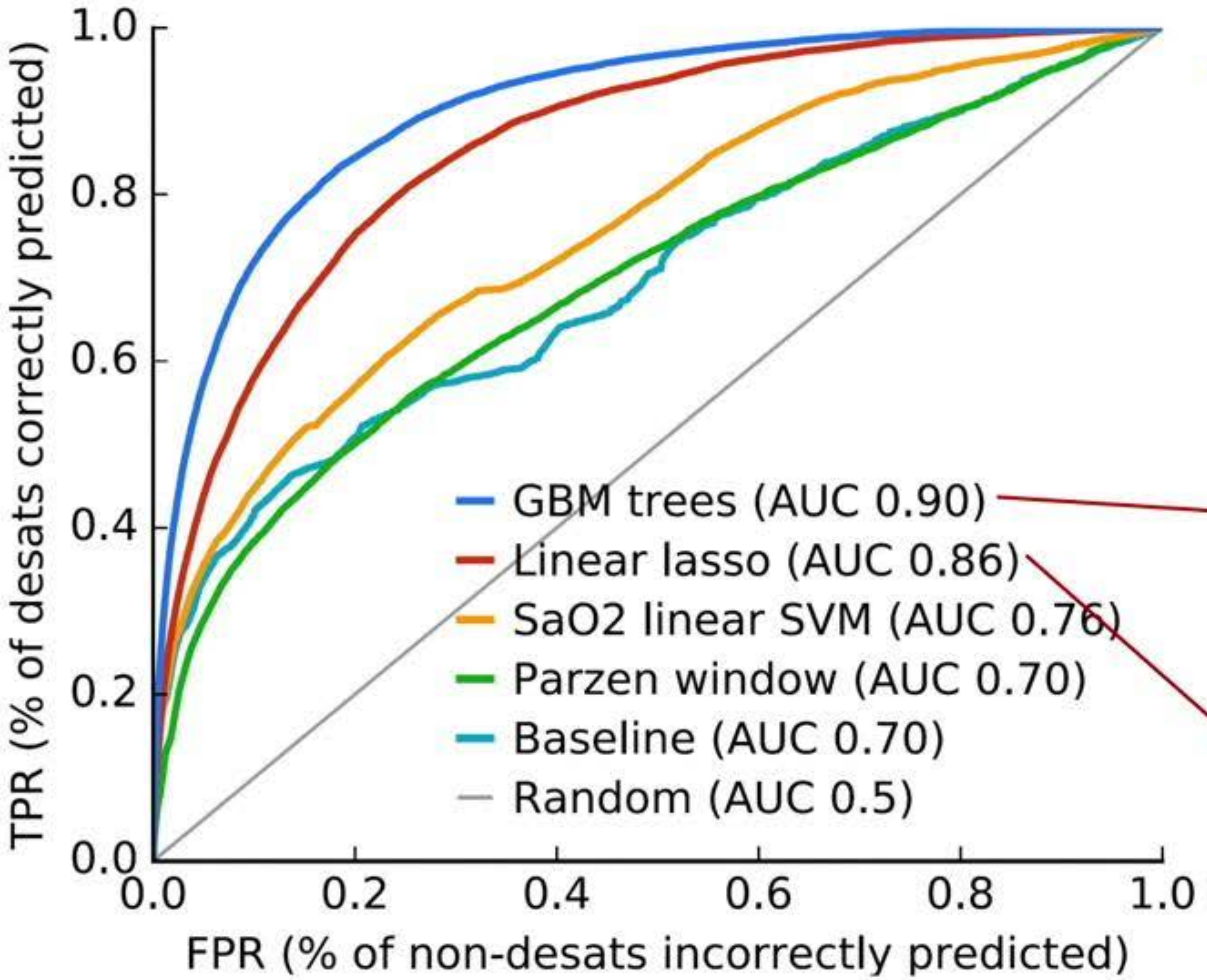

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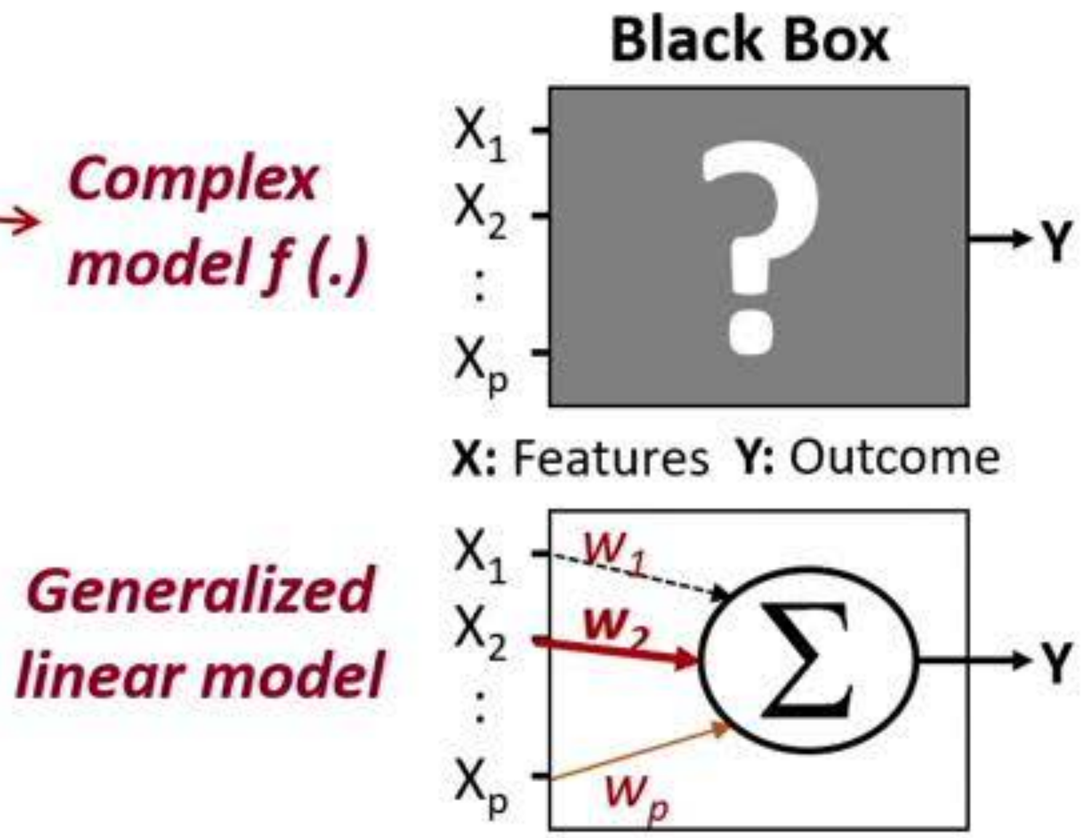

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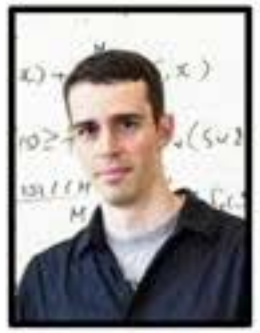

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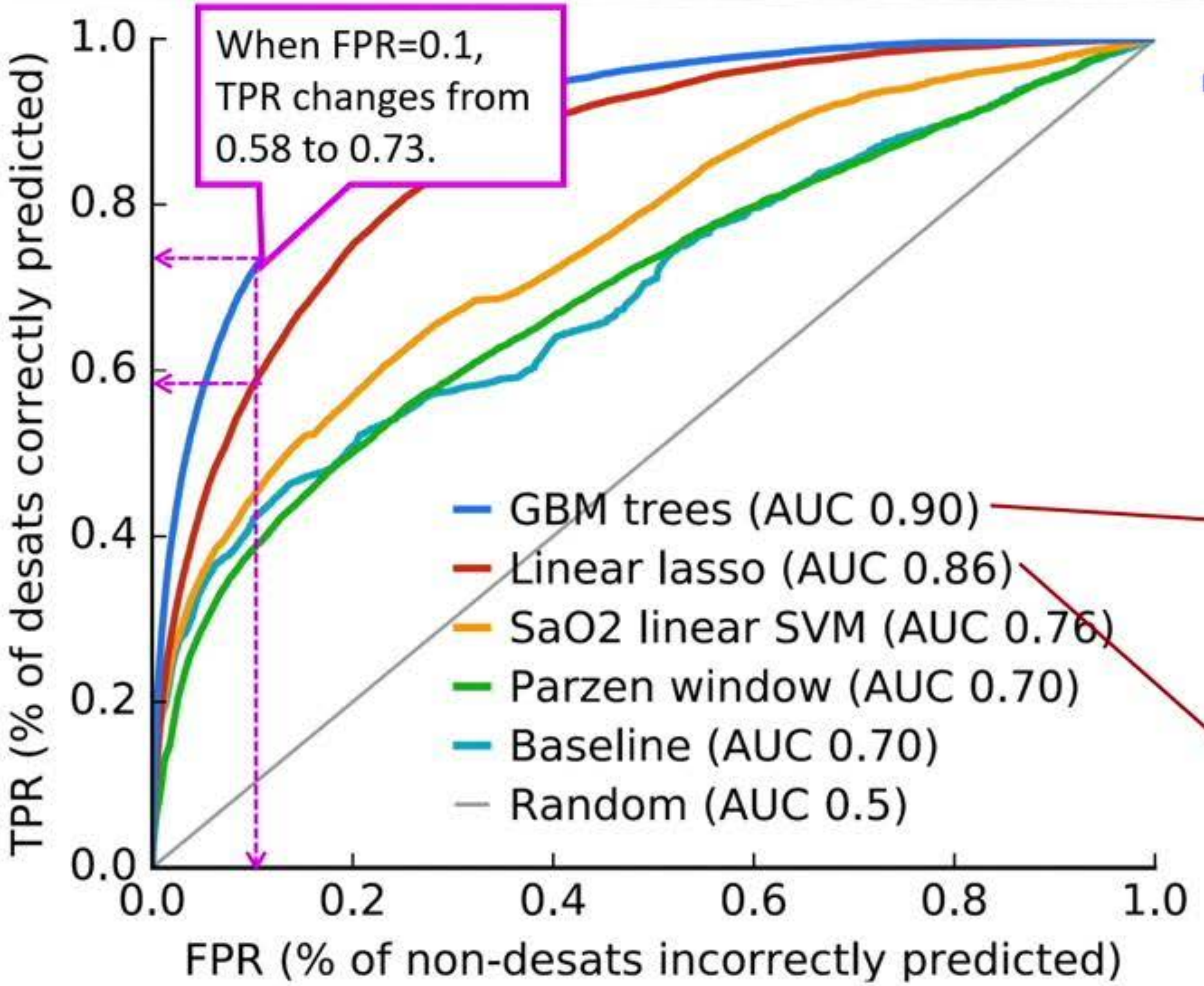

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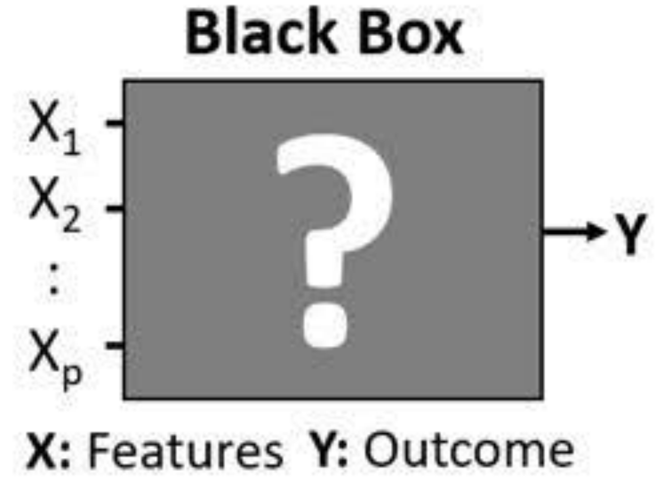
Complex model f (.)



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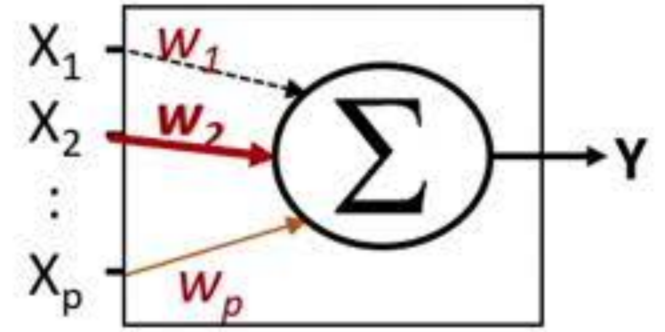
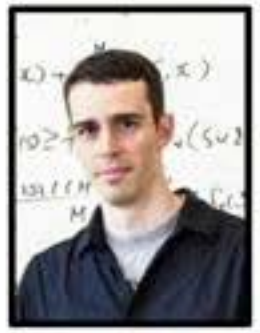


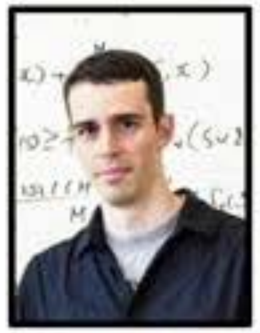
Our solution is to make a prediction with explanations


Scott

- Accuracy vs. interpretability

Scott Lundberg and Su-In Lee. **A Unified Approach to Interpreting Model Predictions**. *NeurIPS (Dec, 2017)* **Oral presentation (top 1%); cited >100 times in 2018;** *NeurIPS workshop on Interpretable ML (2016)* – **Best paper award**

Our solution is to make a prediction with explanations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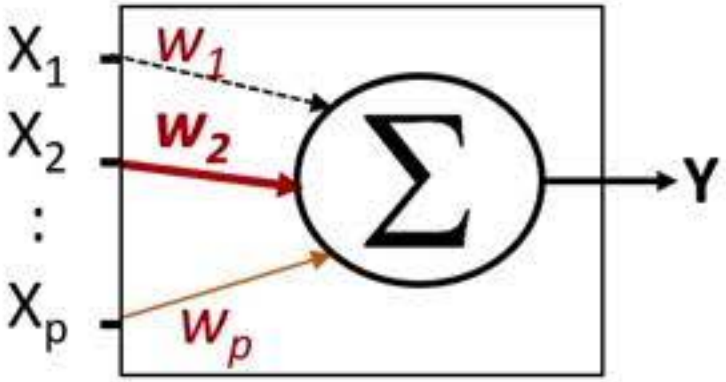
- Accuracy vs. interpretability
  - Simple models often lead to lower performance.

Linear model

X: Features **Y:** Outcome



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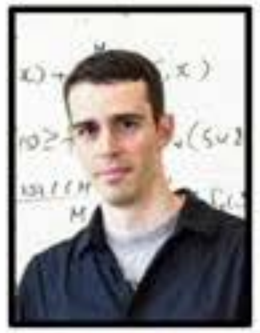

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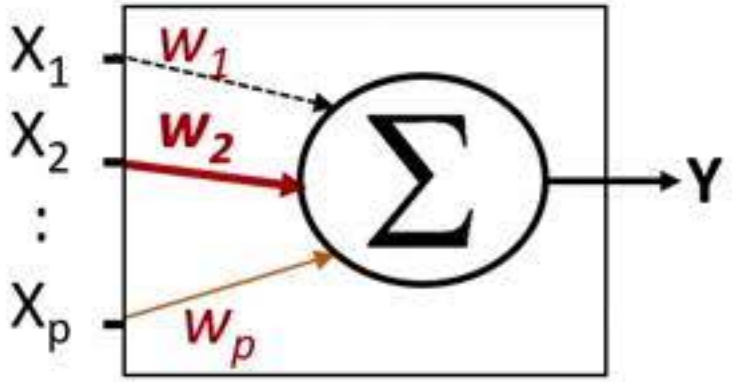

Complex model f (.)

Black Box

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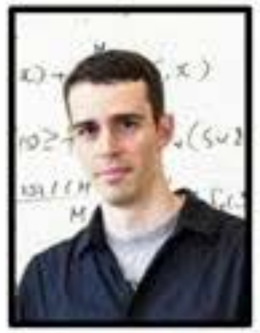

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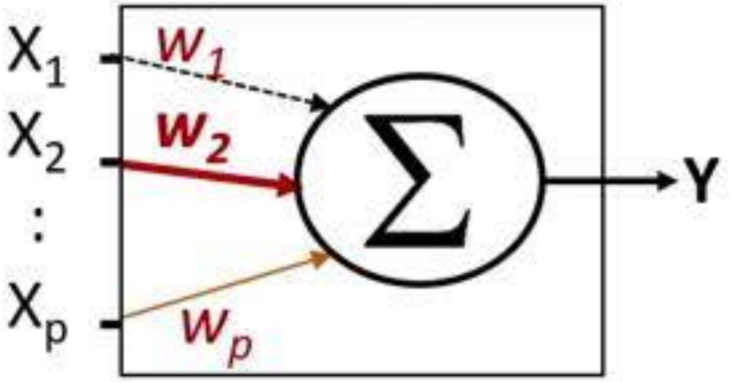
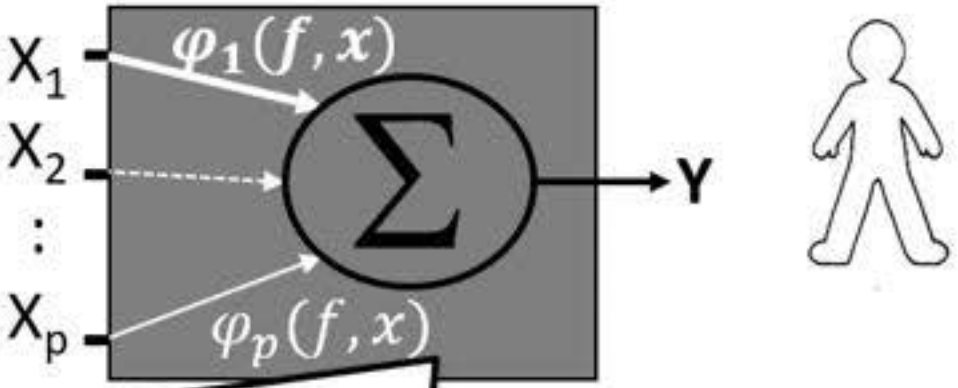


Complex model f (.)

Black Box

Our approach, SHAP

For a particular prediction



- SHAP can estimate feature importance for a particular prediction for any model.

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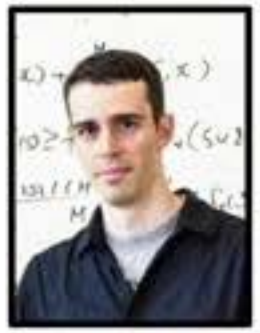


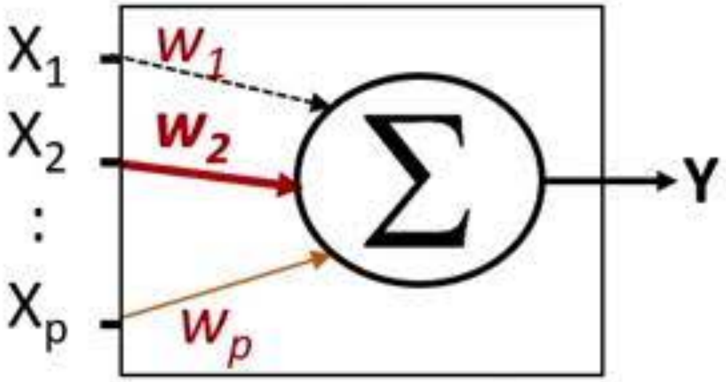
Scott

Eliminating the accuracy vs. interpretability tradeoff
⇨ Broader applicability of ML to medicine

- Accuracy vs. interpretability
  - Simple models often lead to lower performance.
  - Complex models are often considered to be a black box.

Linear model

X: Features **Y:** Outcome



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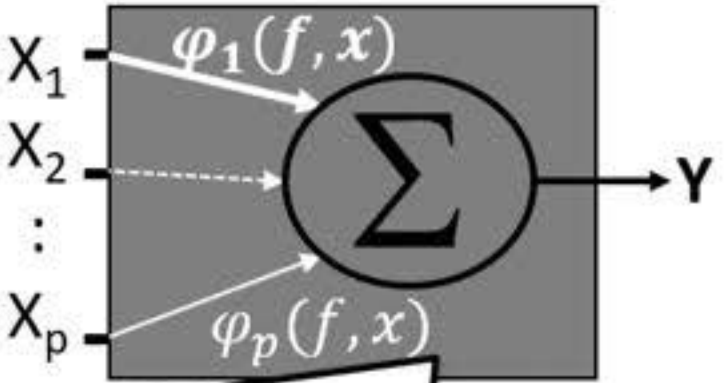

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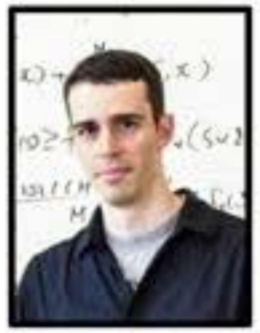
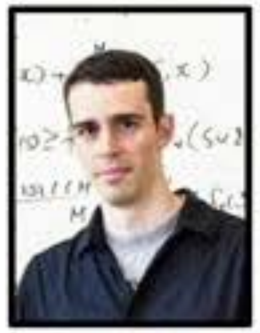
How exactly can we estimate feature importance? – SHapley Additive exPlanation (SHAP) values



Scott

John, a bank customer

How exactly can we estimate feature importance?
– SHapley Additive exPlanation (SHAP) values



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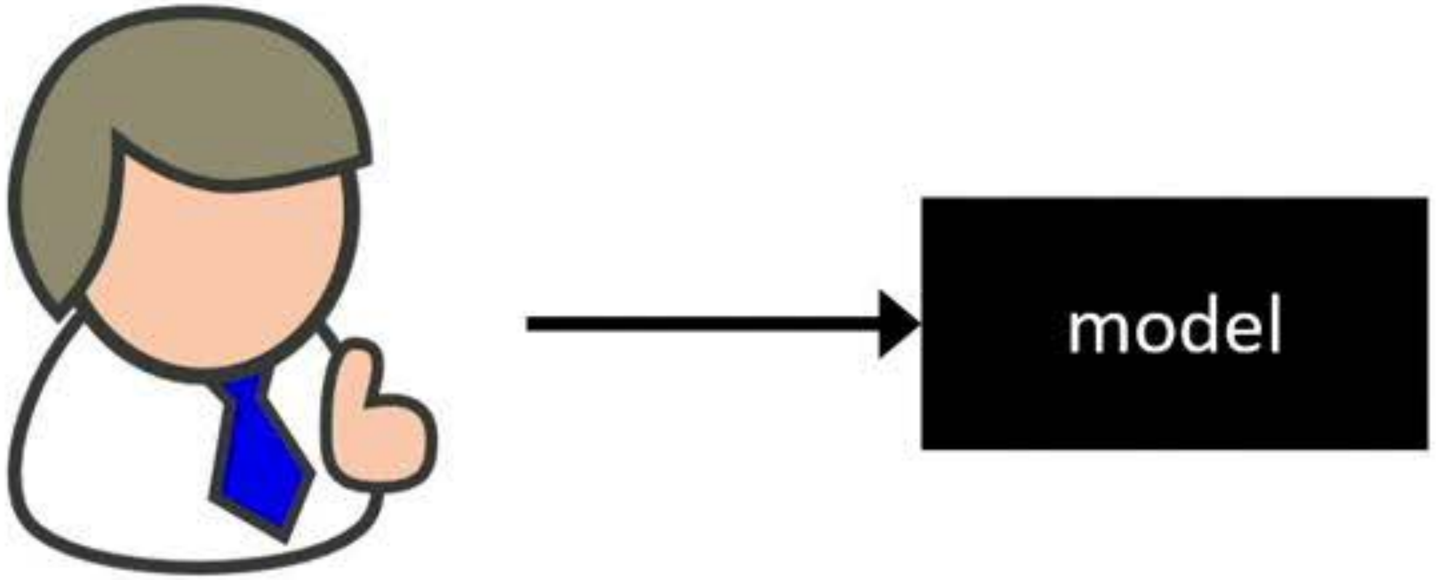

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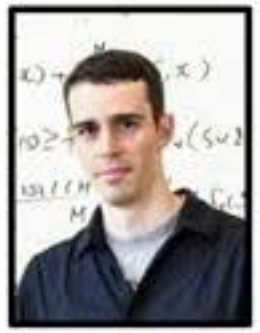

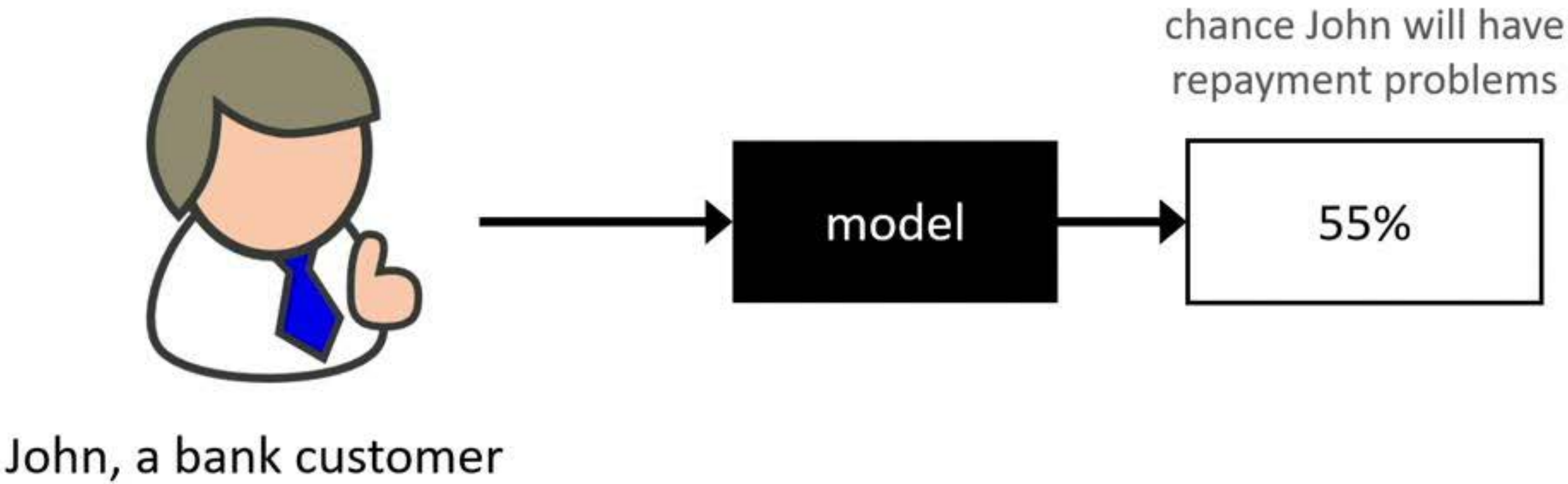

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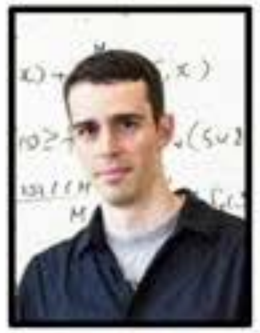

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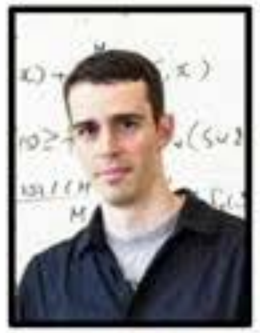
John, a bank customer

→ model → 55%

chance John will have repayment problems

No loan

How exactly can we estimate feature importance? – SHapley Additive exPlanation (SHAP) values



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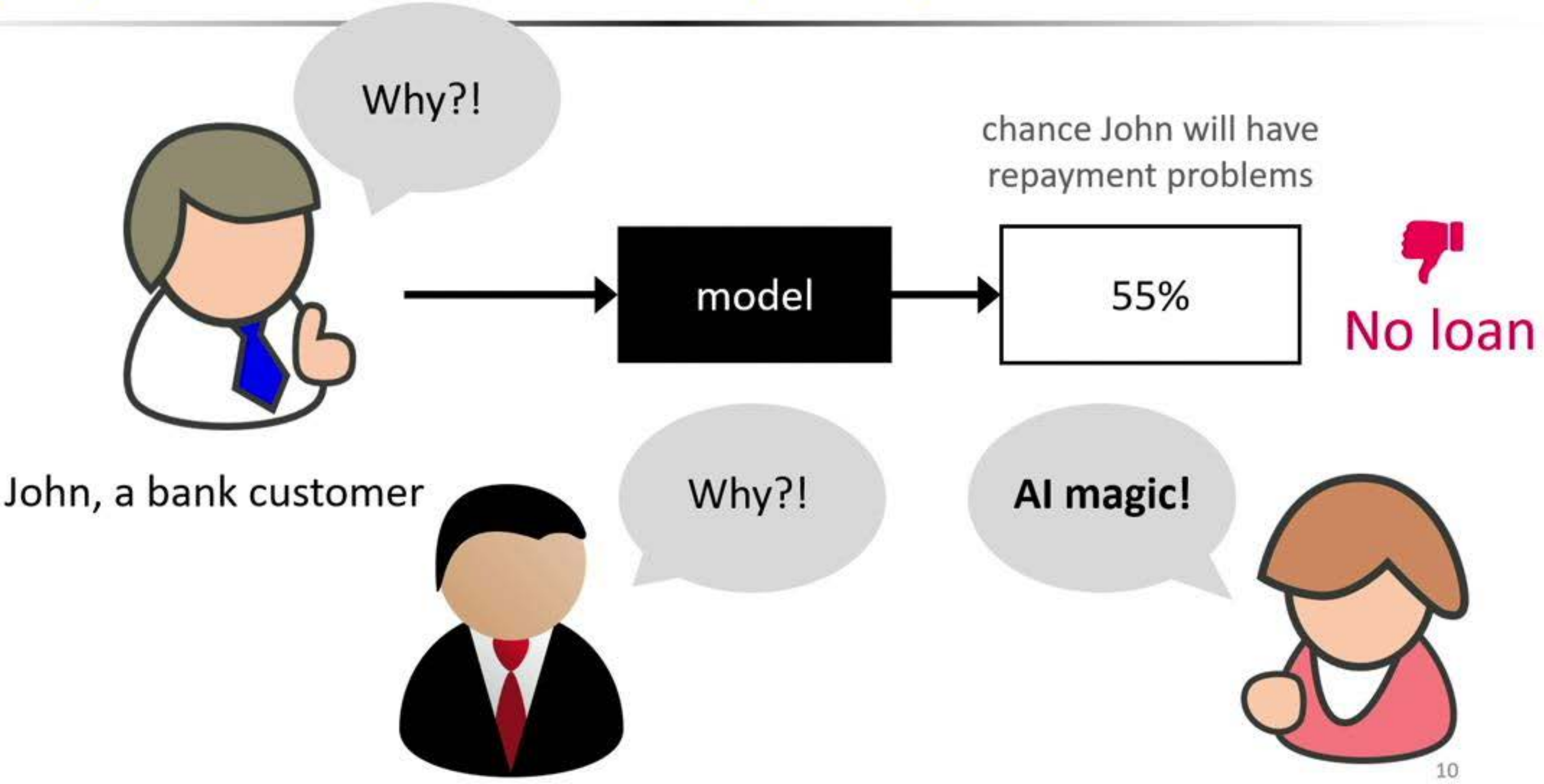

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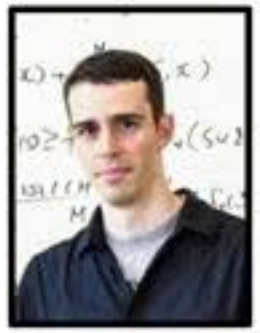

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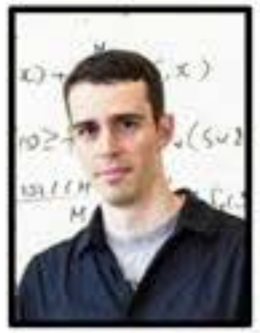
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Base rate

20%

0 $E[f(x)]$

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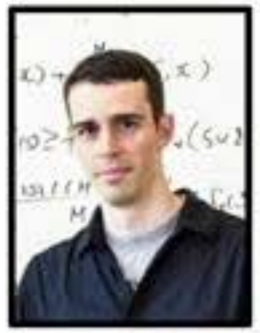


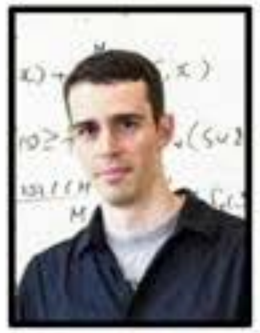
Scott

Base rate — 20% — $E[f(x)]$

Prediction for John — 55% — $f(x)$

$0 \qquad E[f(x)] \qquad f(x)$

How exactly can we estimate feature importance? — SHapley Additive exPlanation (SHAP) values



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Base rate

20%

$E[f(x)]$

Prediction for John

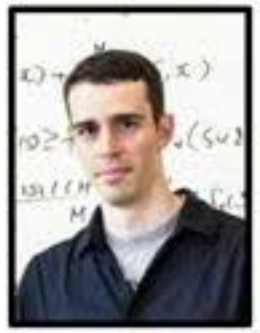
55%

$f(x)$

0

How did we get here?

How exactly can we estimate feature importance? — SHapley Additive exPlanation (SHAP) values



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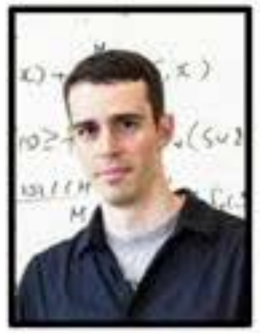

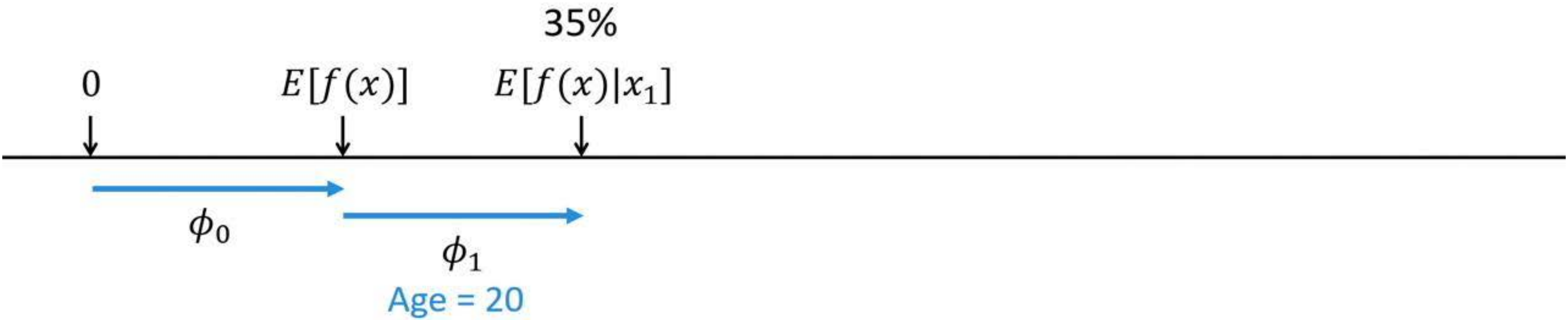

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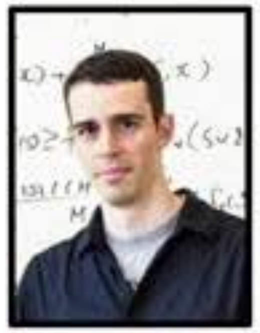

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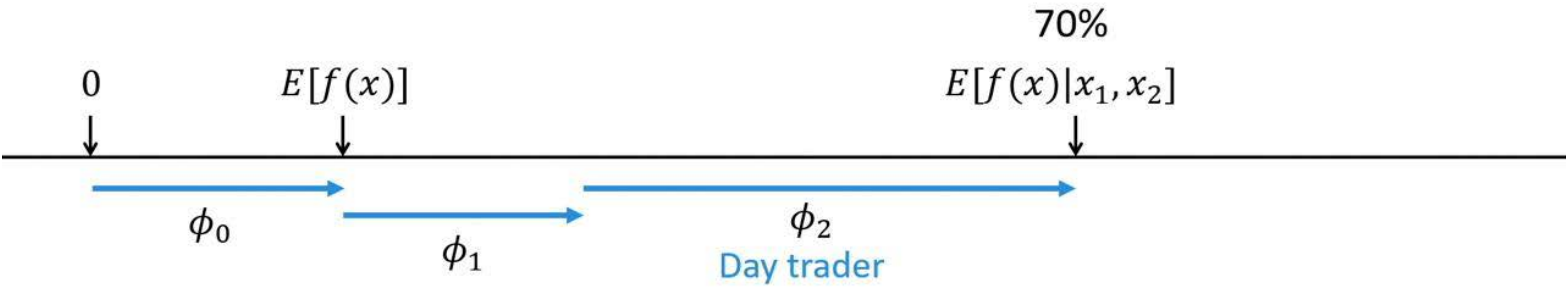

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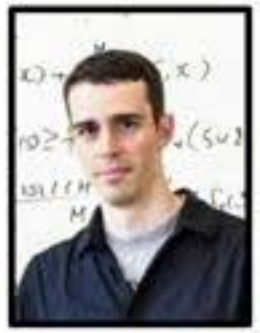

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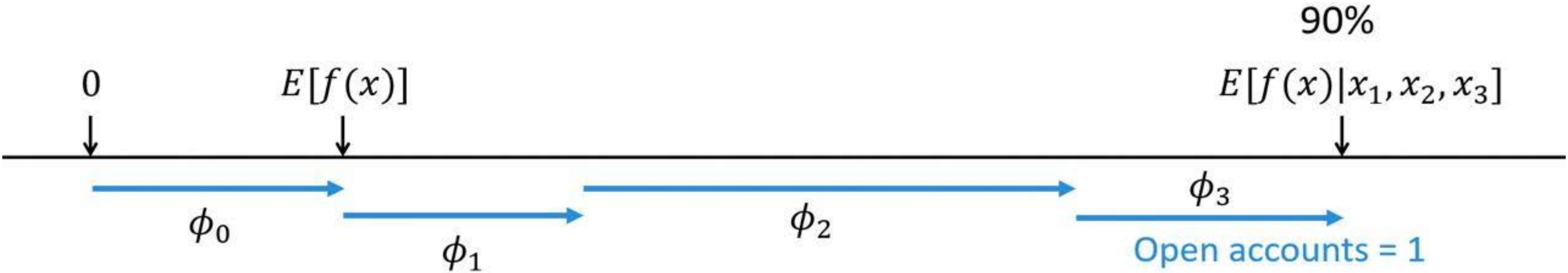

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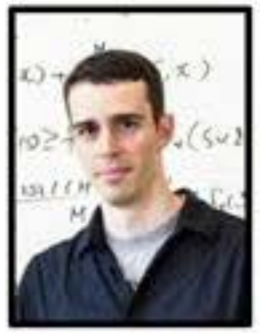

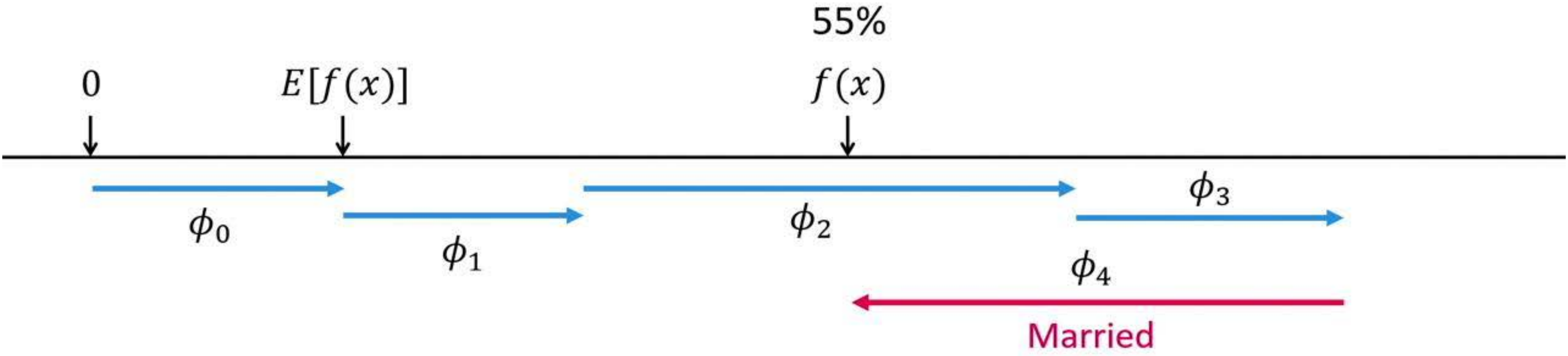

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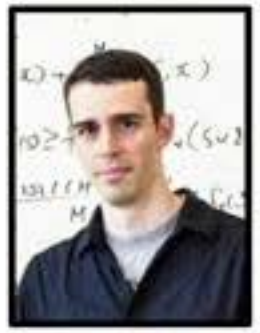
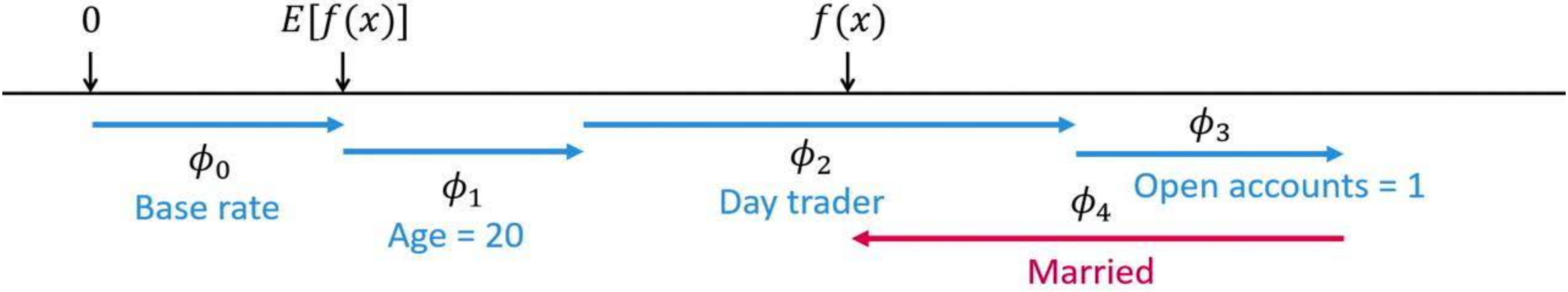


Scott

The order matters!



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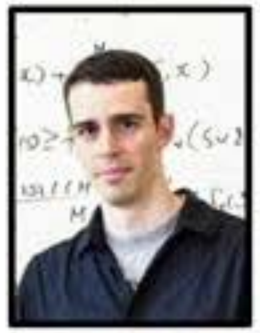

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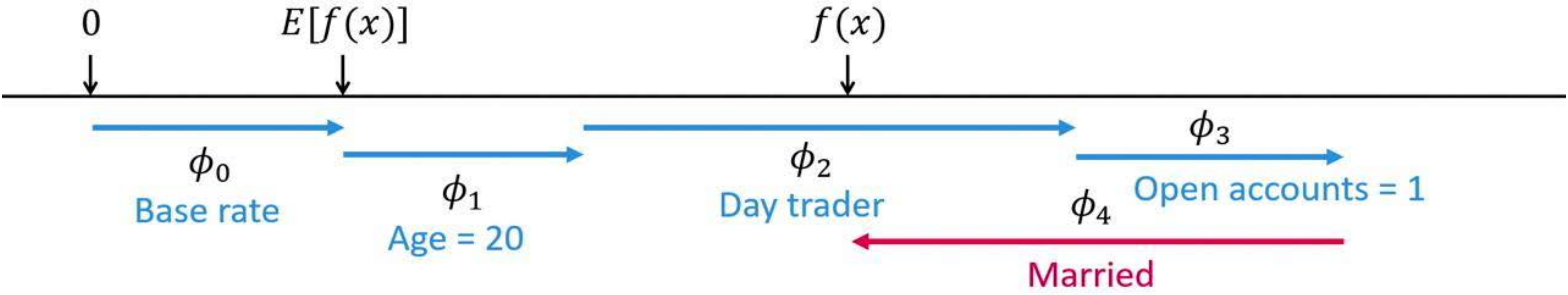
The order matters!

SHAP values result from averaging over all N! possible orderings



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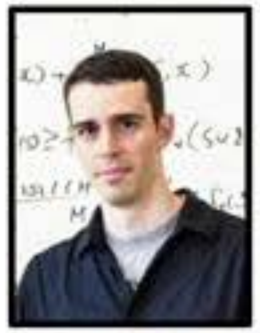
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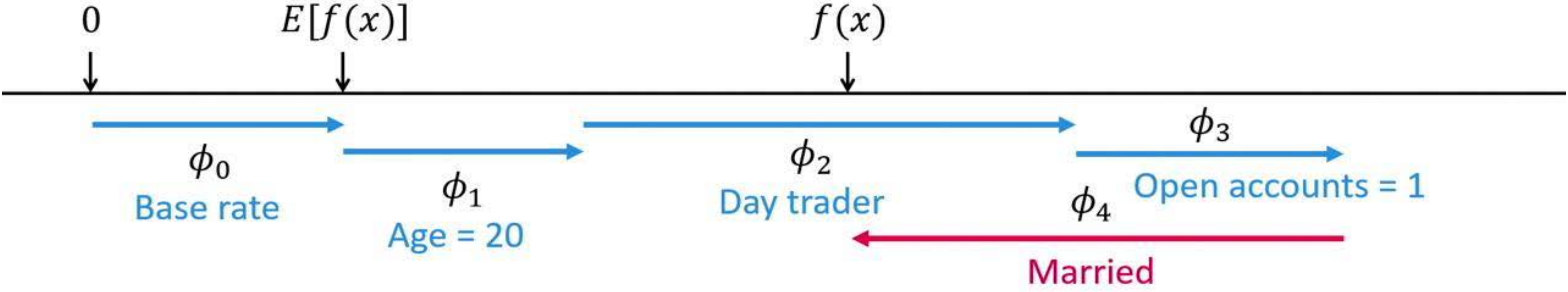
They are the only solution that satisfies three important properties



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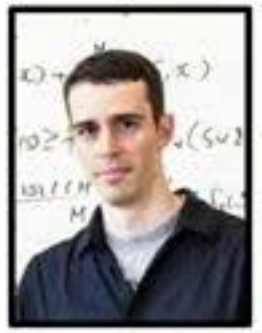

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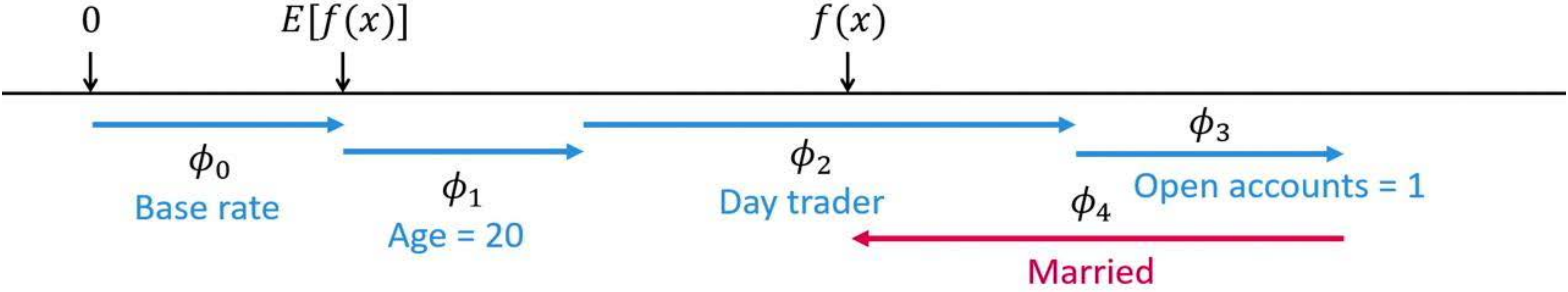
We need to develop efficient methods to estimate or compute exact SHAP values.



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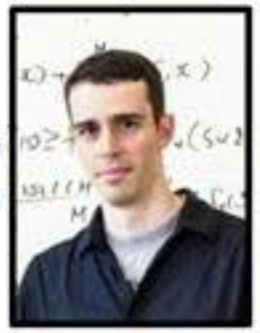
Prescience efficiently computes SHAP values on a predict made on a single time point for a particular patient.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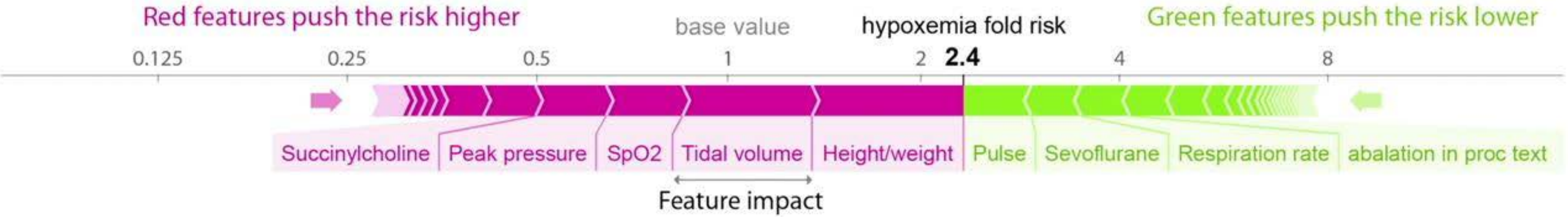

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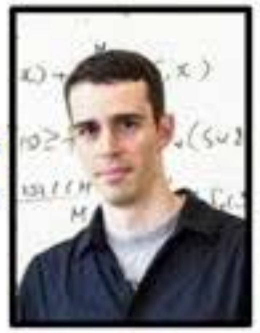

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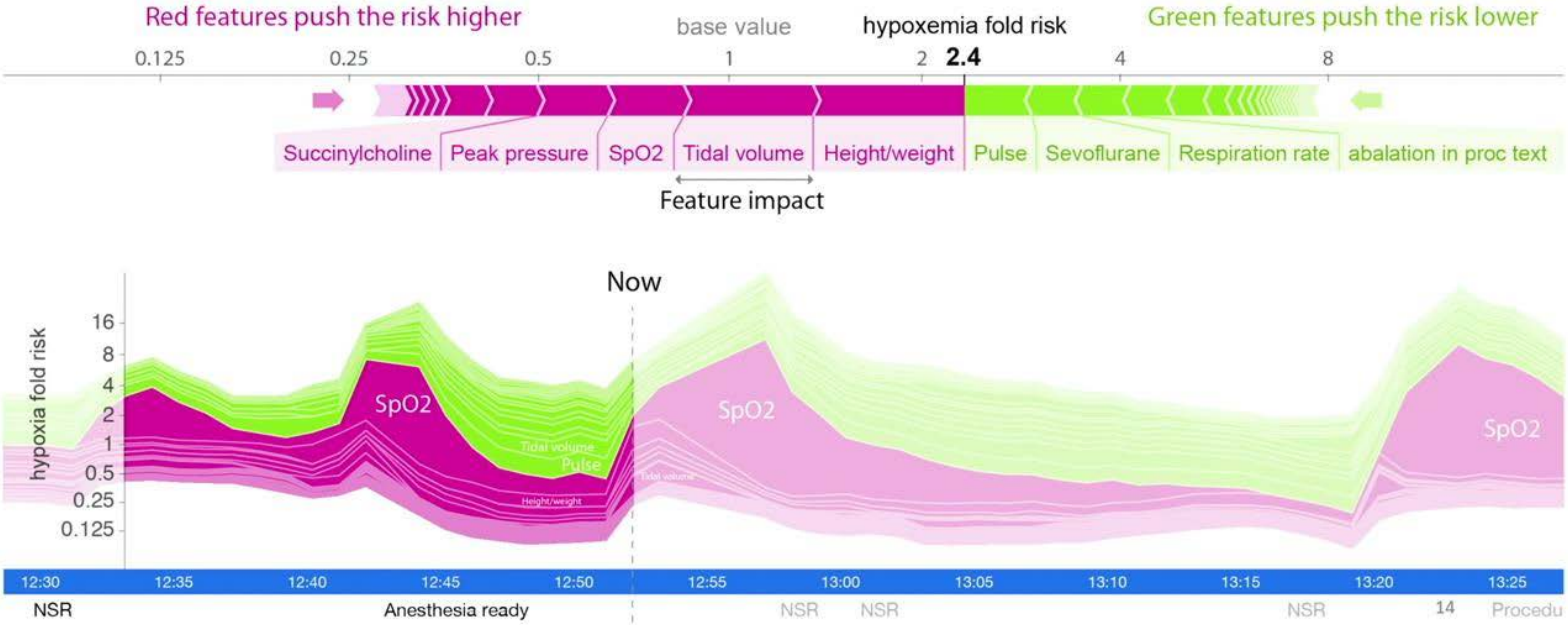
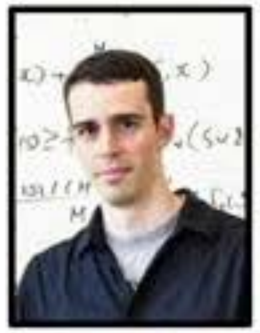


Prescience improves anesthesiologist's ability to predict hypoxemia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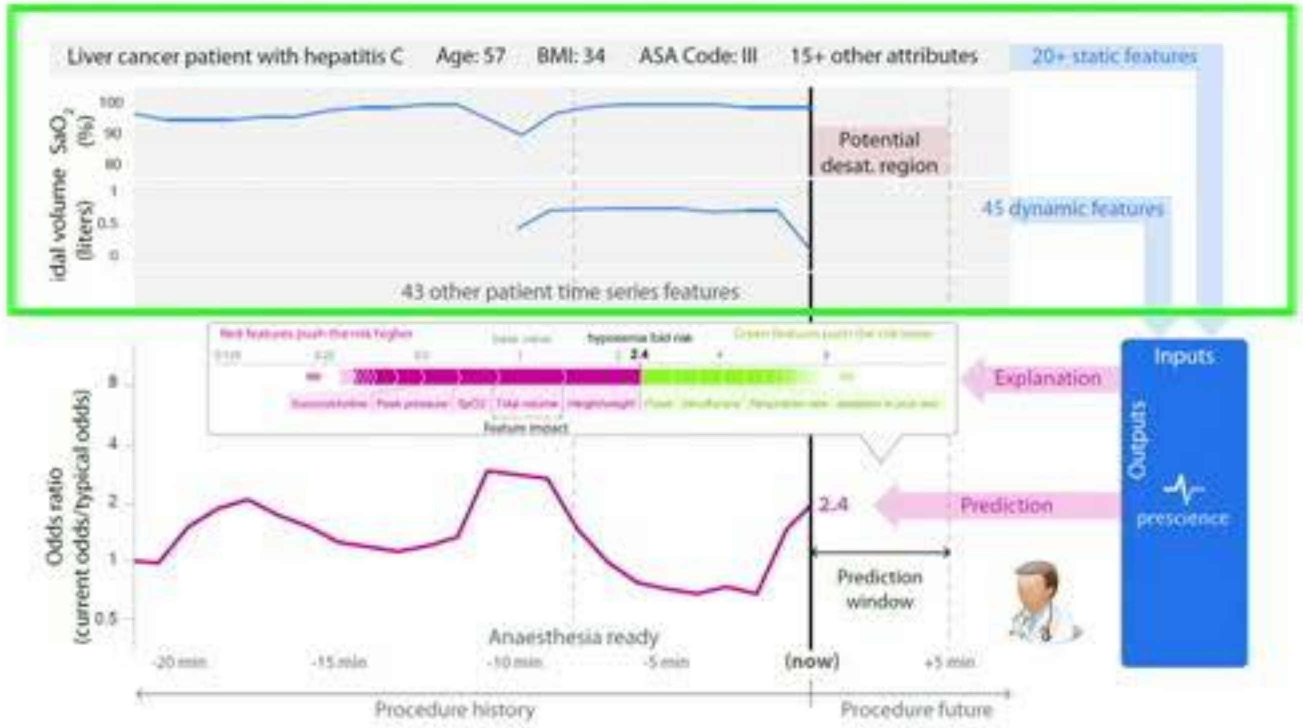
- We replayed prerecorded surgery data in a web-based visualization to 5 anesthesiologists.



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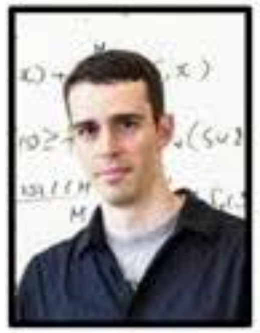

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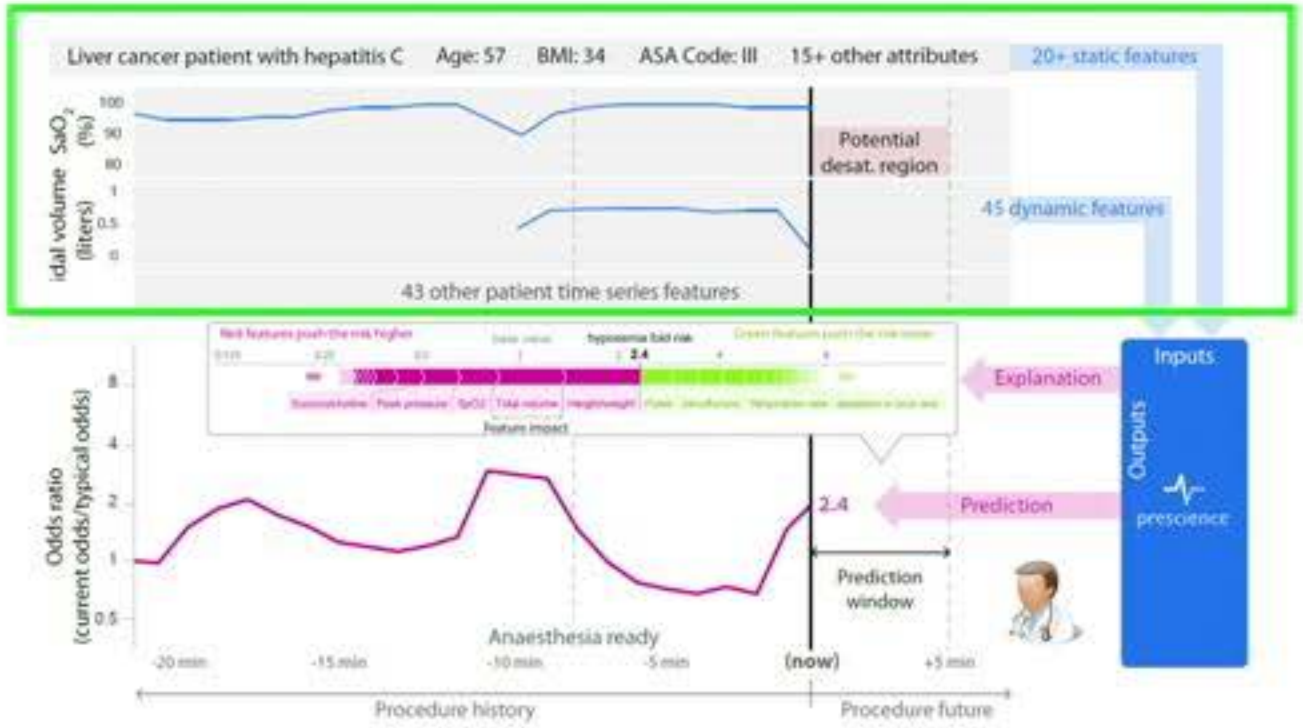
- We replayed prerecorded surgery data in a web-based visualization to 5 anesthesiologists.
- Each anesthesiologist provided a relative risk of hypoxemia for ~270 cases **without** or **with** the aid of Prescience.



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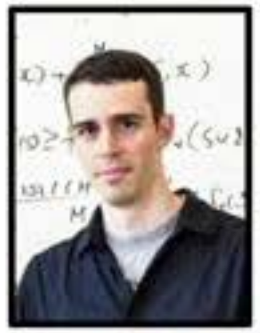

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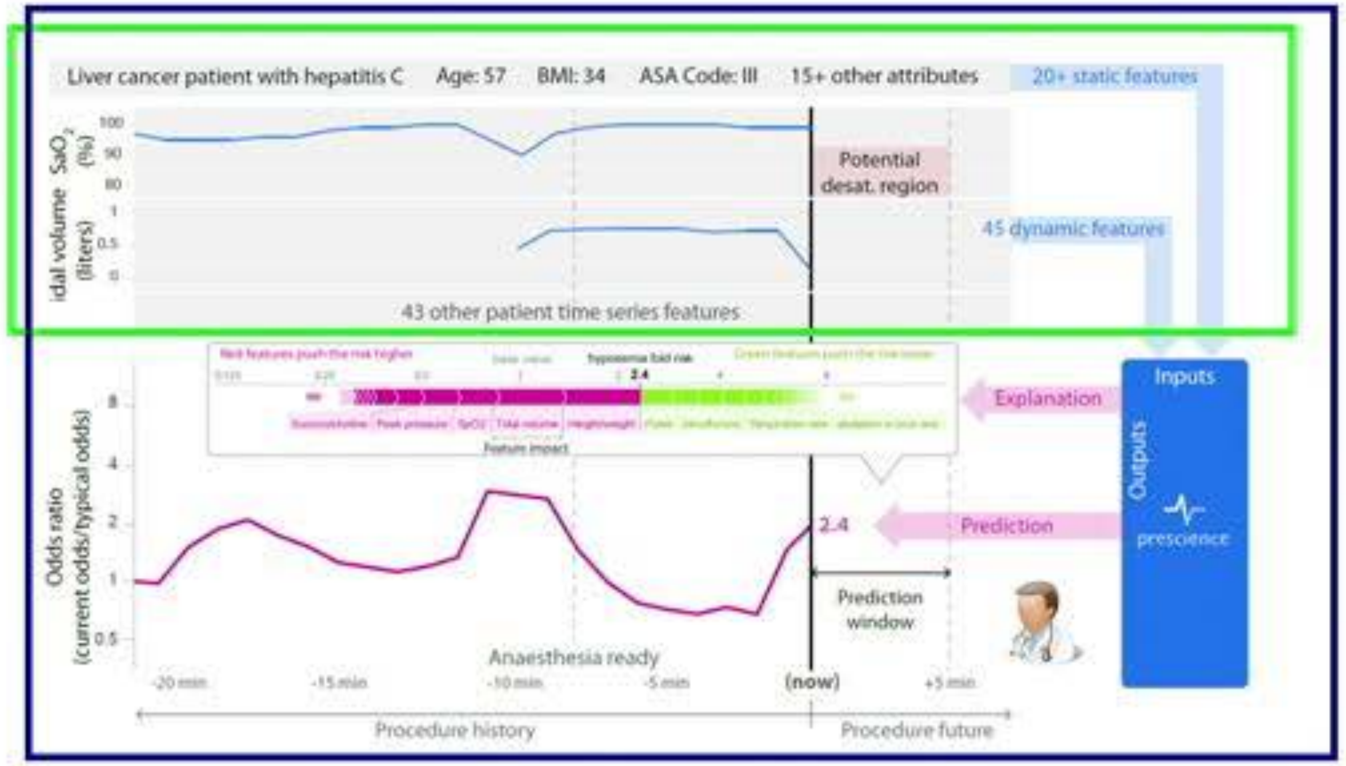

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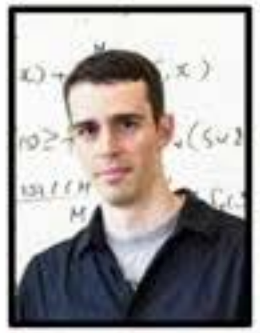

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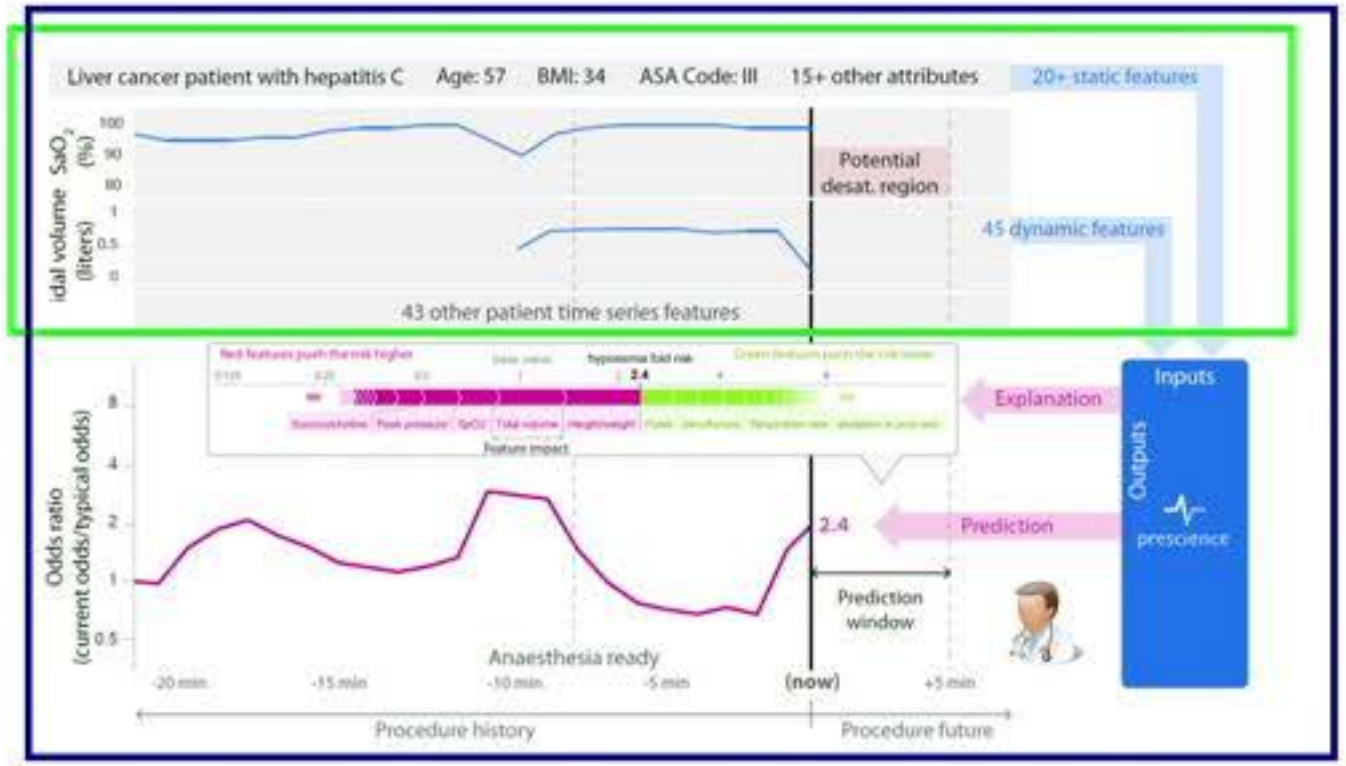

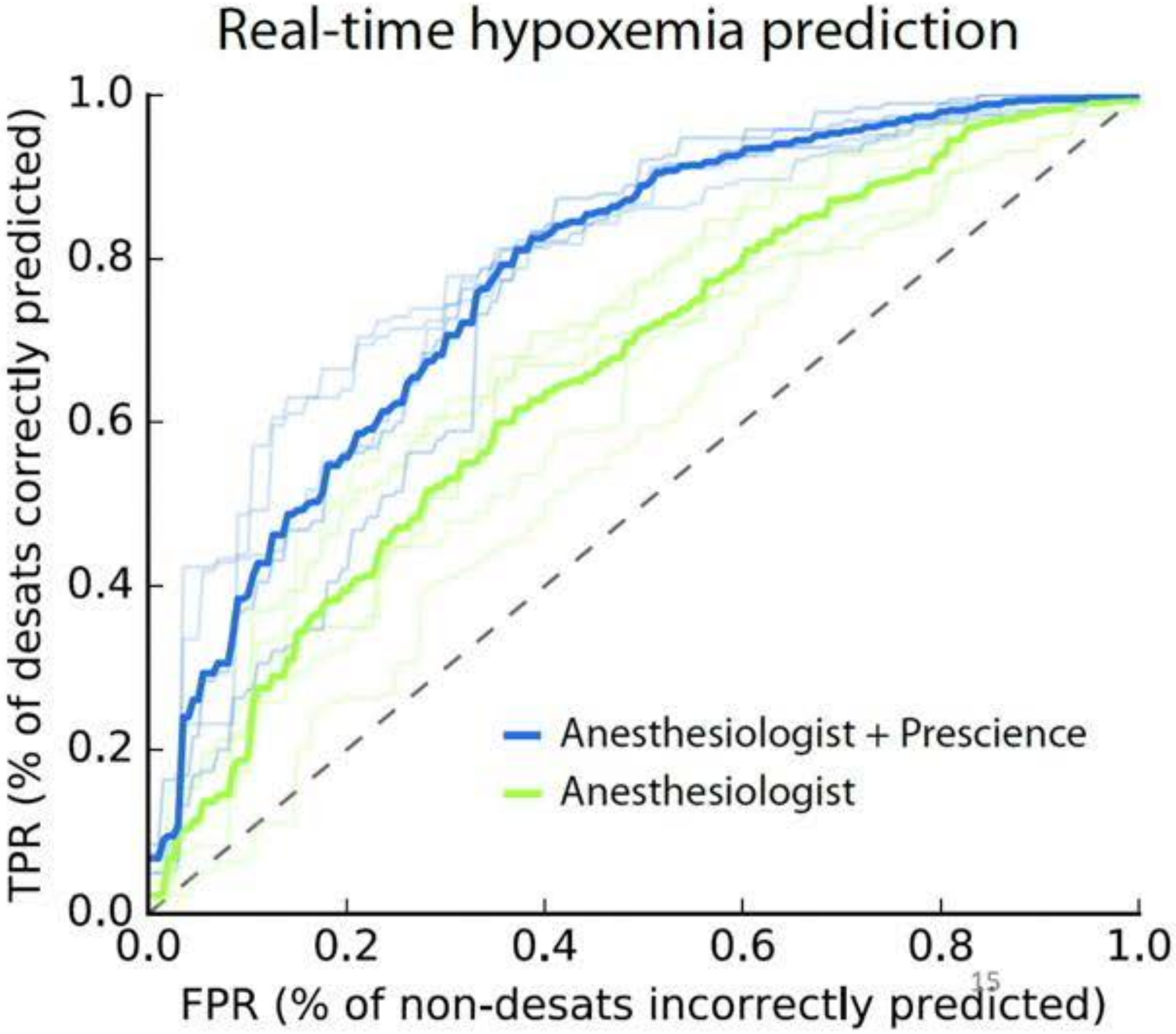

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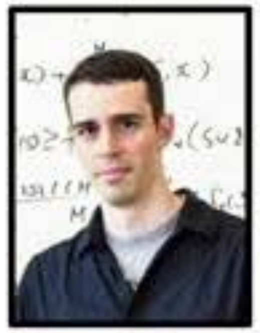

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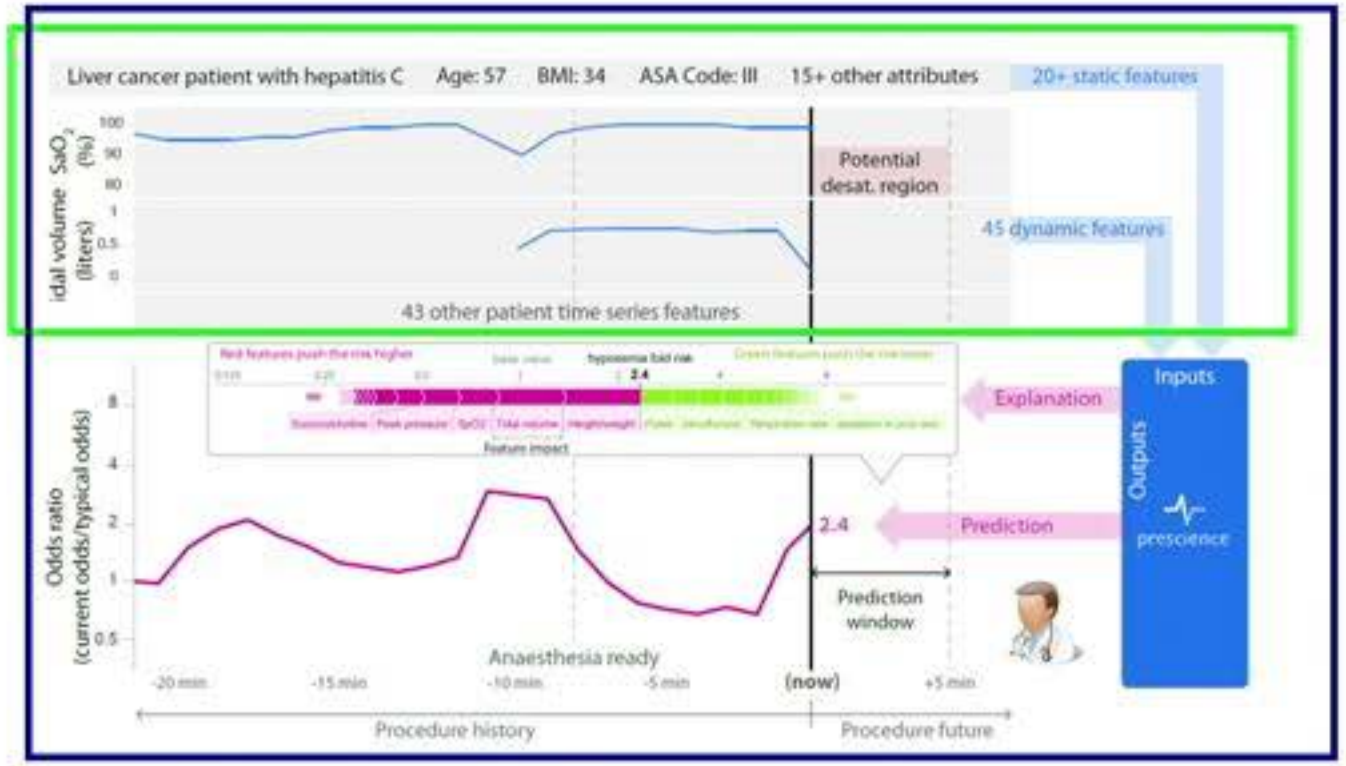

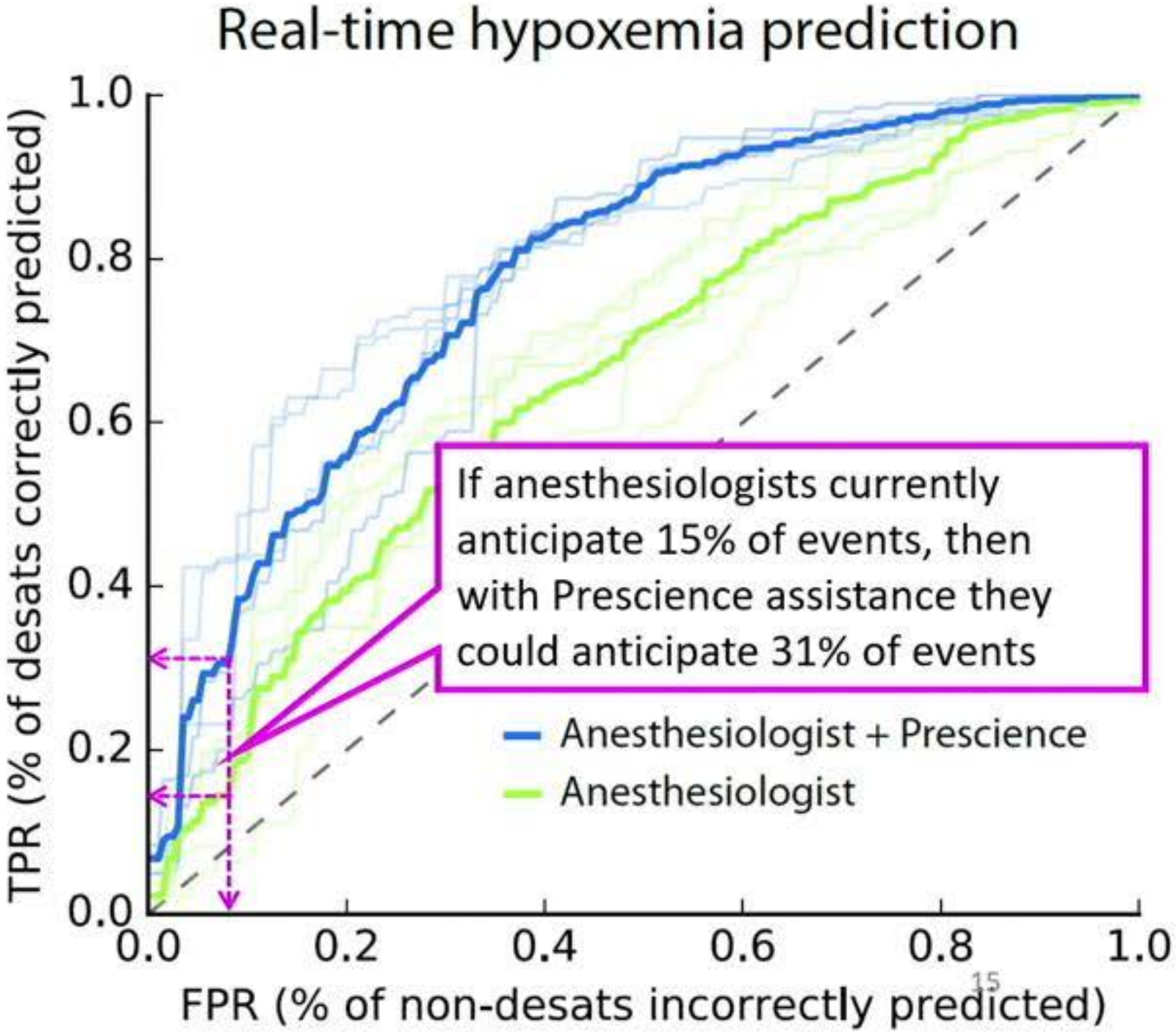

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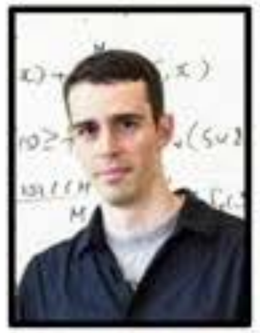

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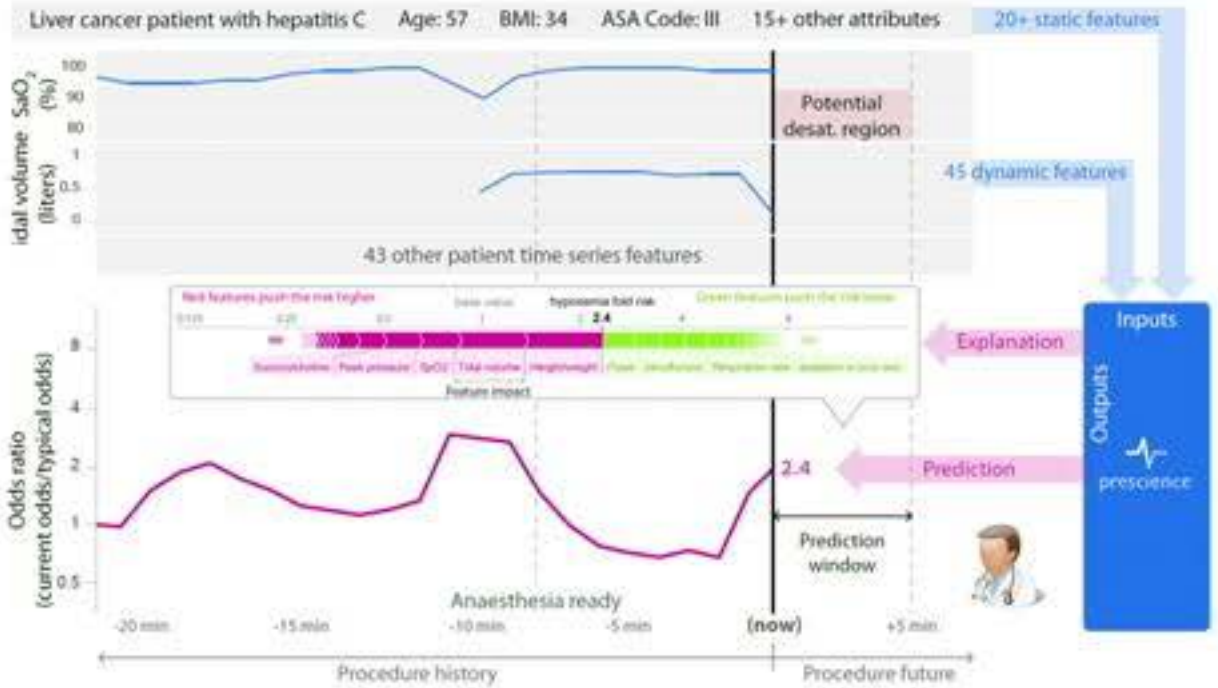
- What if we just let Prescience predict the hypoxemia risk?



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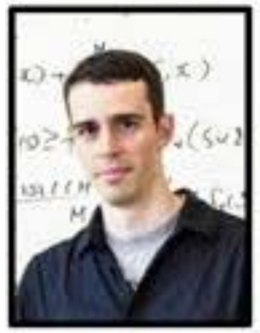

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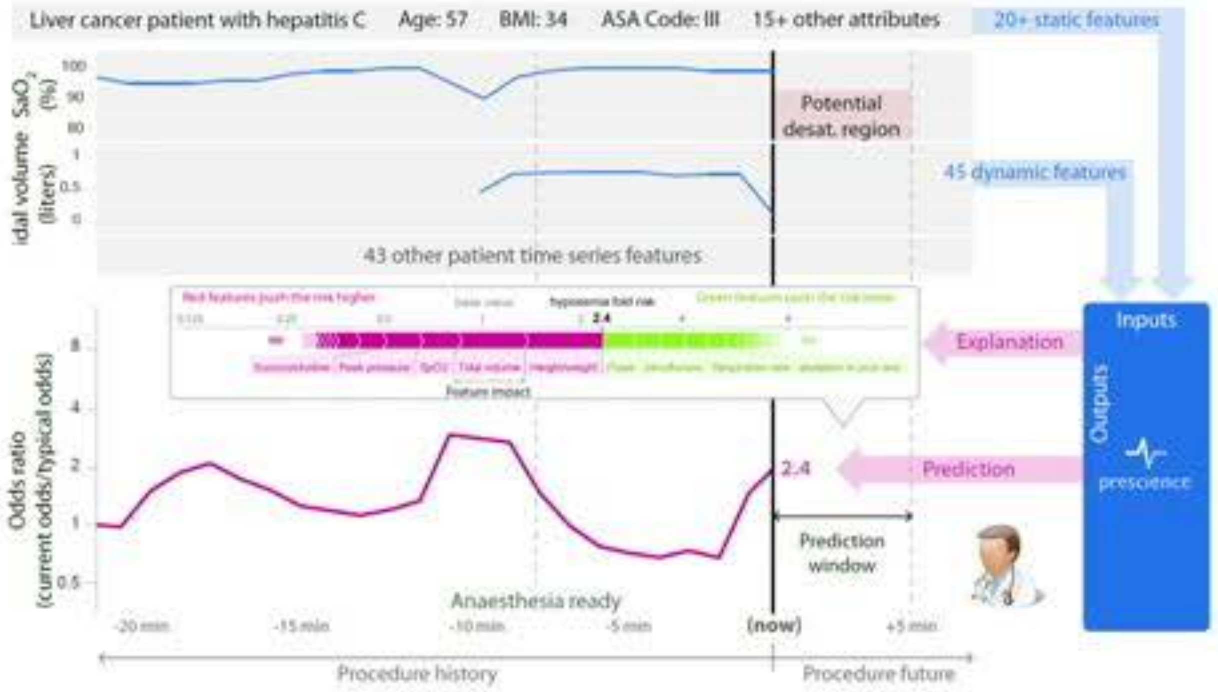
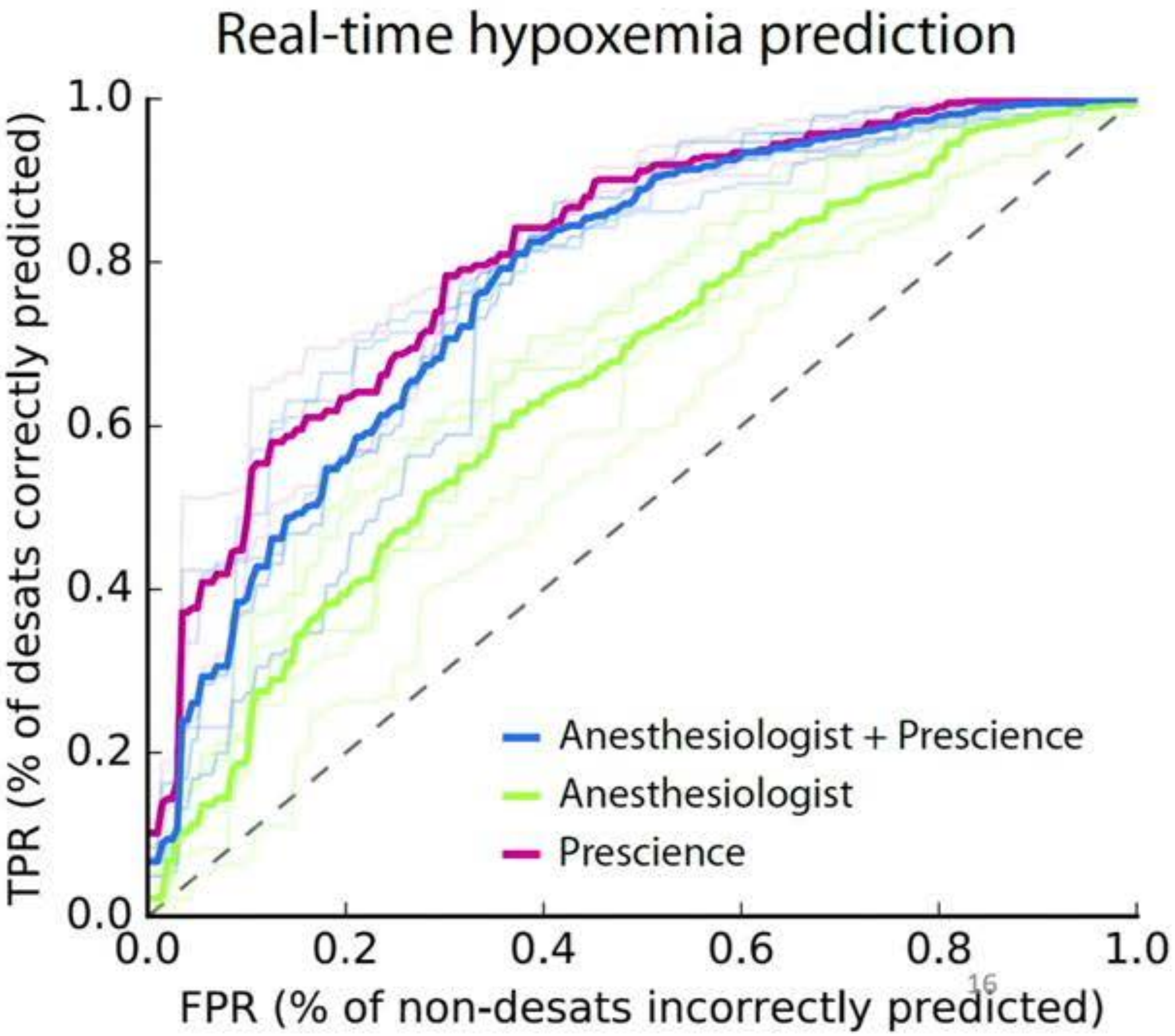
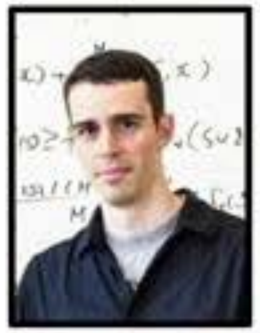




Prescience improves anesthesiologist's ability to predict hypoxemia



Scott

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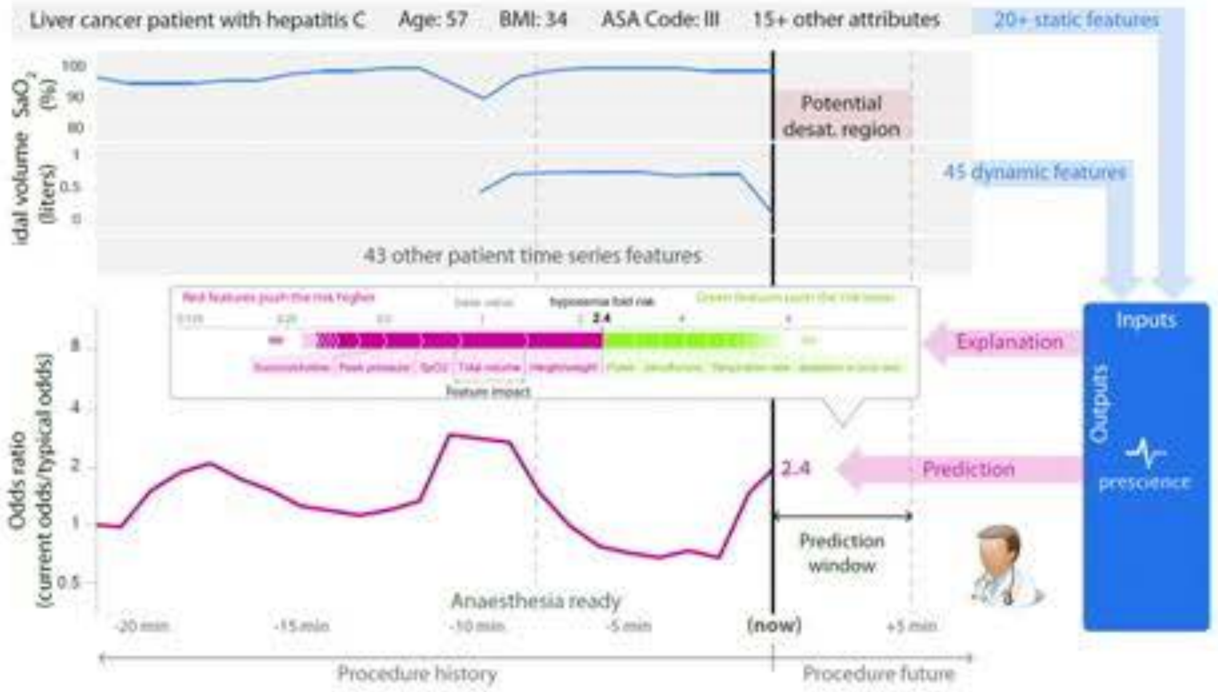

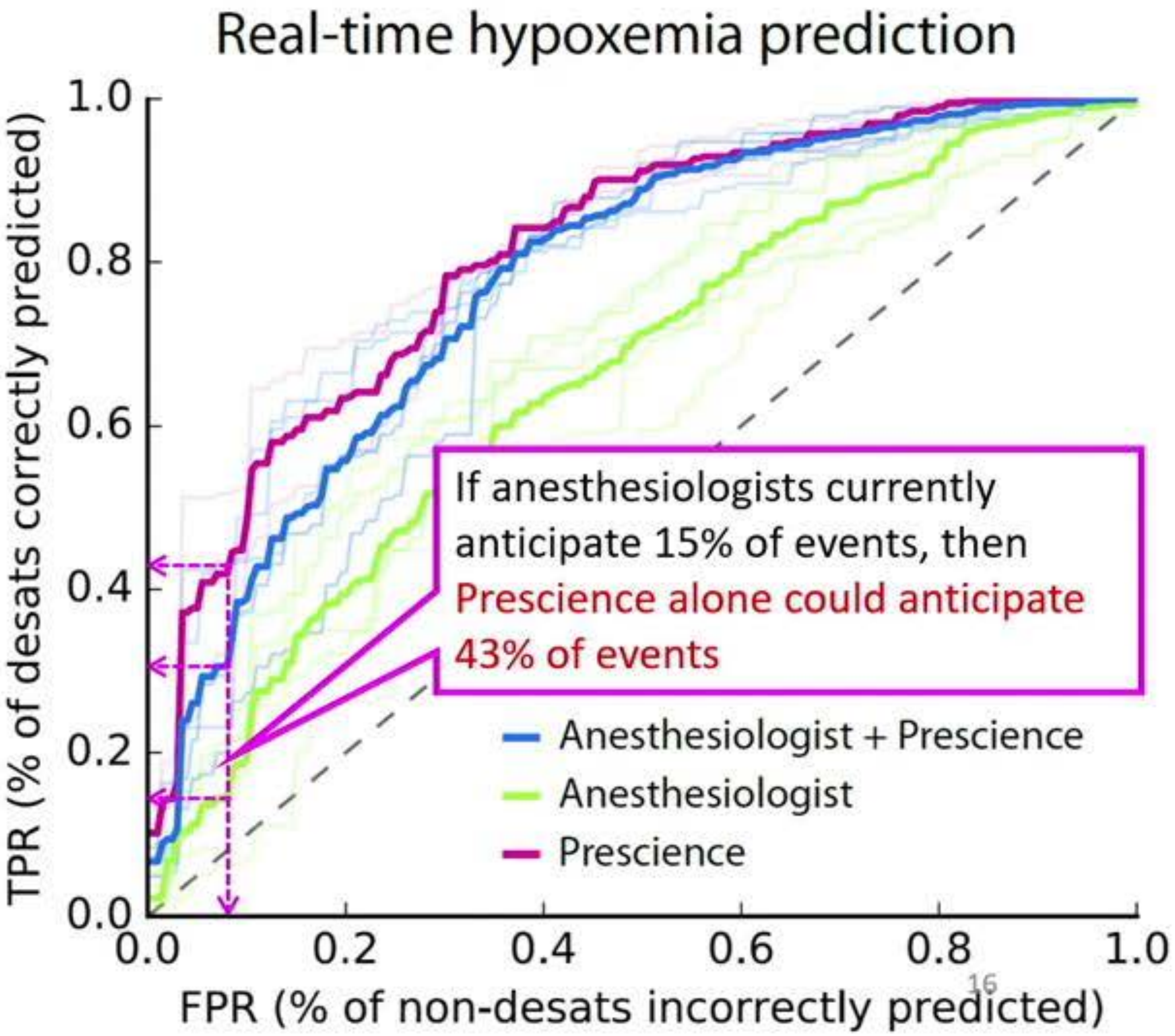

We are improving prediction accuracy further by developing PHASE (PHysiologicAl Signal Embedding)

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Hugh Chen, Scott Lundberg, and Su-In Lee. **PHASE: Physiological Signal Embeddings via Interpretable Stacked Models.**

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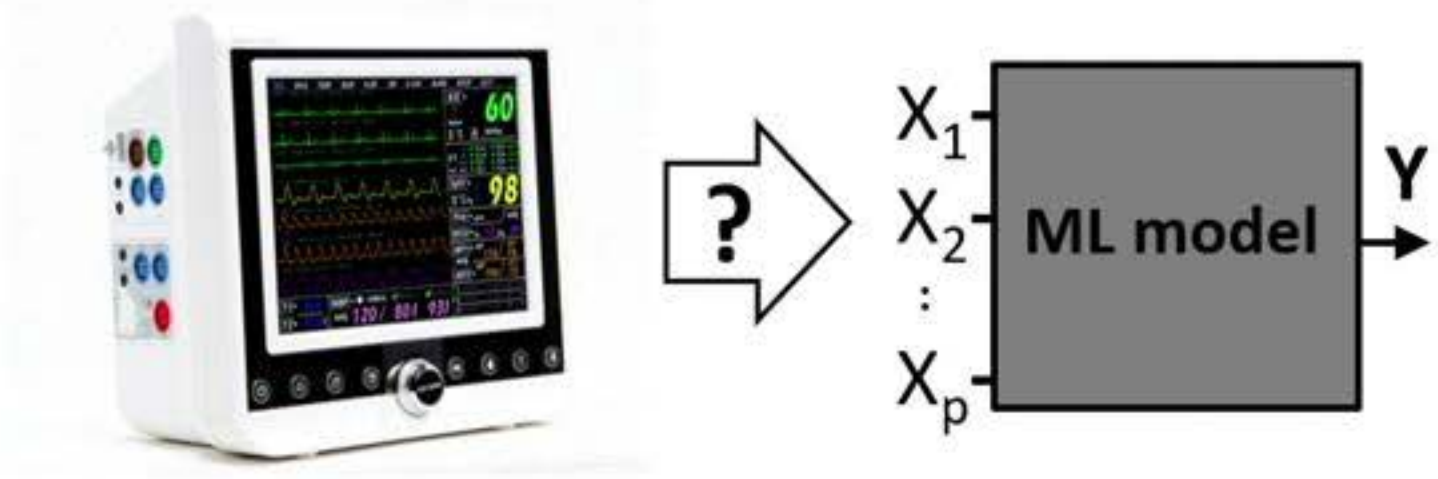

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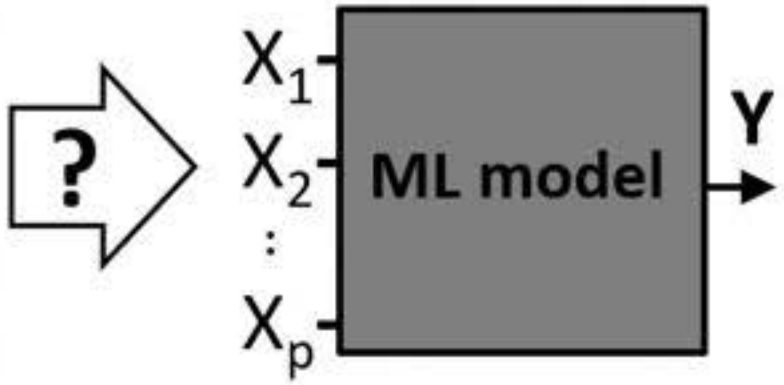

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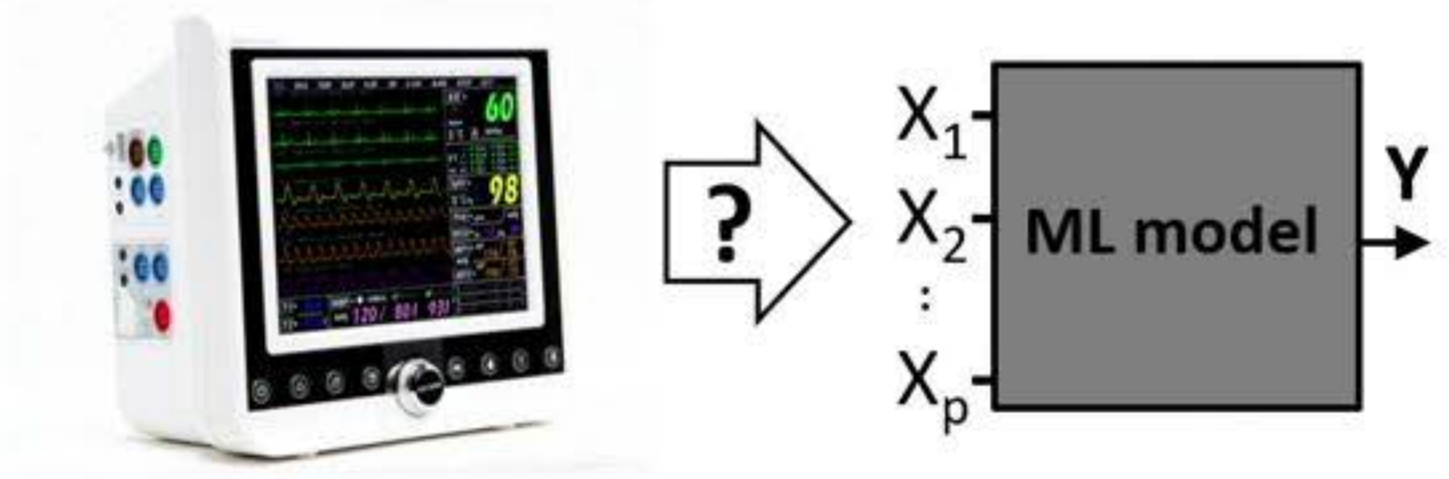

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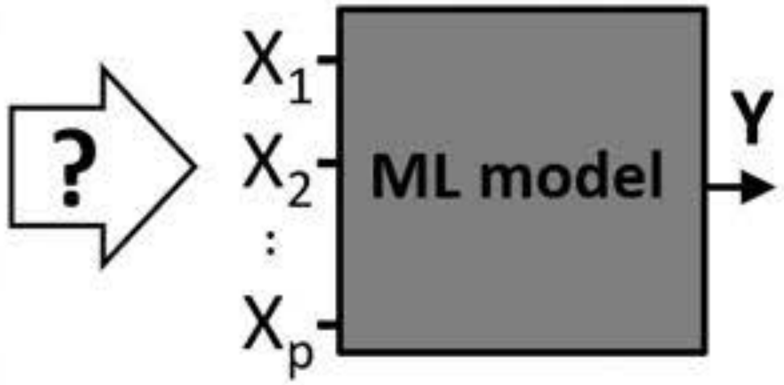

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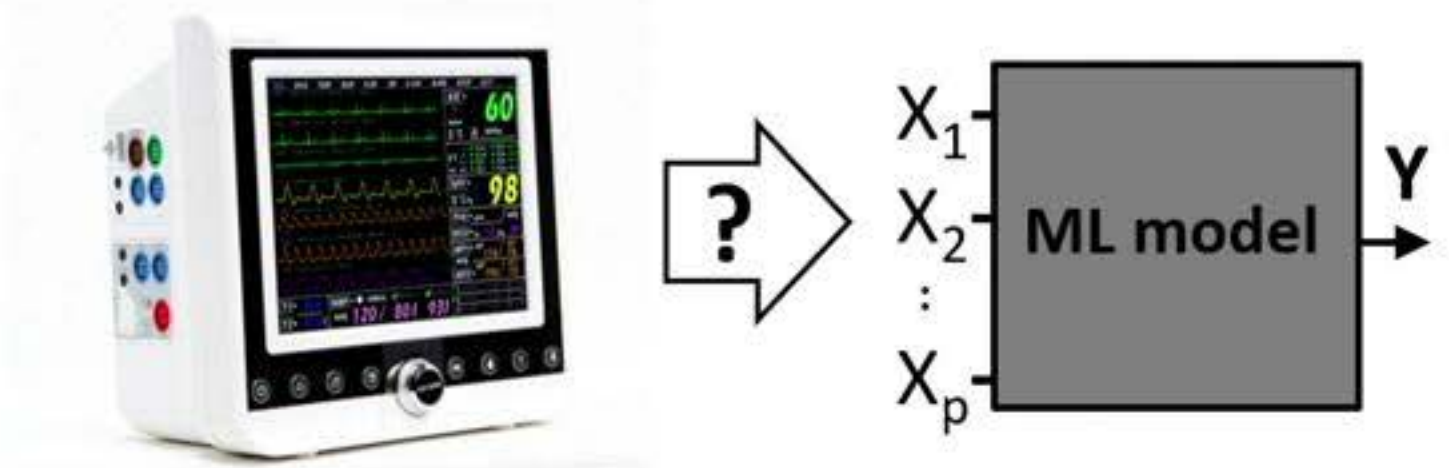

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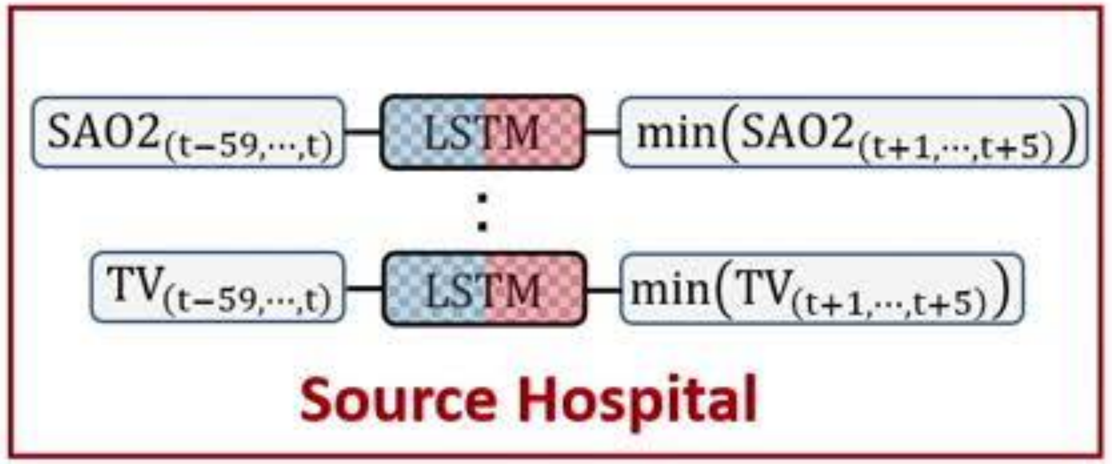

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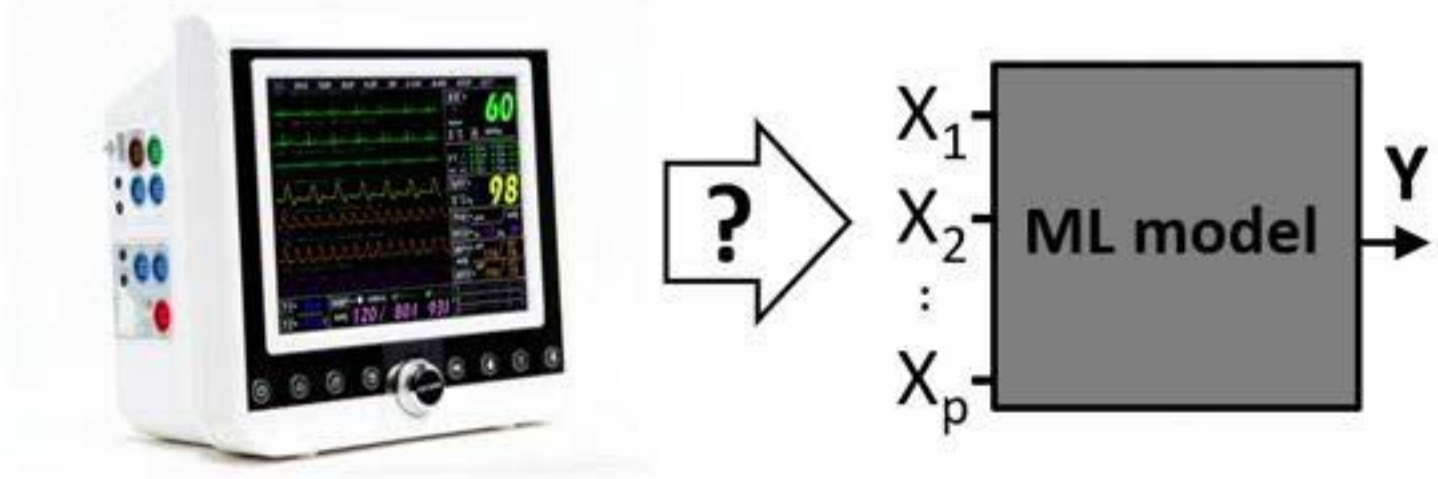

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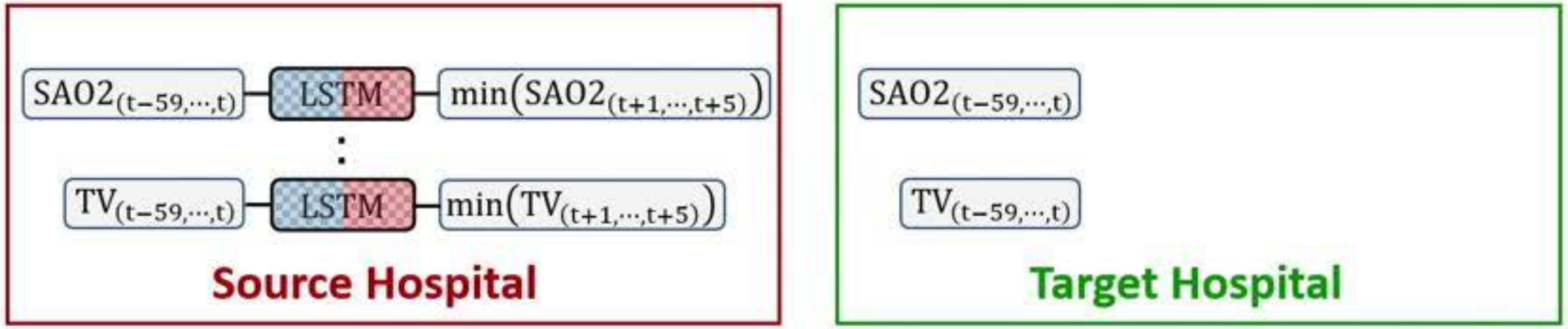

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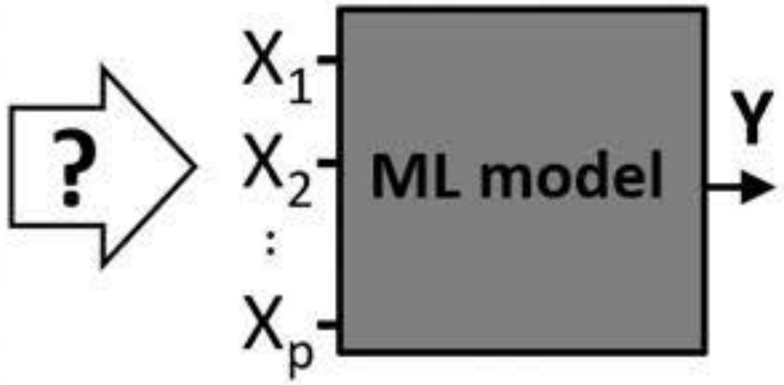

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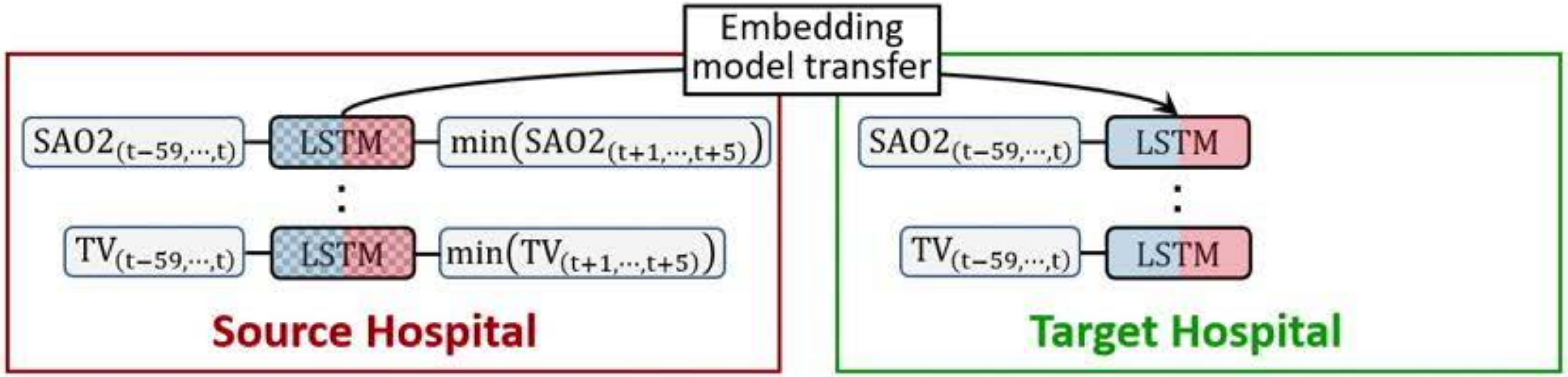

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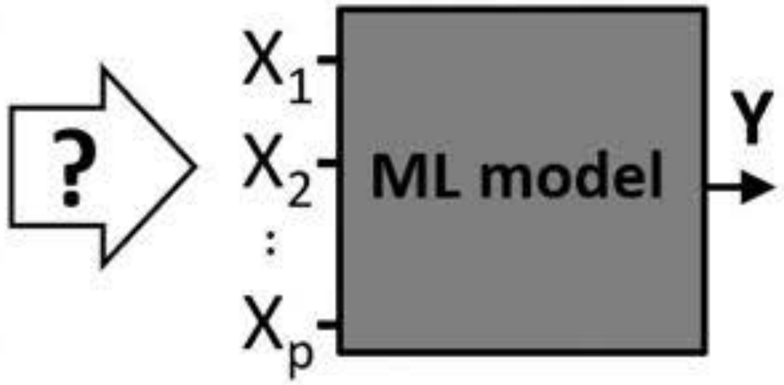

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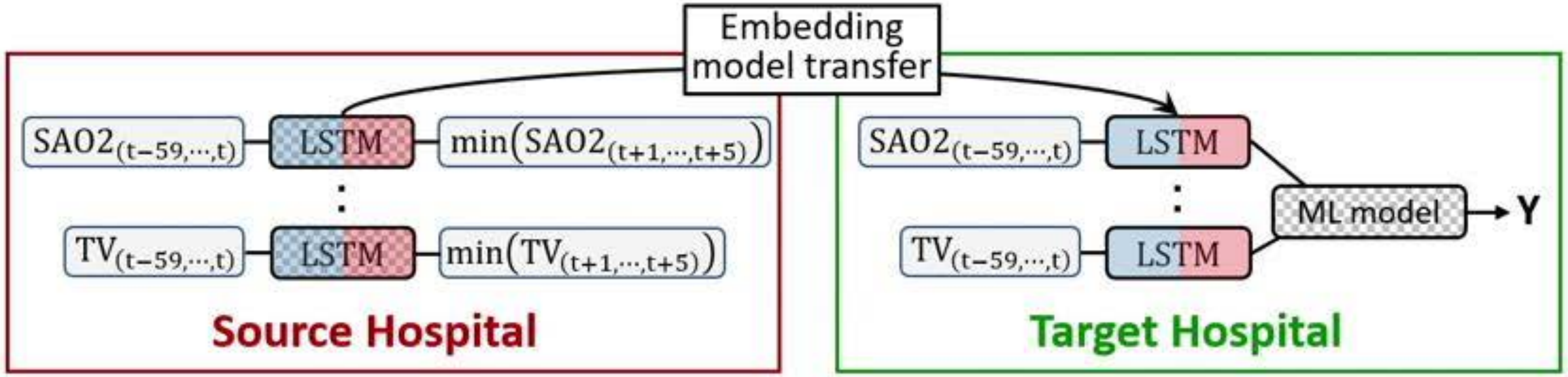

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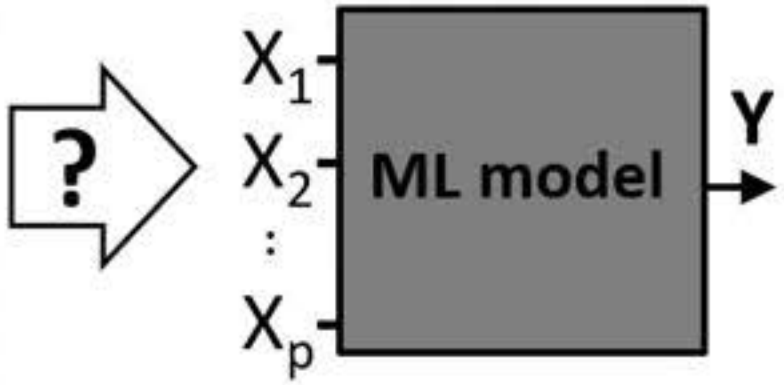

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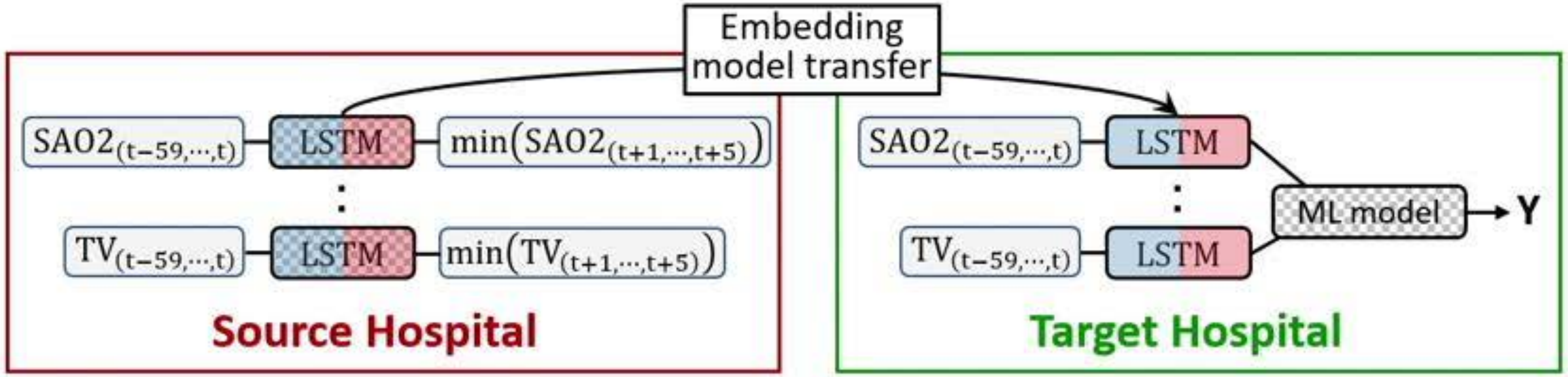

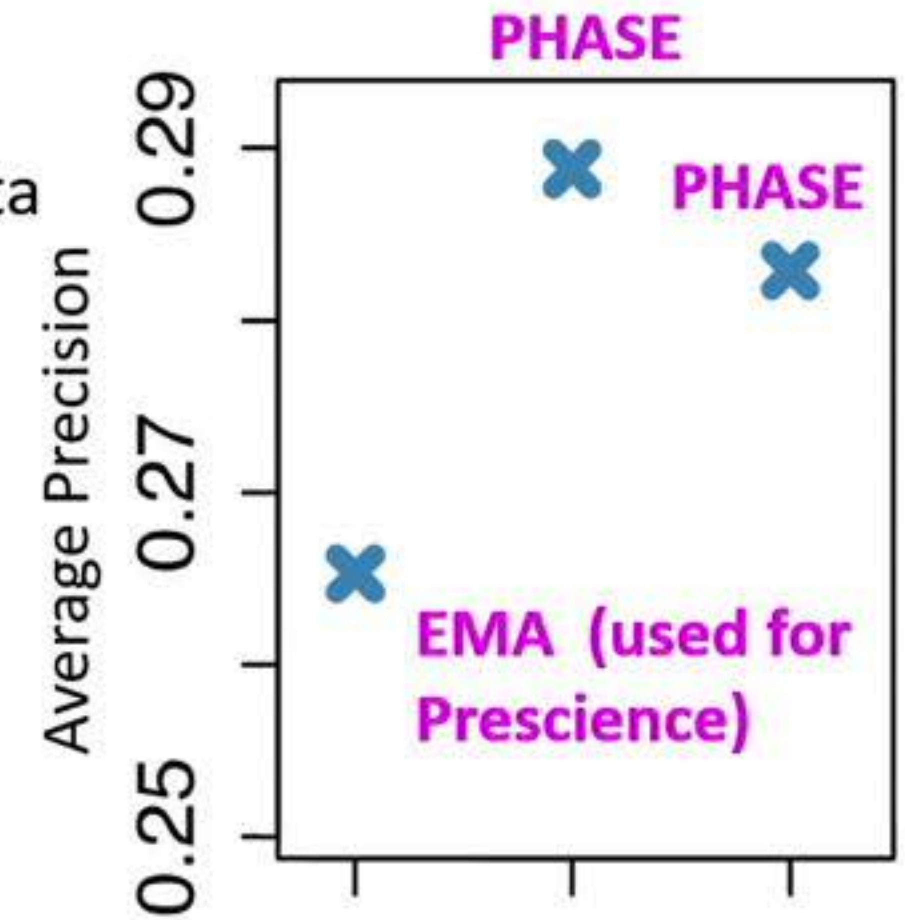

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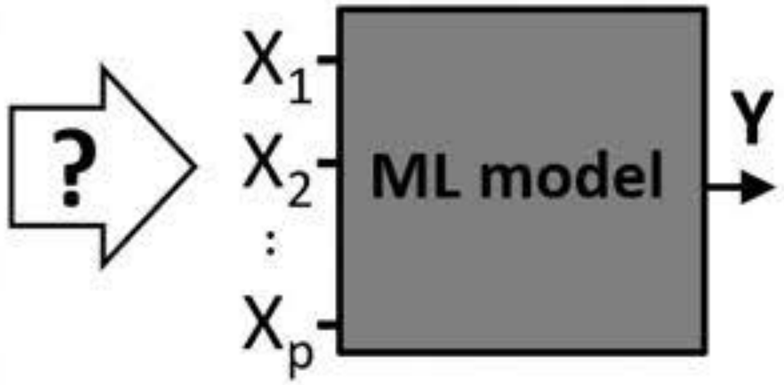

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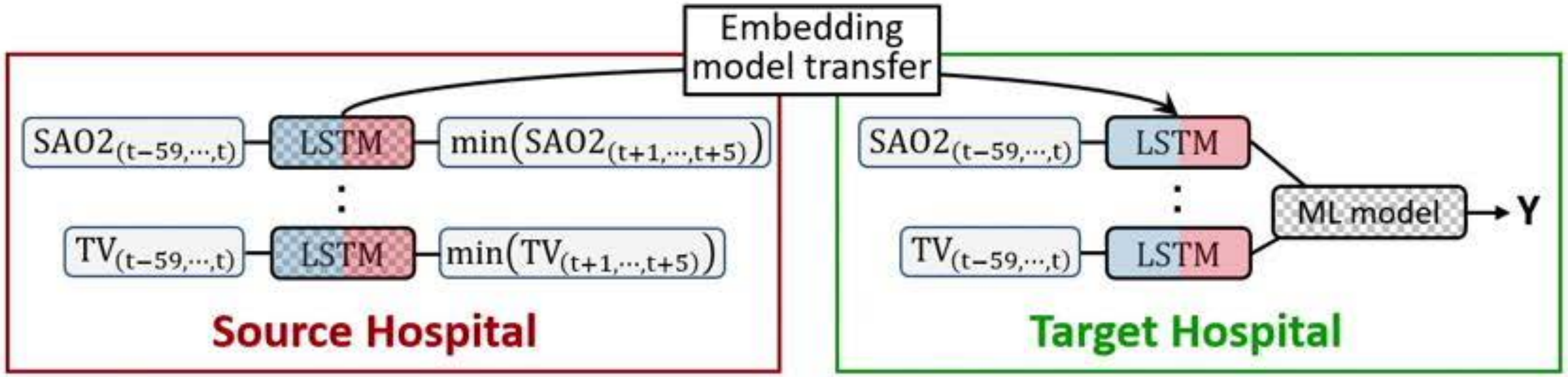
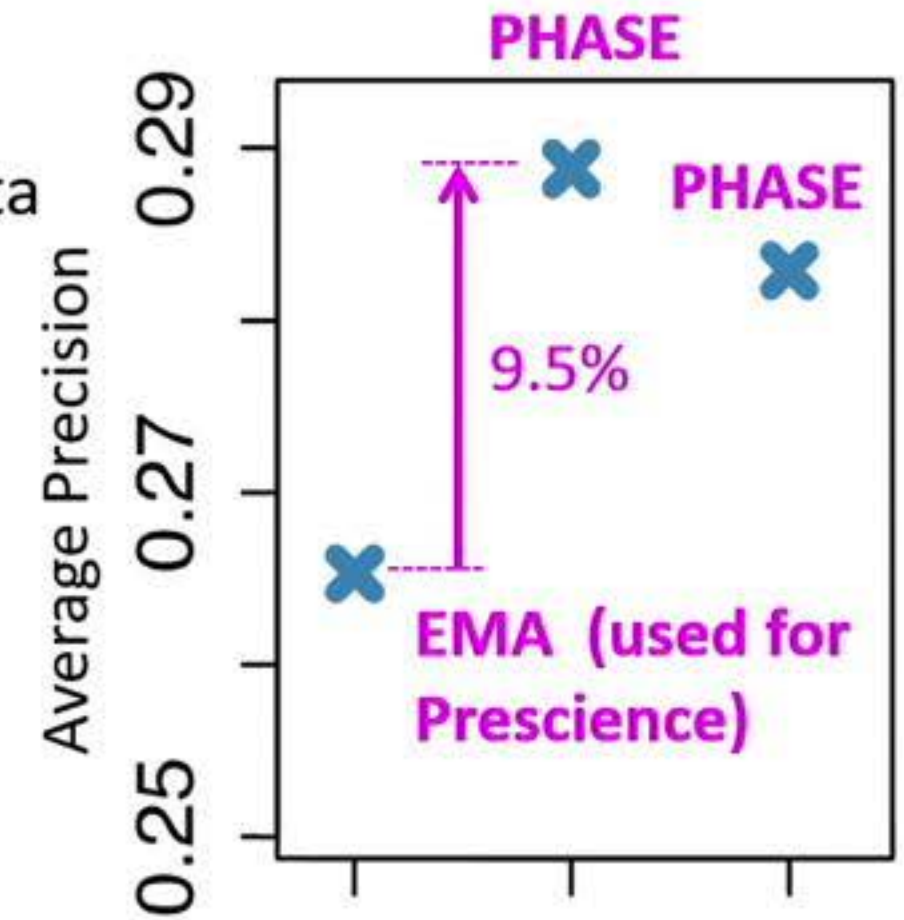




Hugh Chen, Scott Lundberg, and Su-In Lee. **PHASE: Physiological Signal Embeddings via Interpretable Stacked Models.**

Making tree ensembles interpretable

Scott

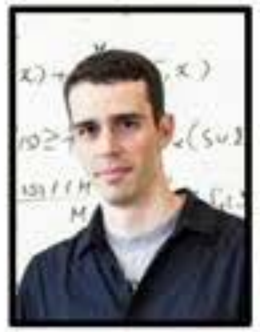
Gabe

Hugh

- Why tree ensembles? 

Scott Lundberg, Gabe Erion, Hugh Chen, and Su-In Lee. **Accurate and Interpretable Machine Learning with Trees.**

Making tree ensembles interpretable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- Why tree ensembles? 
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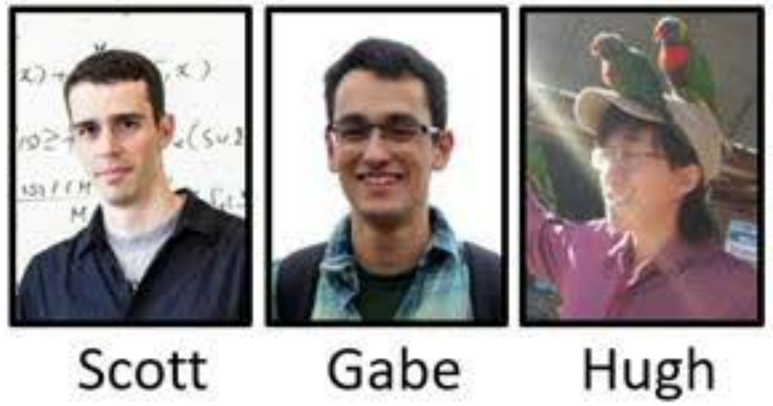
Making tree ensembles interpretable



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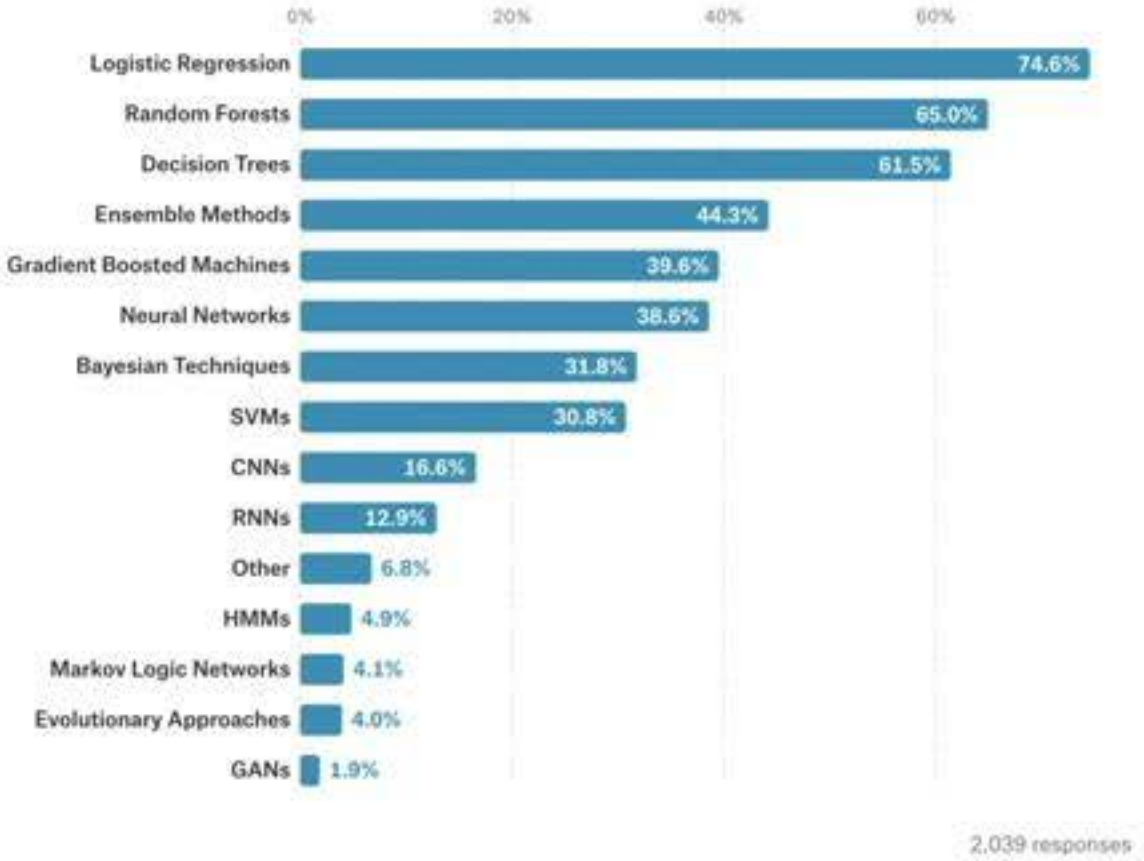

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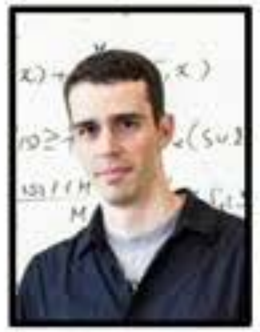

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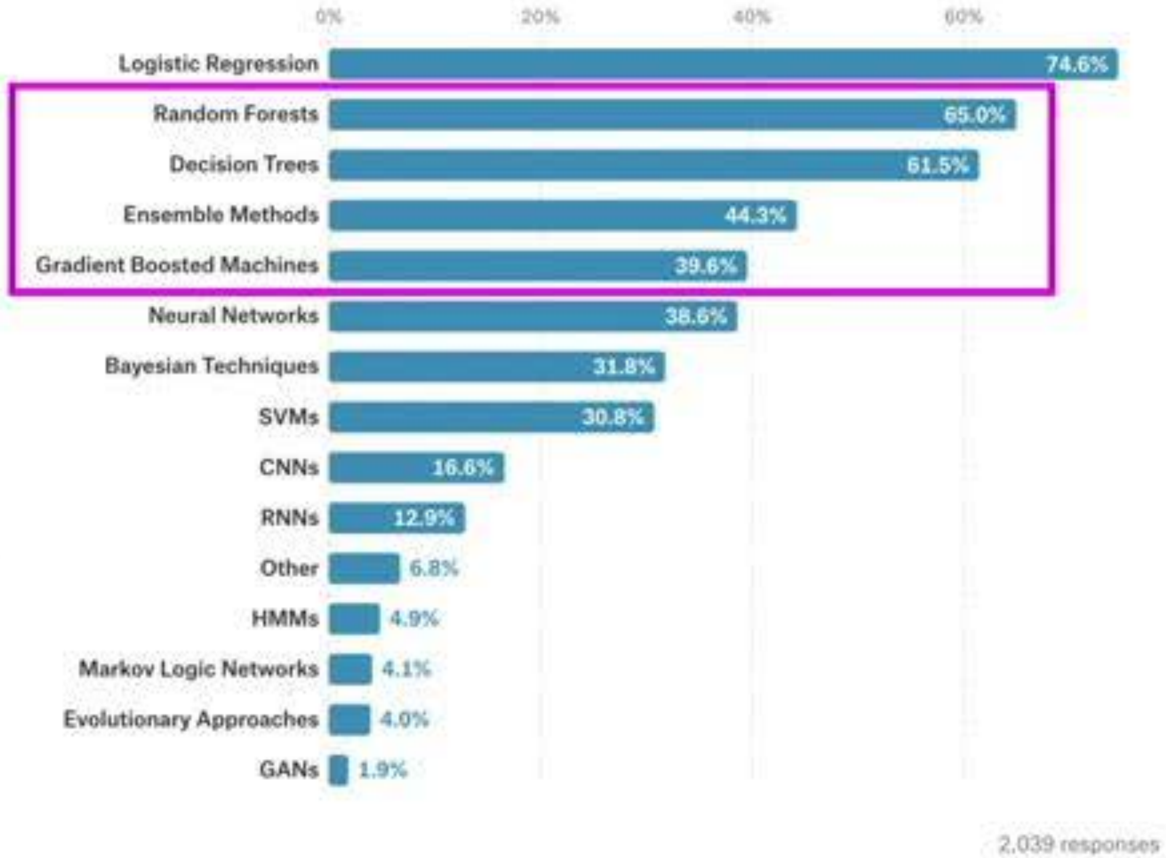

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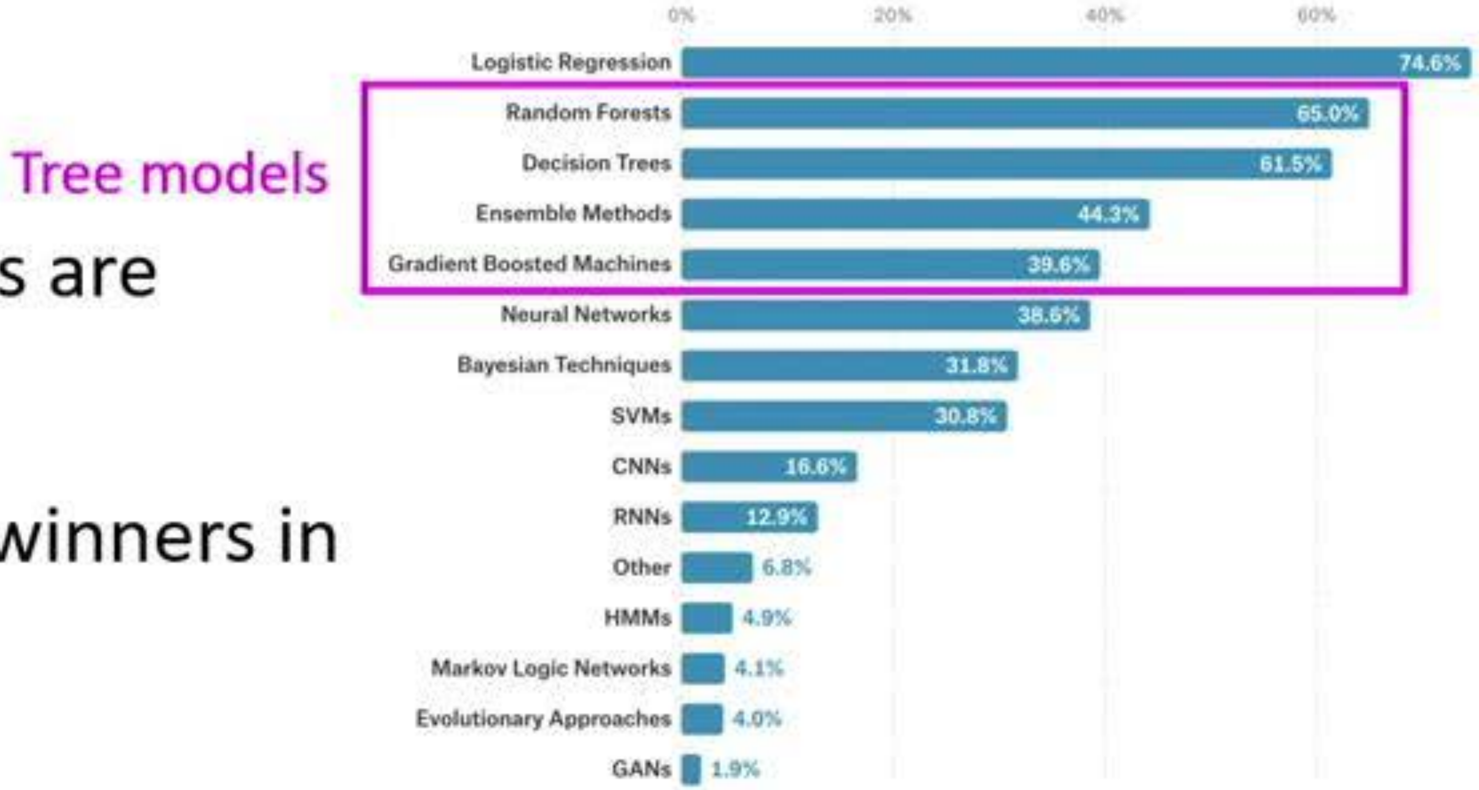

- Tree SHAP reduces the exact computation of SHAP values from exponential to polynomial time.

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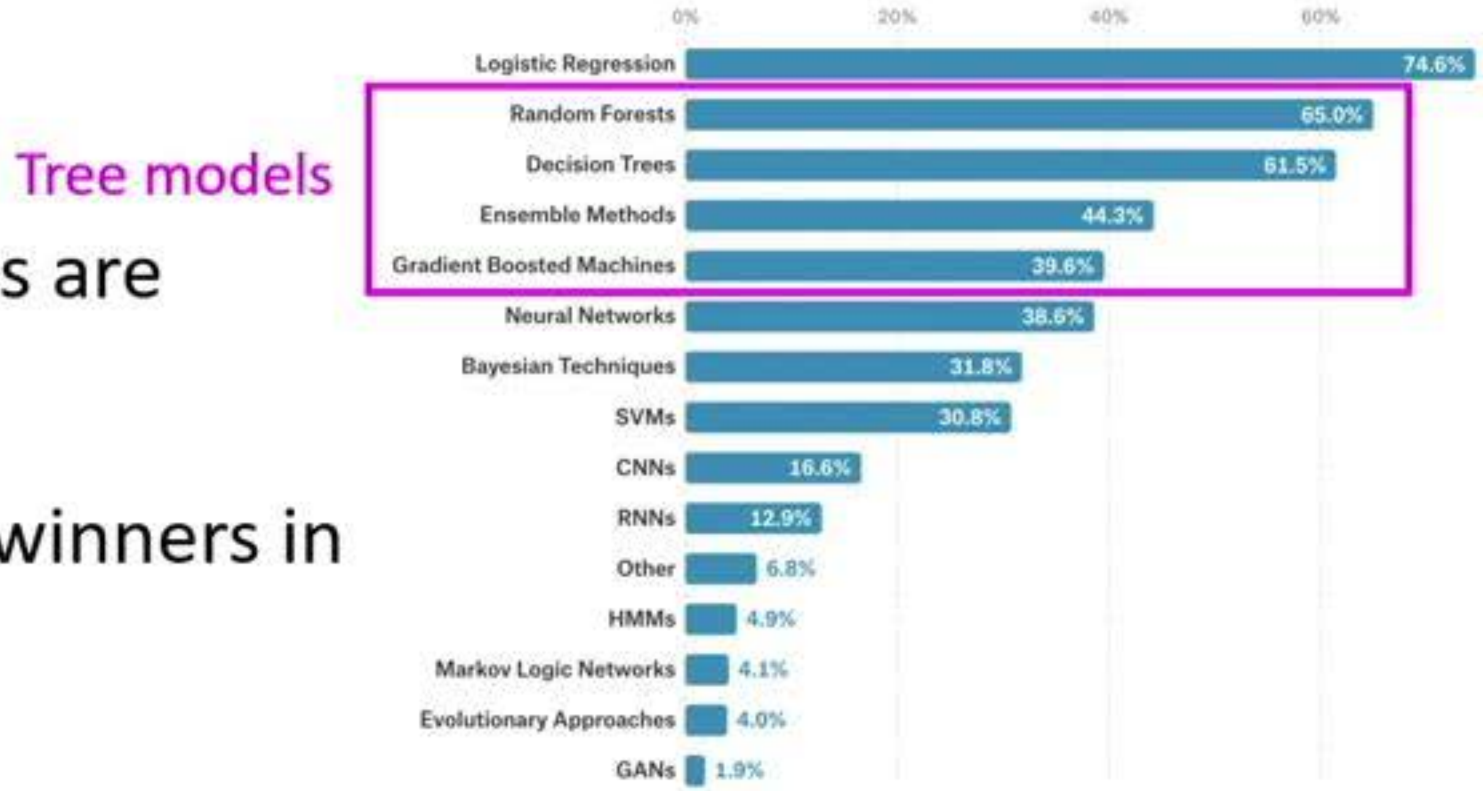

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Direct Solution $O(TL2^M)$ **Exponential**

to

Tree SHAP $O(TLD^2)$ **Polynomial**

Scott Lundberg, Gabe Erion, Hugh Chen, and Su-In Lee. **Accurate and Interpretable Machine Learning with Trees.**

Using SHAP values as building blocks for interpretable ML: SHAP summary plot

Scott Gabe Hugh

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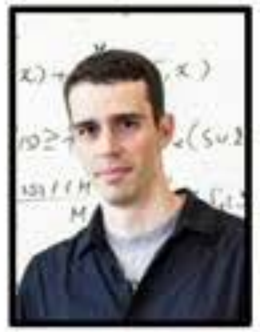

Scott

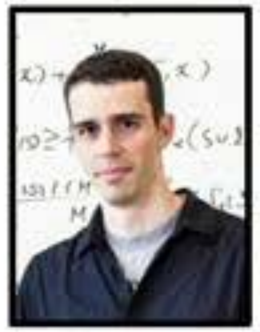

Gabe


Hugh

- NHANES I

National Health & Nutrition Examination Survey

Using SHAP values as building blocks for interpretable ML: SHAP summary plot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  National Health & Nutrition Examination Survey

  - X: 14 common measurements

Using SHAP values as building blocks for interpretable ML: SHAP summary plot


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XGBoost (Cox Proportional Hazards model)

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9,932 individuals

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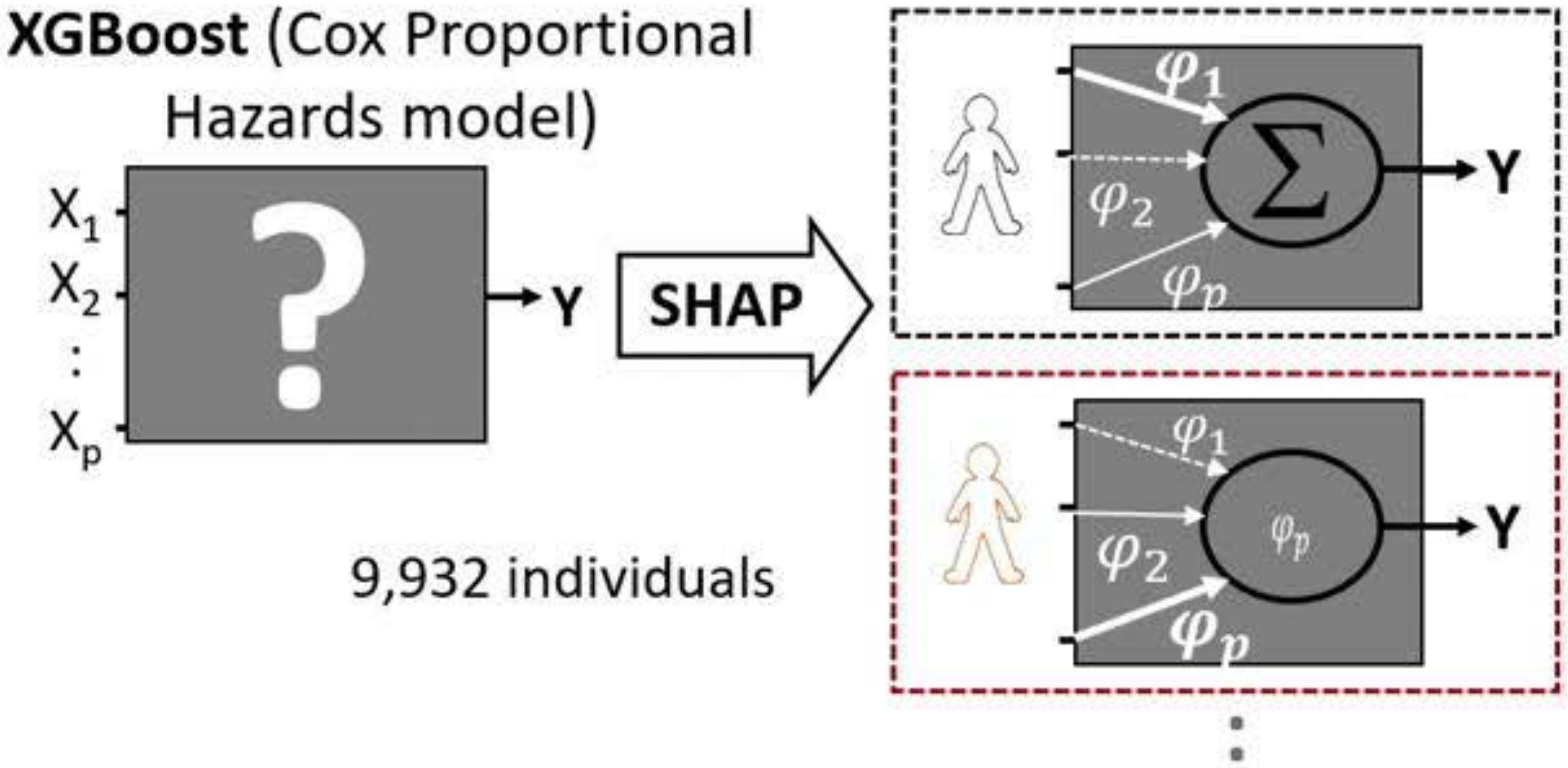

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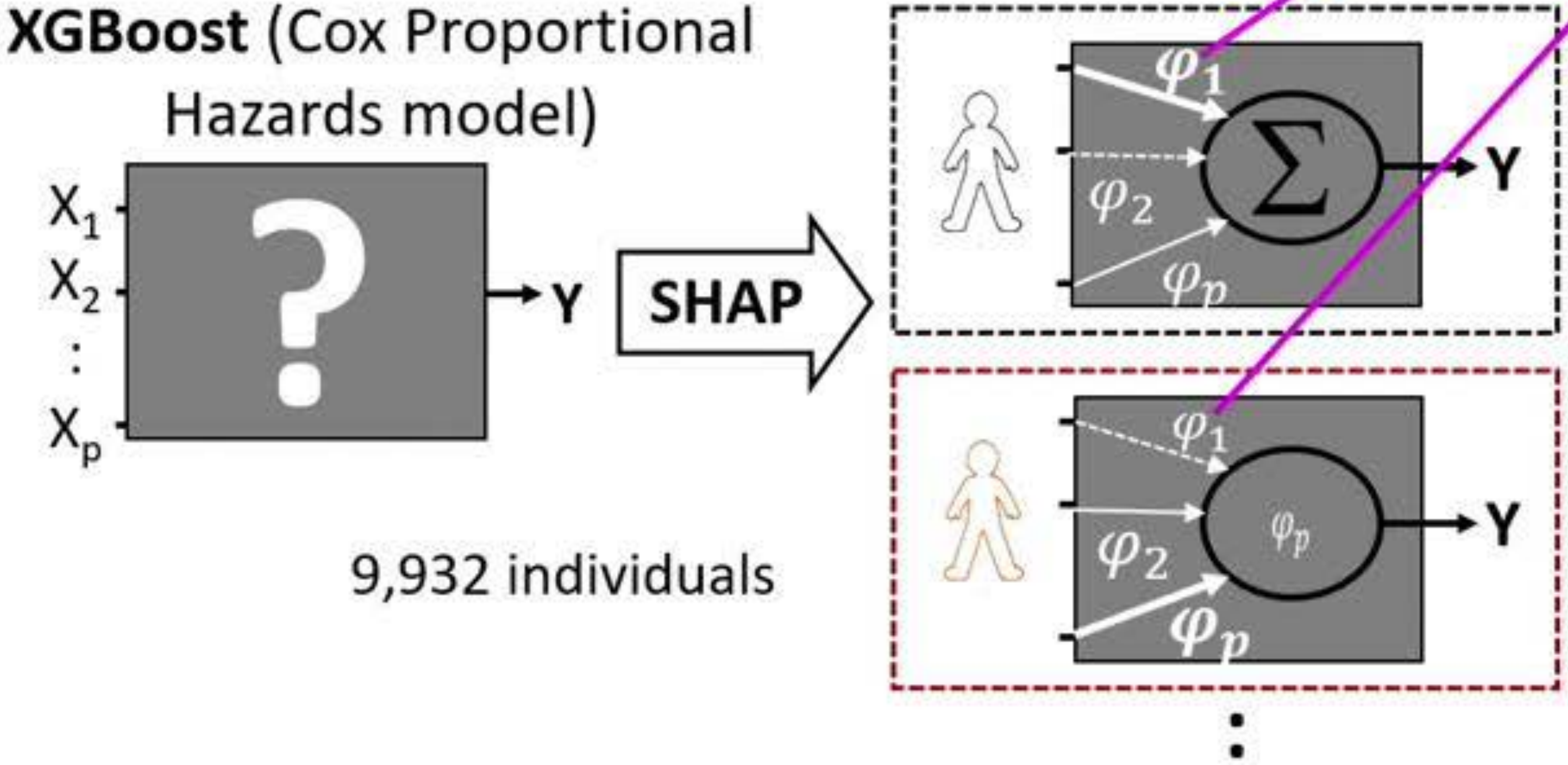

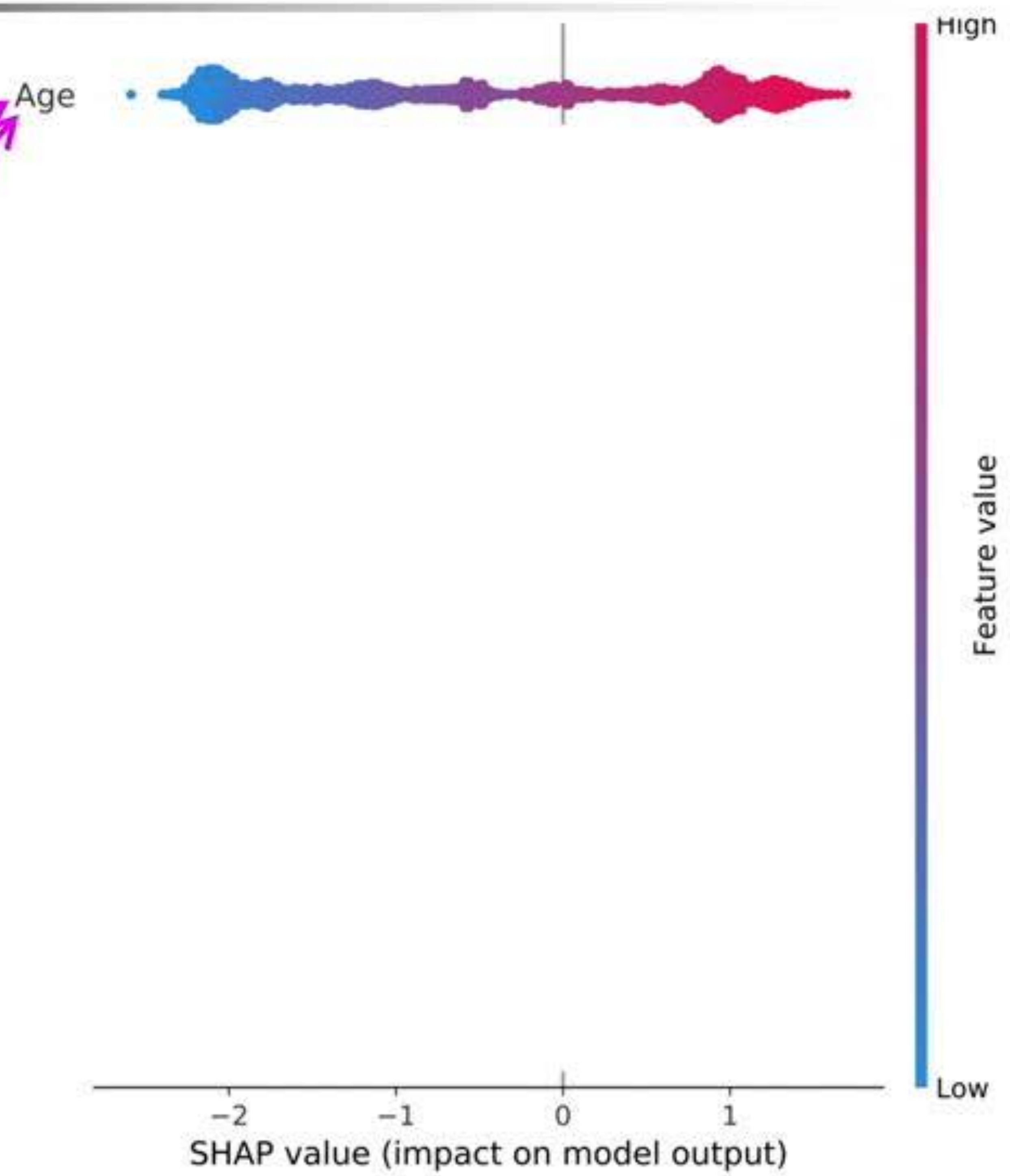

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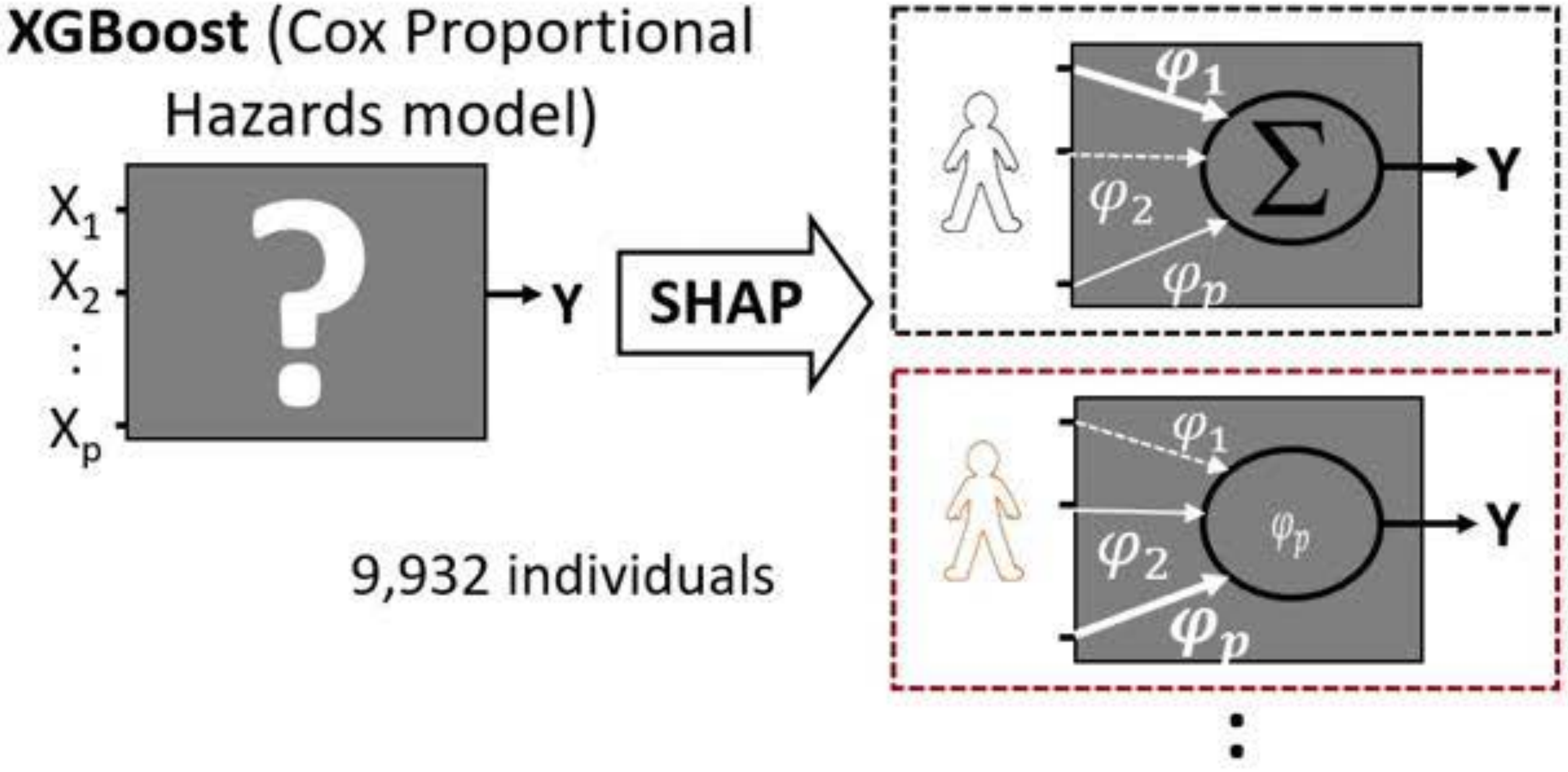

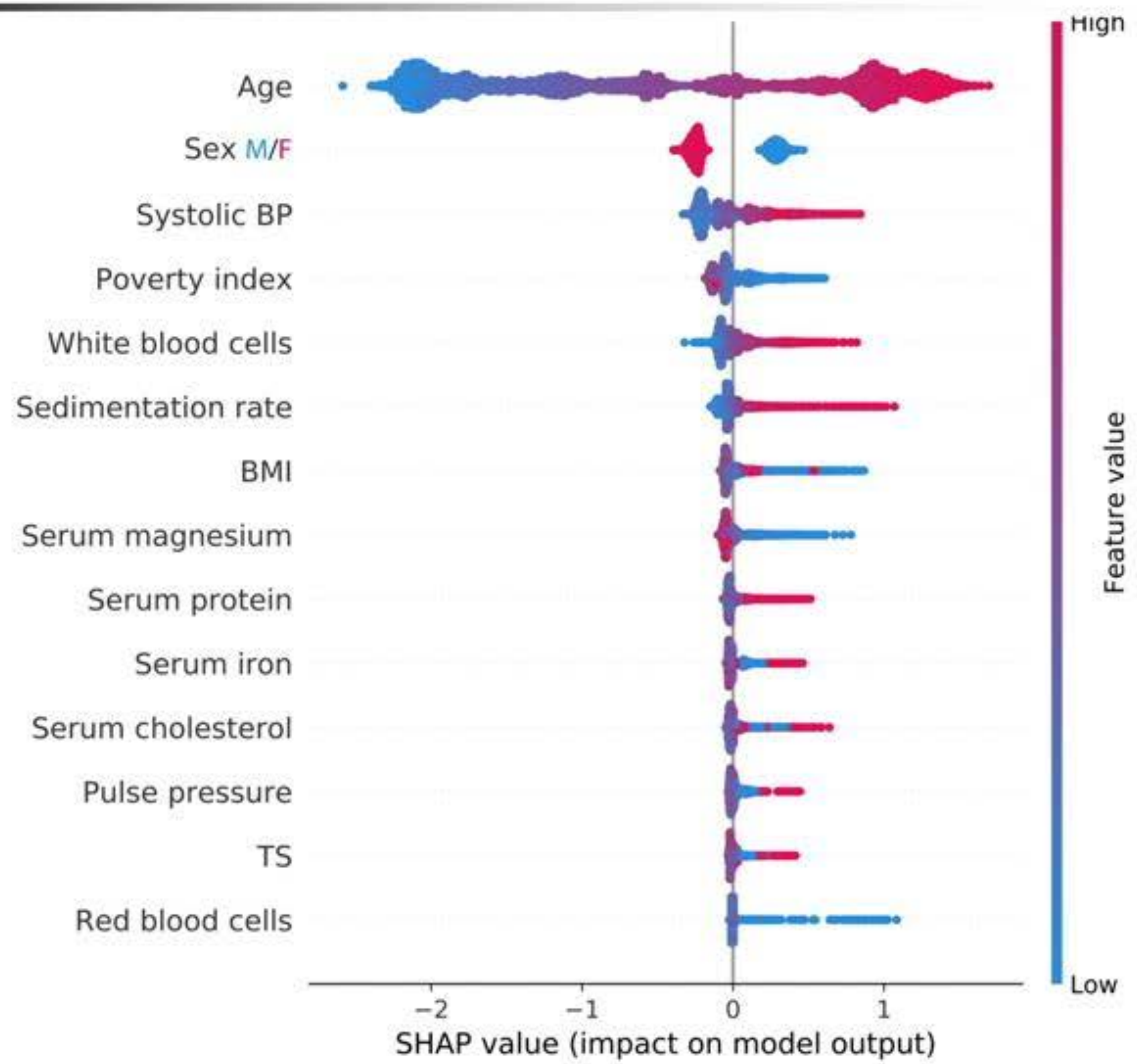

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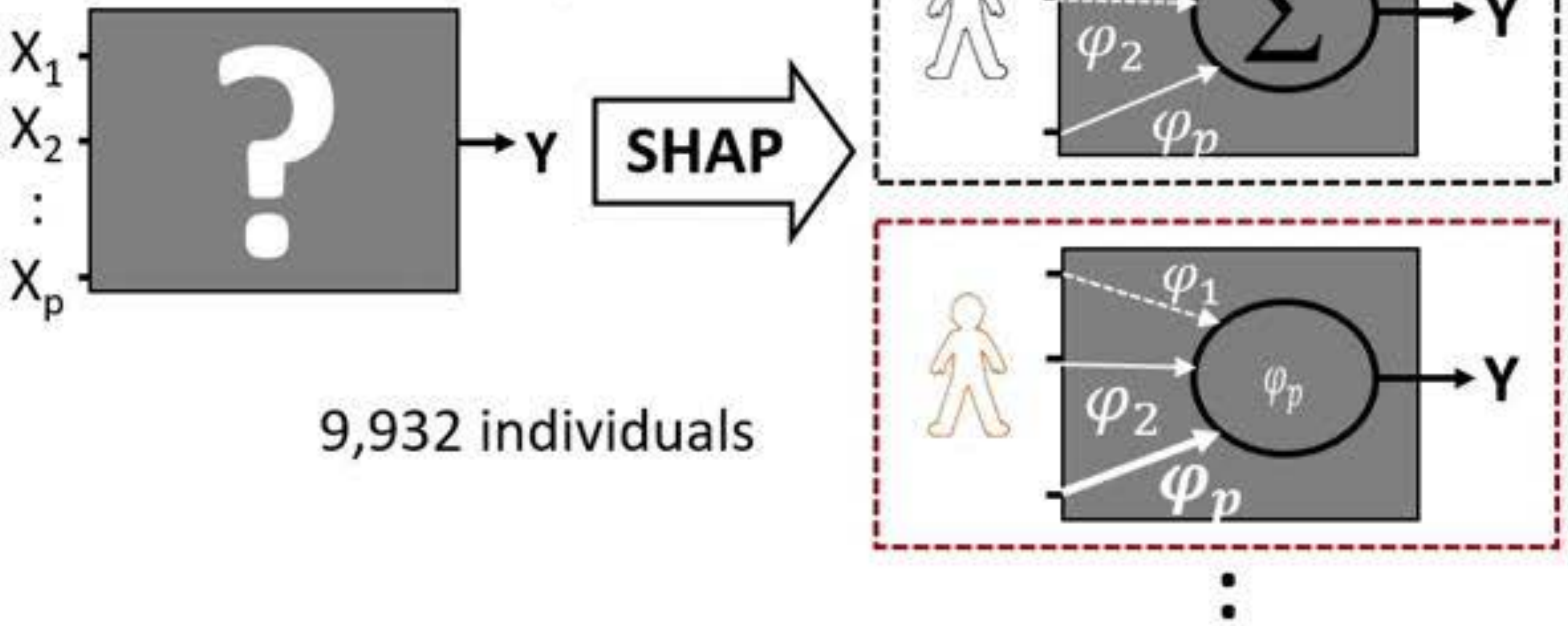

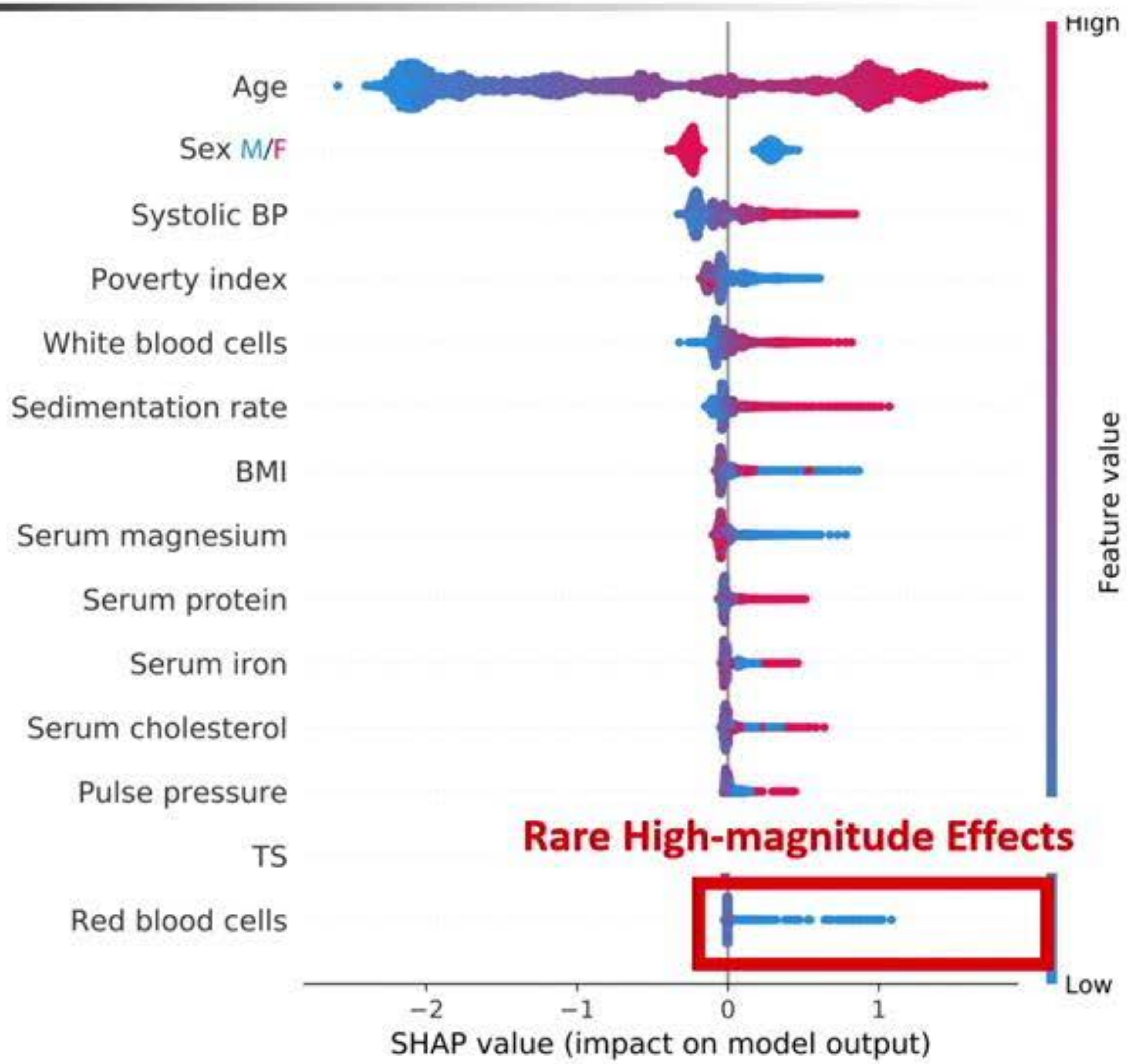

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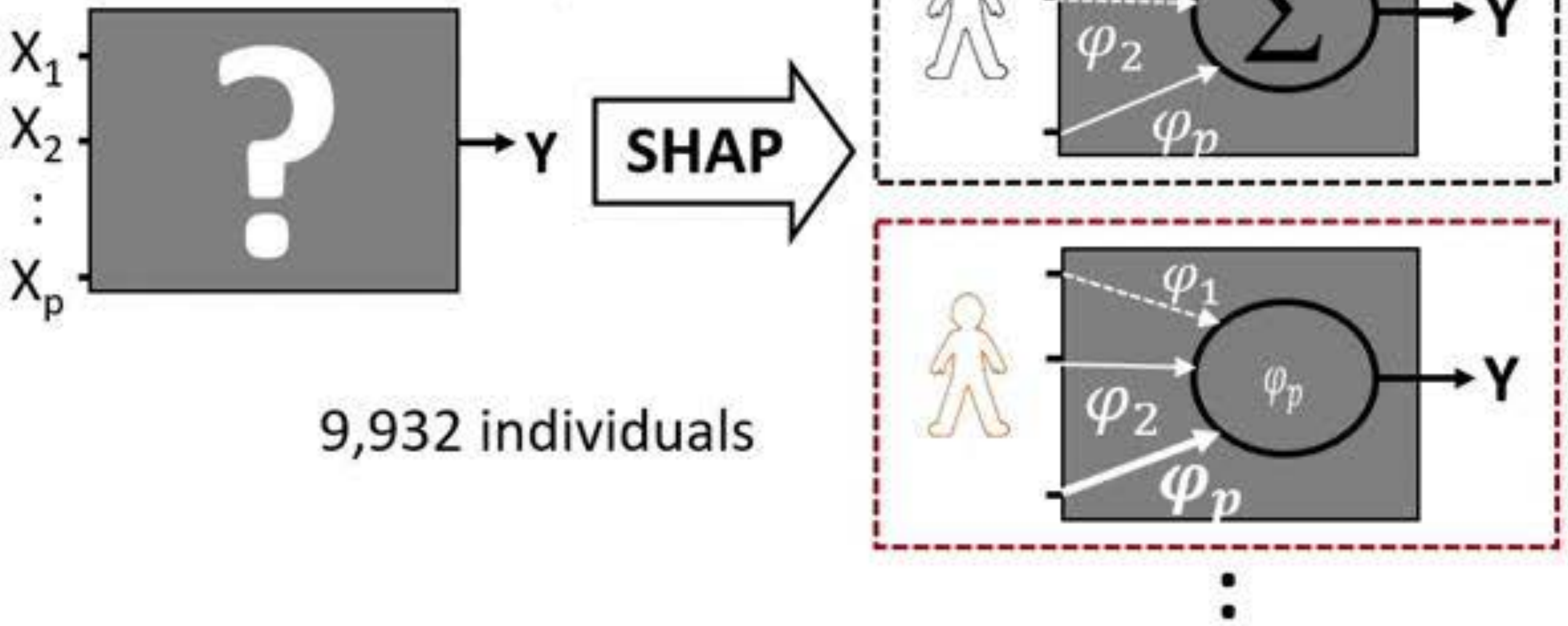

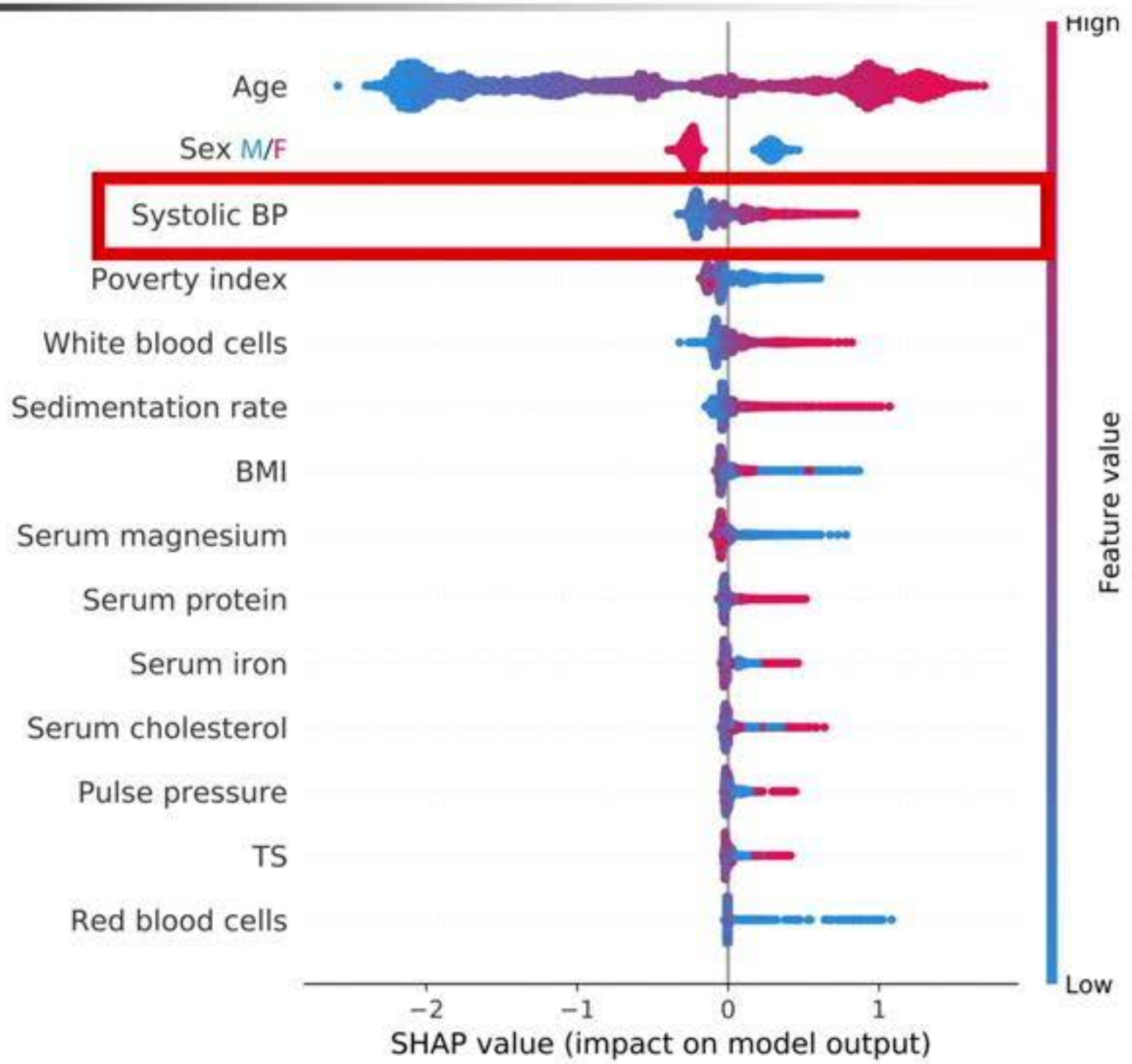

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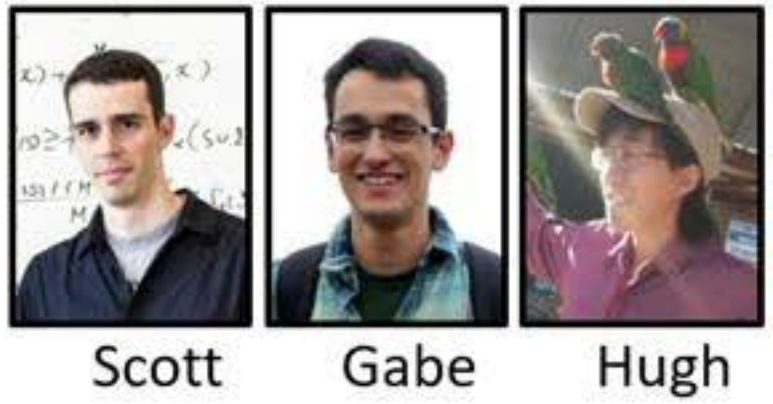

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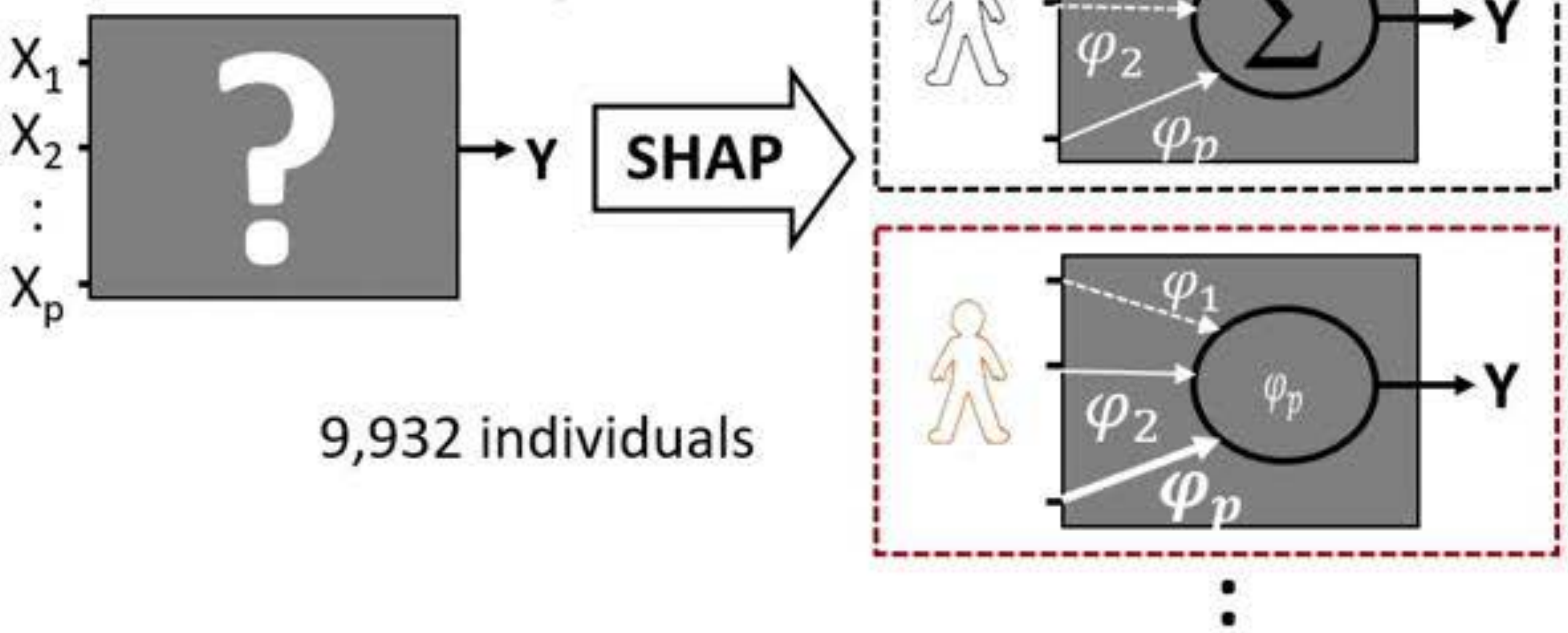

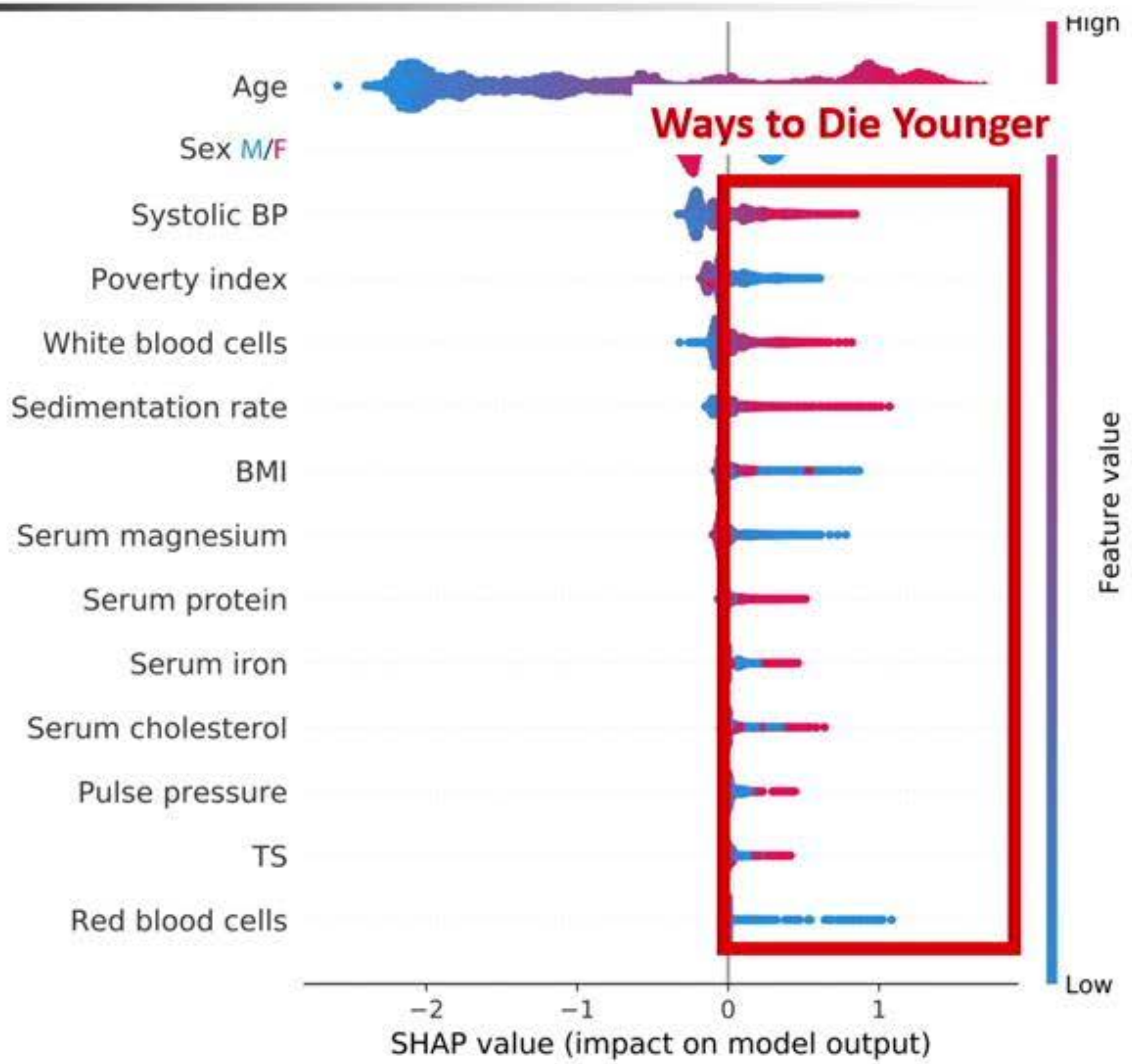

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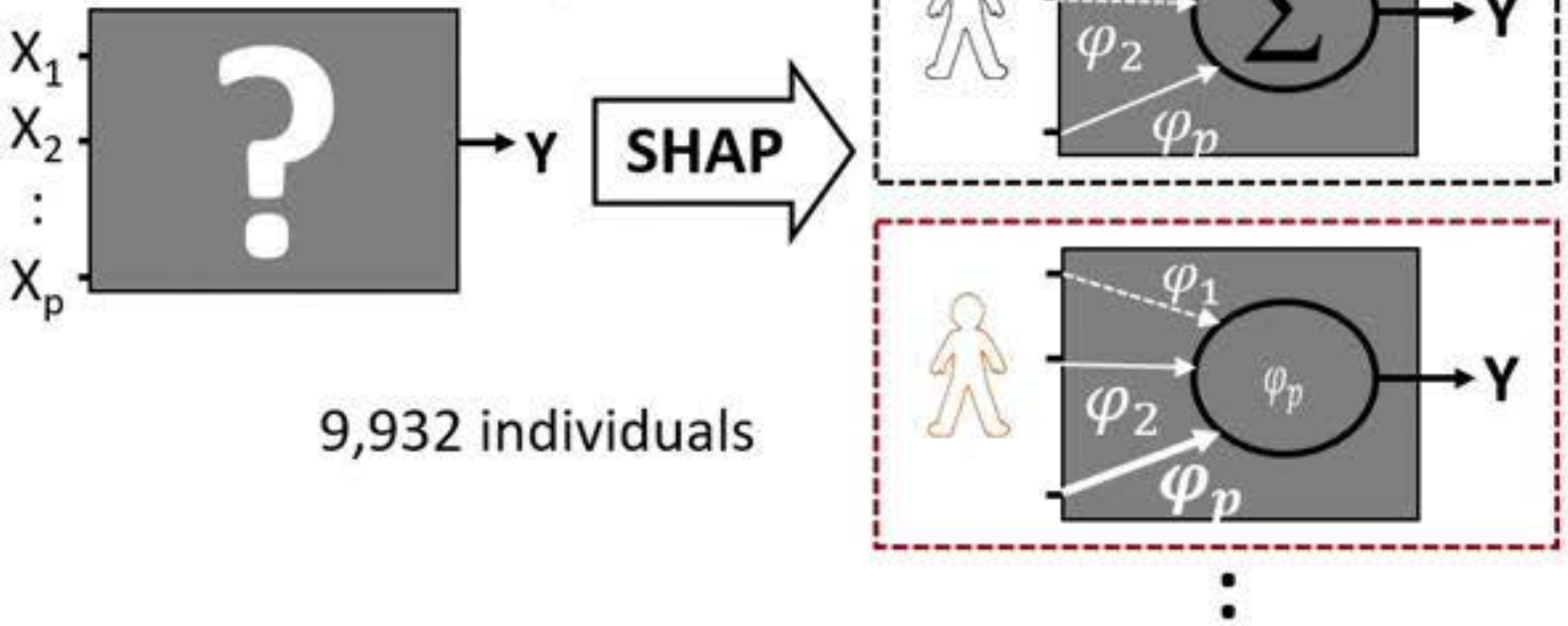

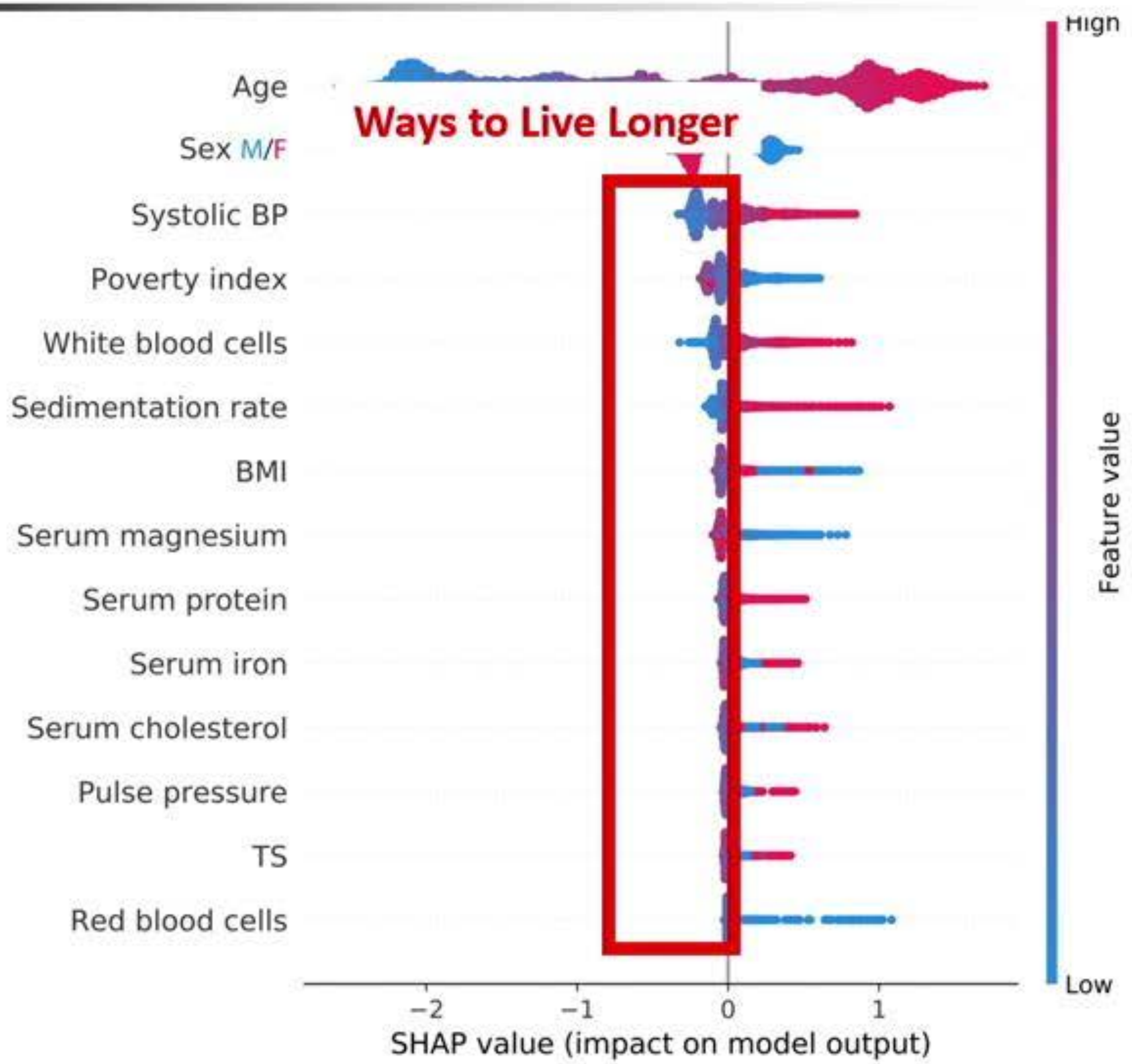

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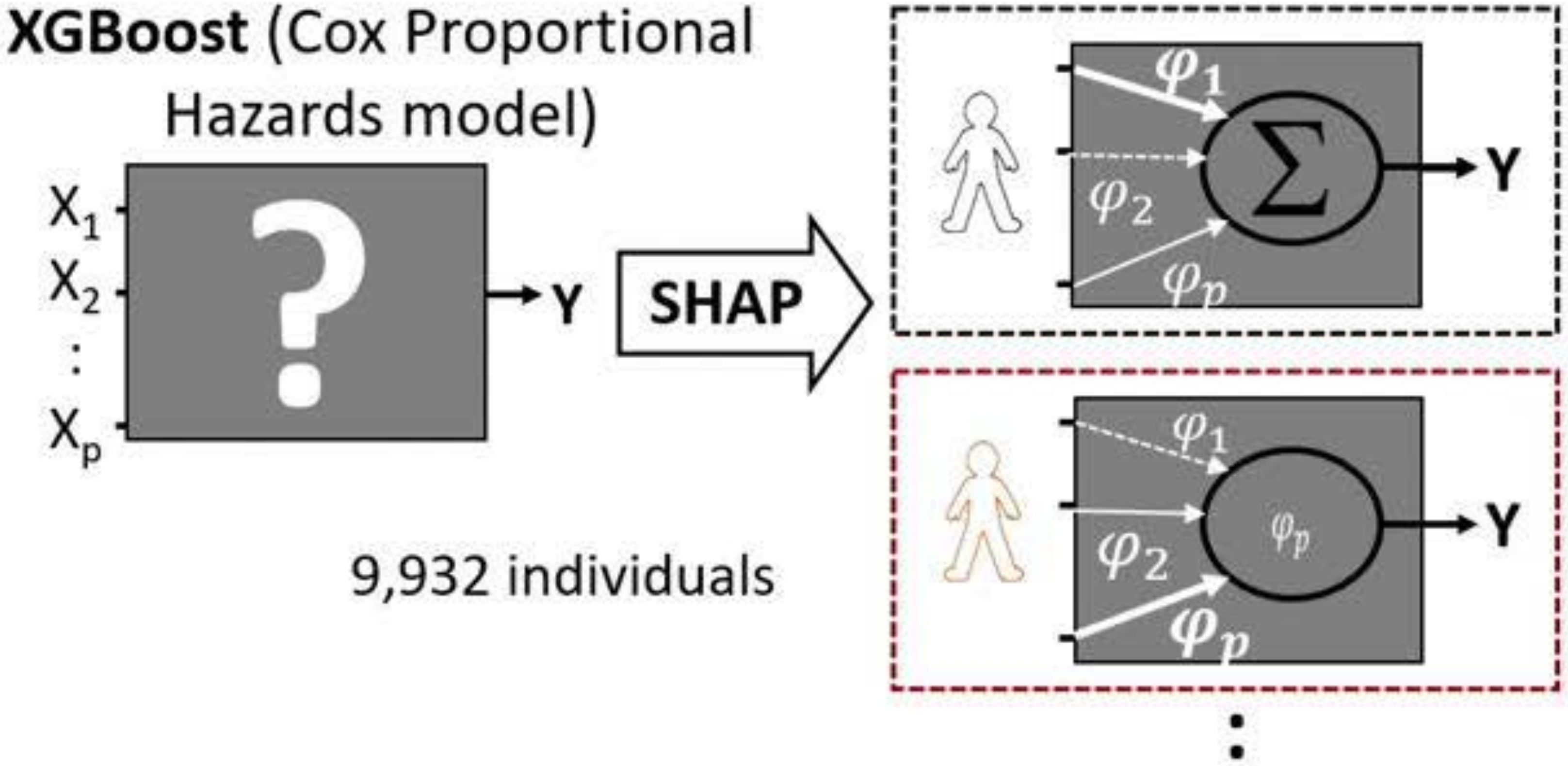

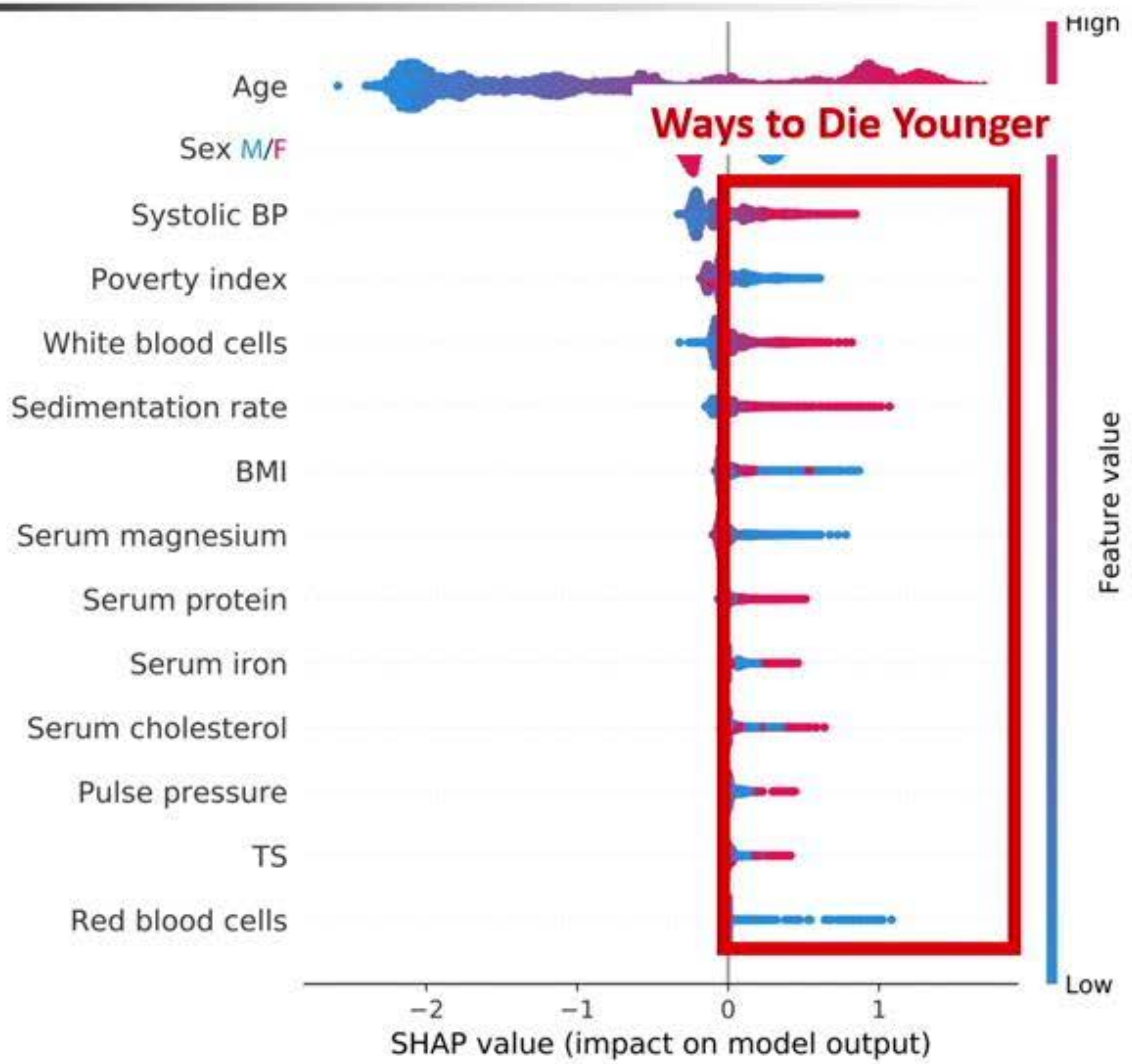

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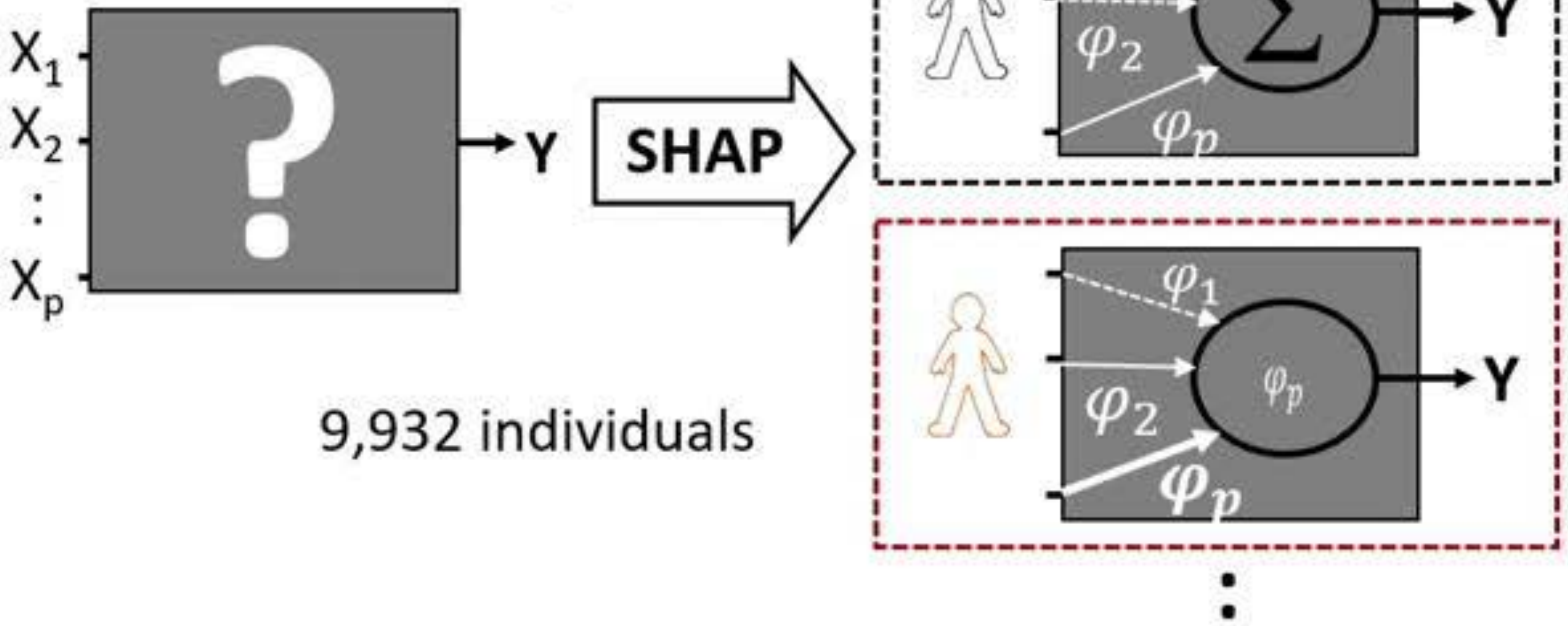

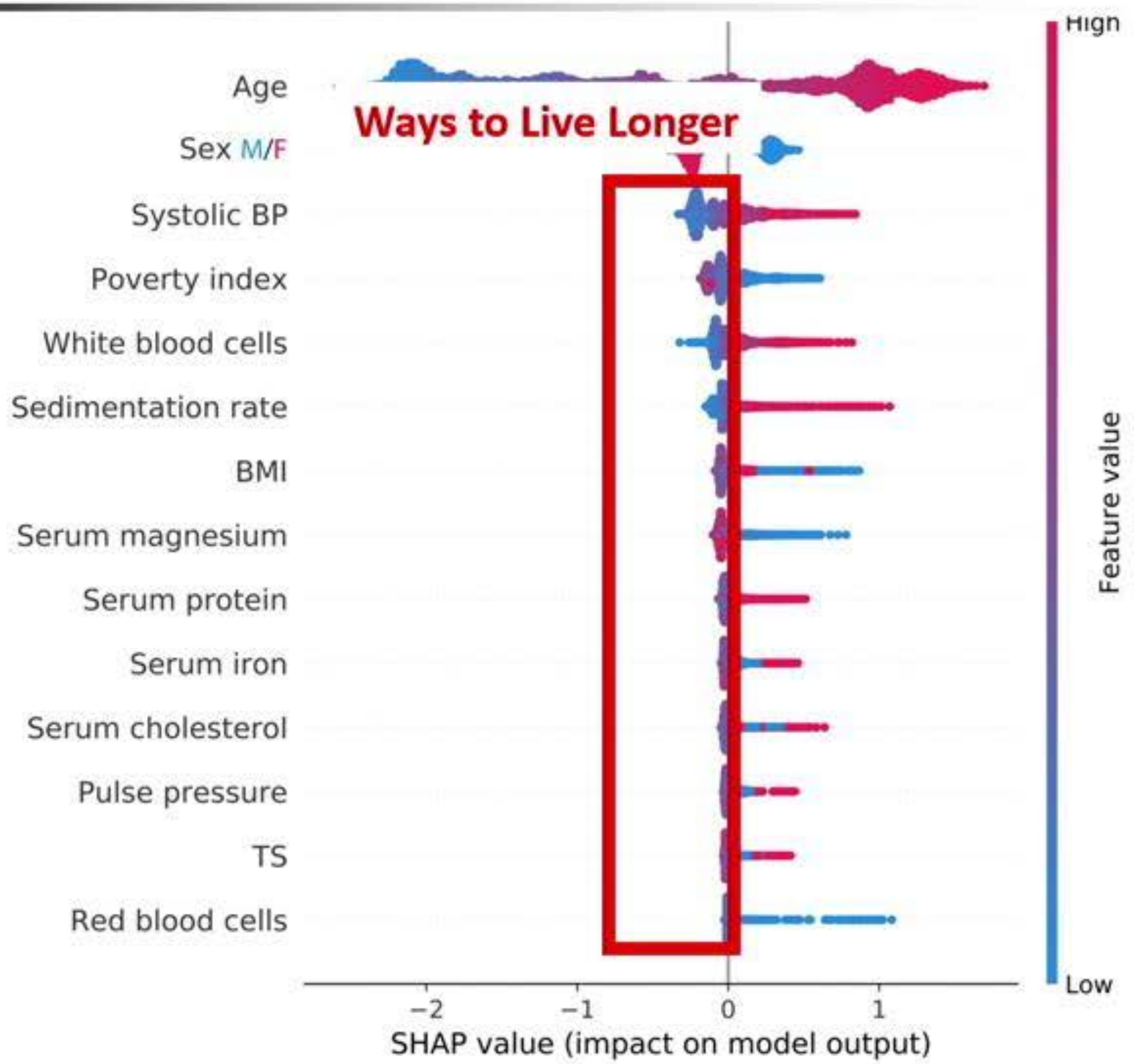

Using SHAP values as building blocks for interpretable ML: SHAP dependence plot


Scott


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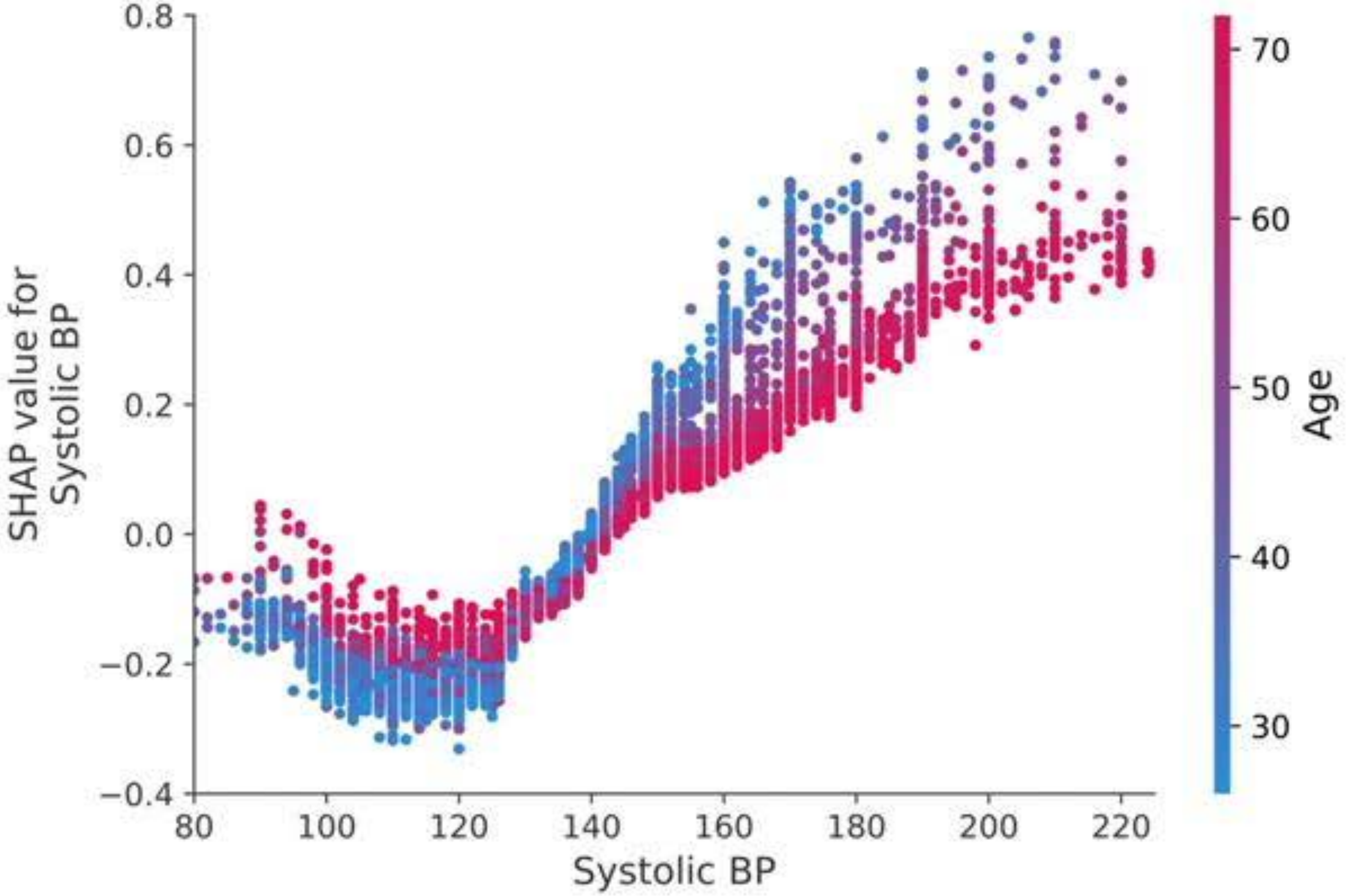
Hugh



Scott Lundberg, Gabe Erion, Hugh Chen, and Su-In Lee. **Accurate and Interpretable Machine Learning with Trees.**

Using SHAP values as building blocks for interpretable ML: SHAP dependence plot


Scott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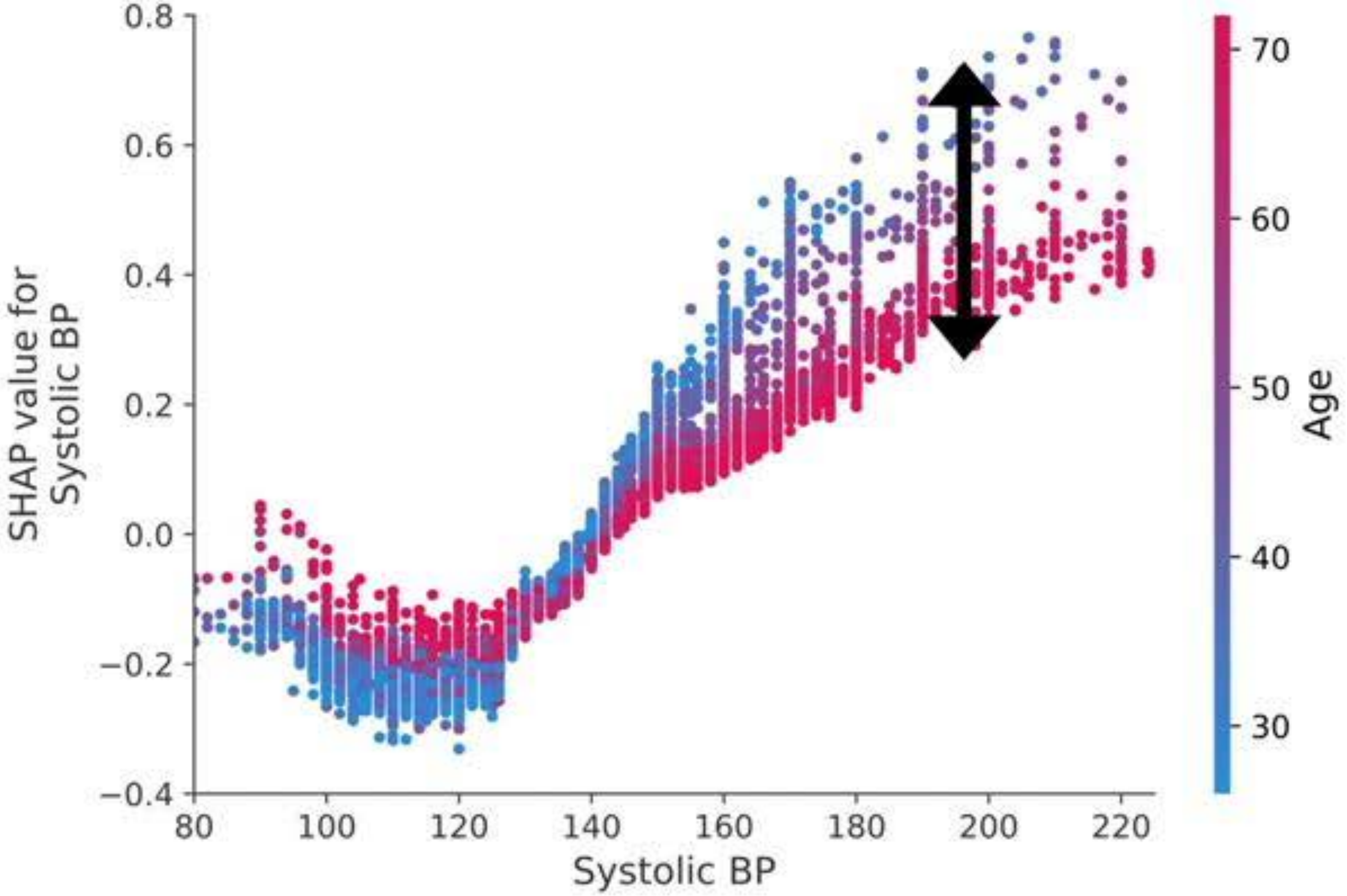
Hugh

Interaction effect:
Early onset high blood pressure is worse



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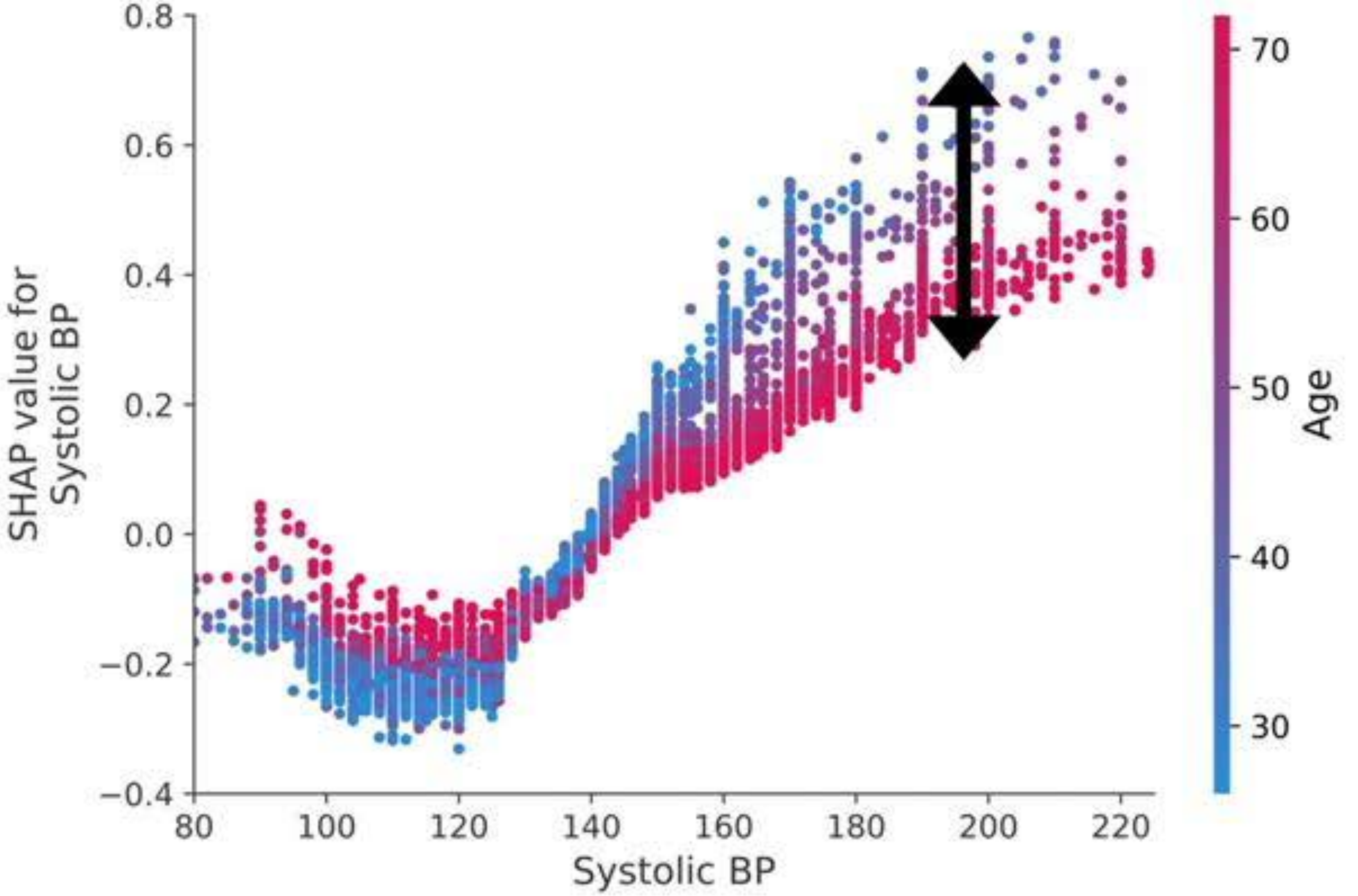

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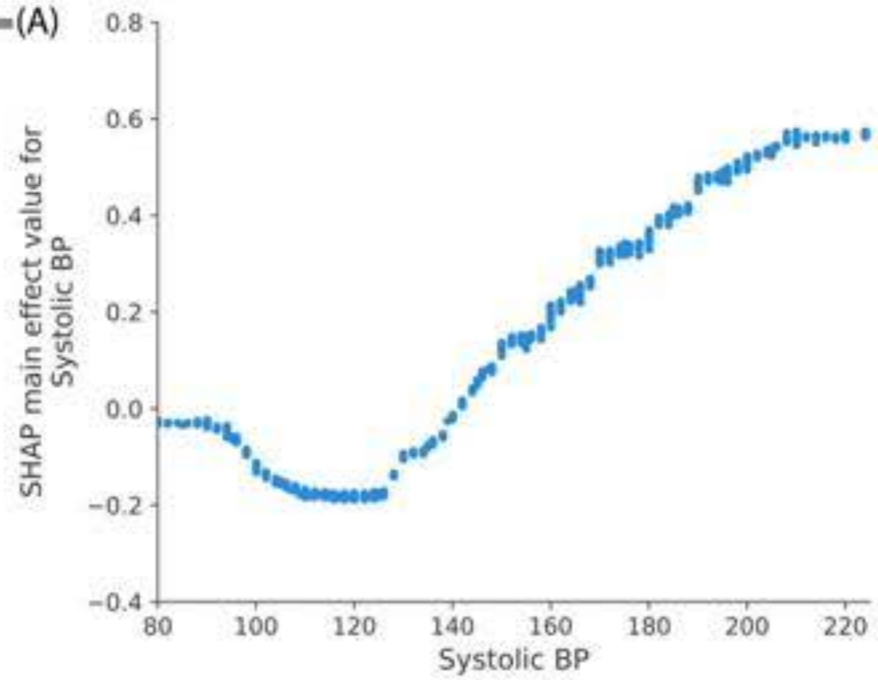

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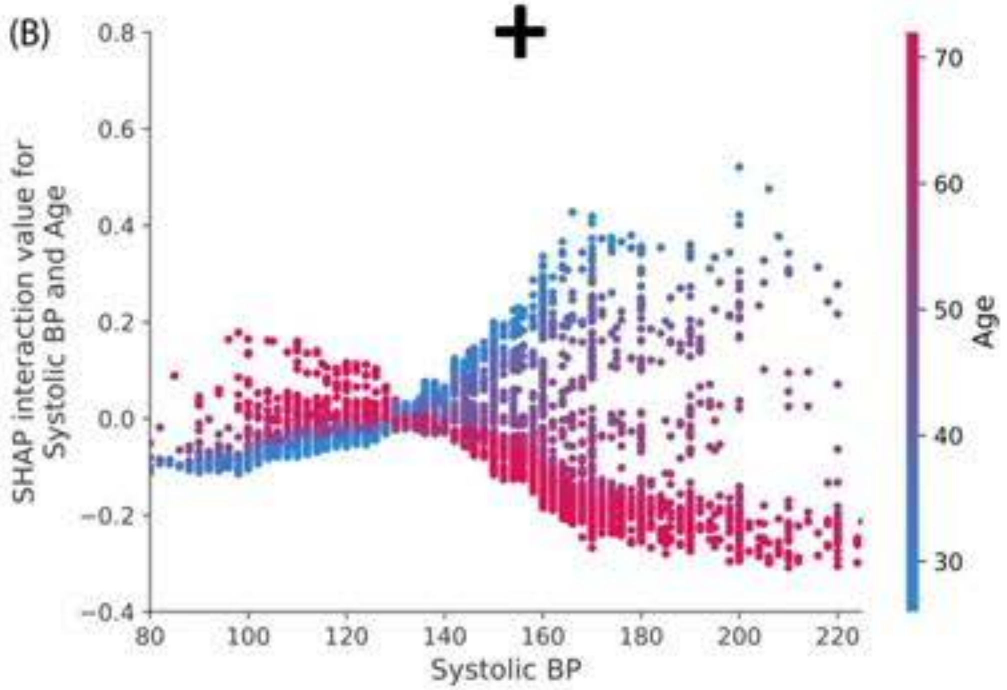

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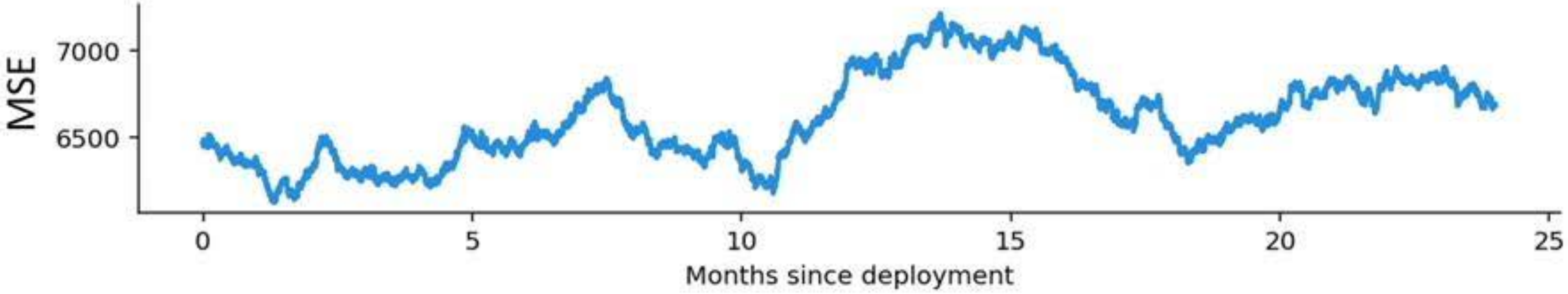
Surgery duration prediction error



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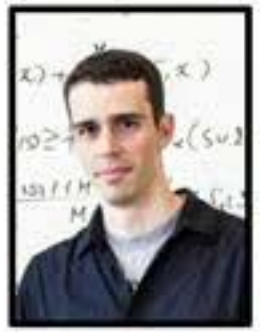
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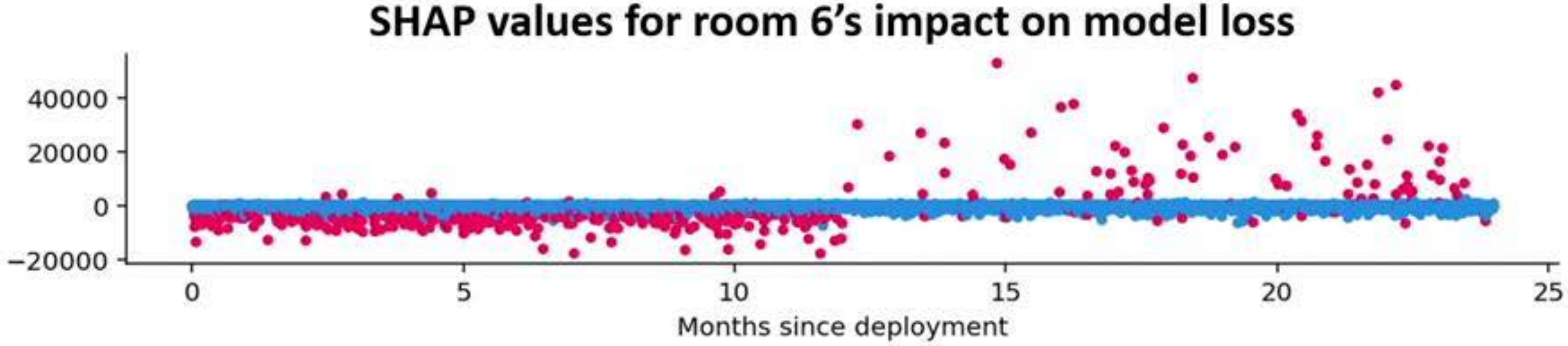


Interpretable ML can transform important areas of medicine

Prediction & decision support systems in hospitals

- Make interpretable predictions from complex models.

Cancer precision medicine

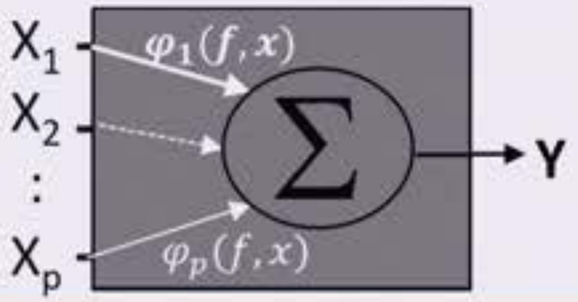
- Learn interpretable feature representations.

Alzheimer's disease therapeutic target discovery

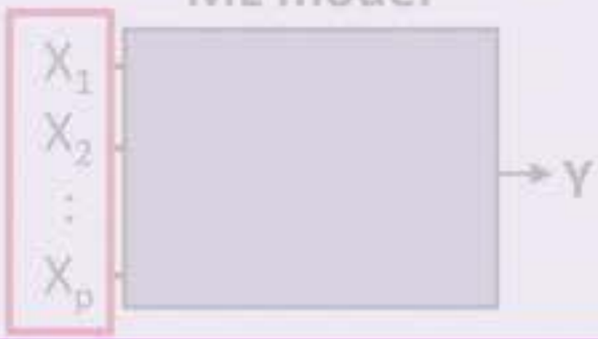
- Integrate data sets for statistical power and interpretability.

General ML techniques

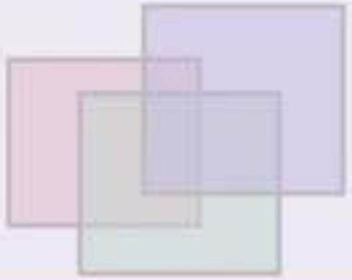
Black Box



ML model



Data integration



Bedside applications

Basic science

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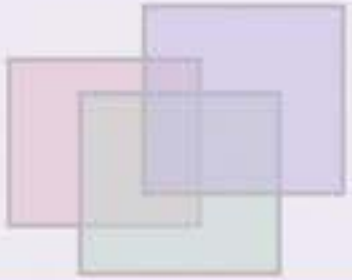

Bedside applications

Basic science

Precision medicine in cancer treatment

Patient X

Lee*, Celik*, et al. (2018)
*Nature Comm. (*co-first authors)*

Precision medicine in cancer treatment

- Acute myeloid leukemia (AML)
  - Cancer of the blood and bone marrow cells
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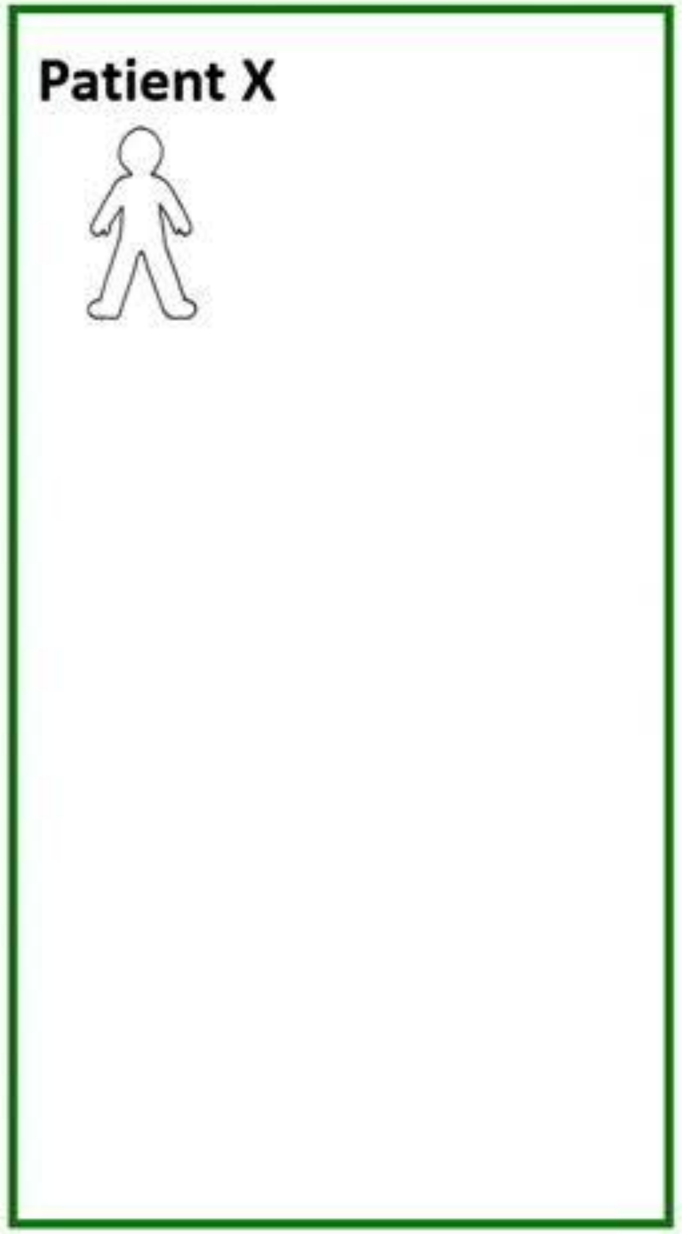

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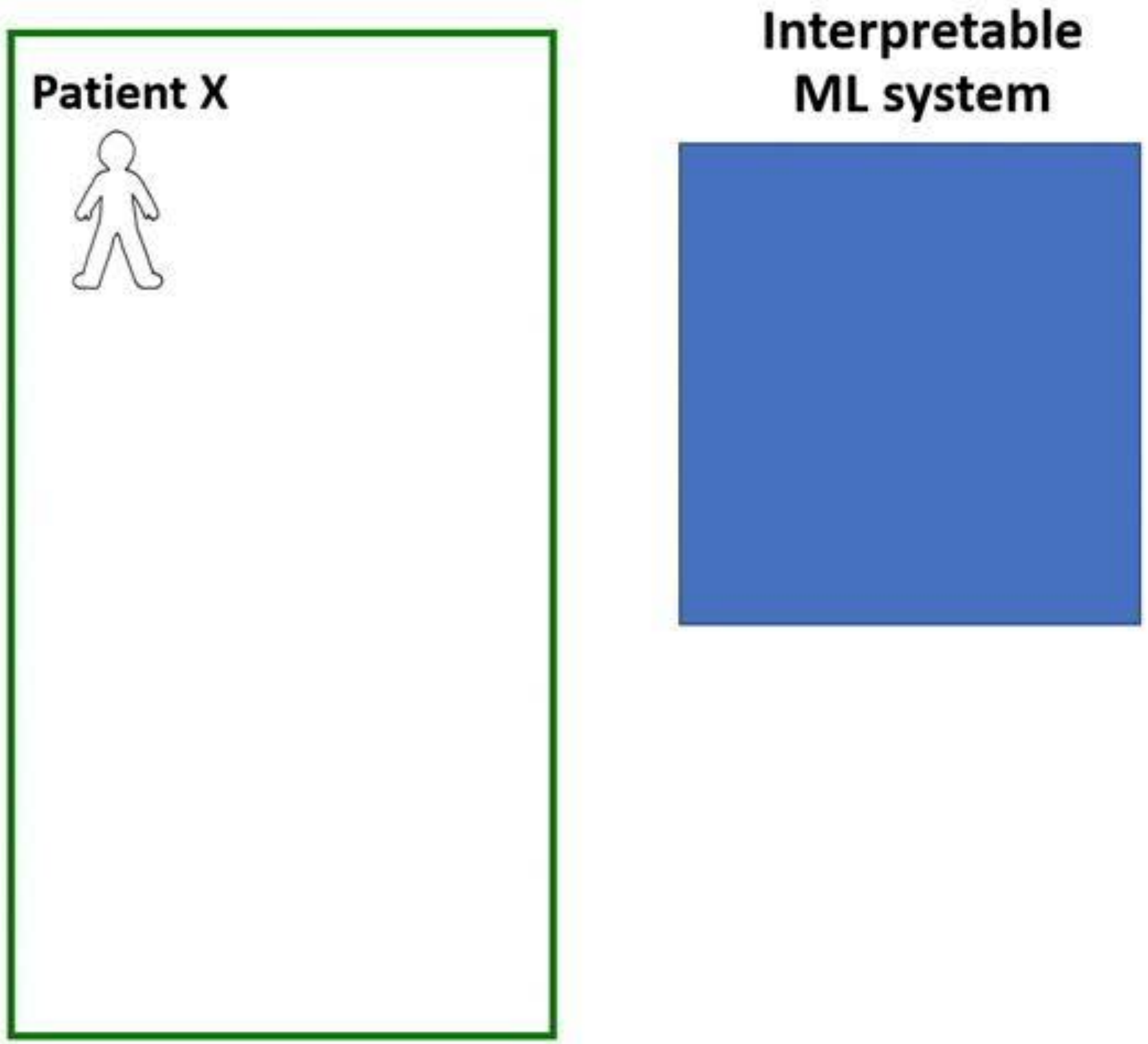

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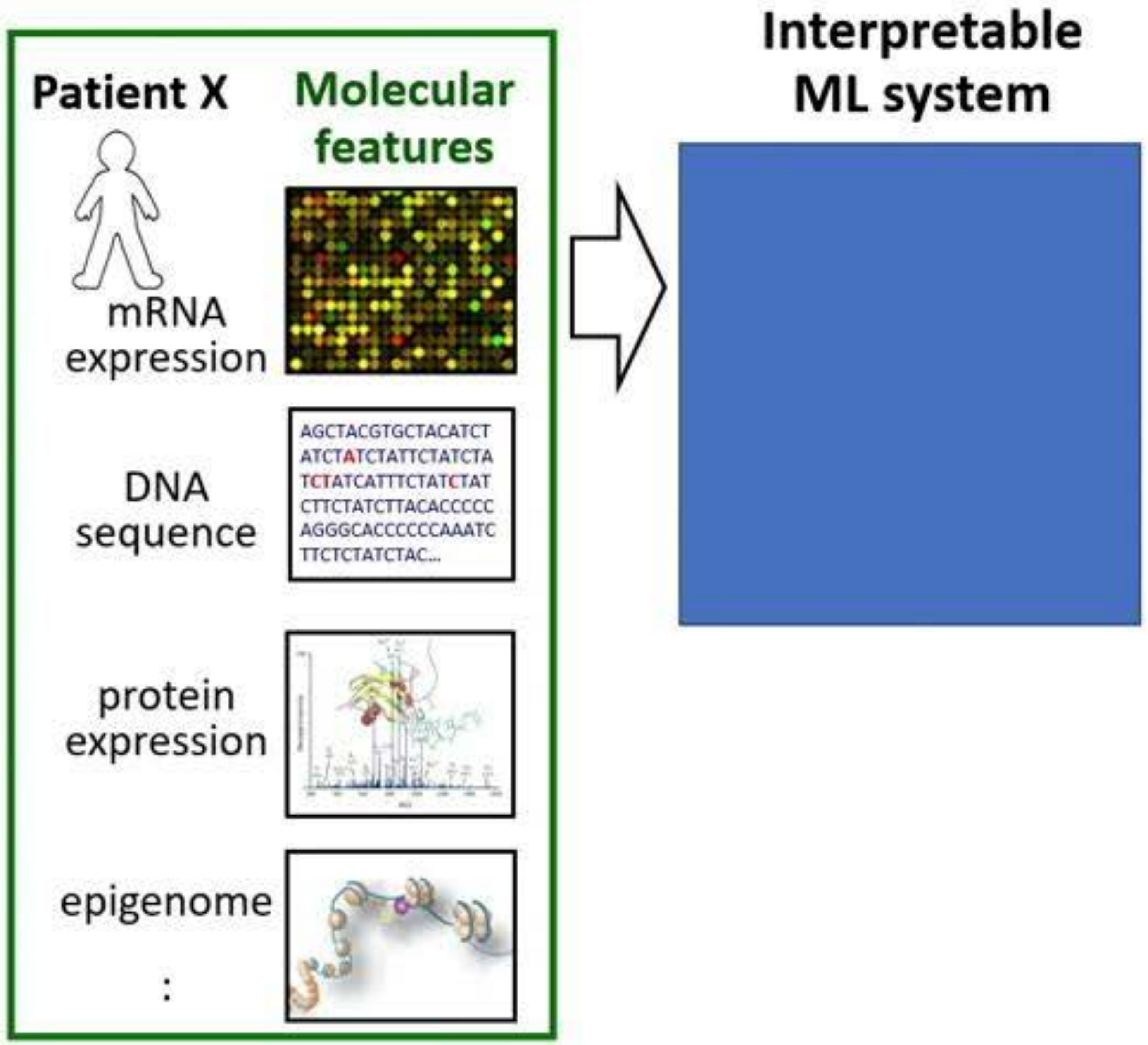

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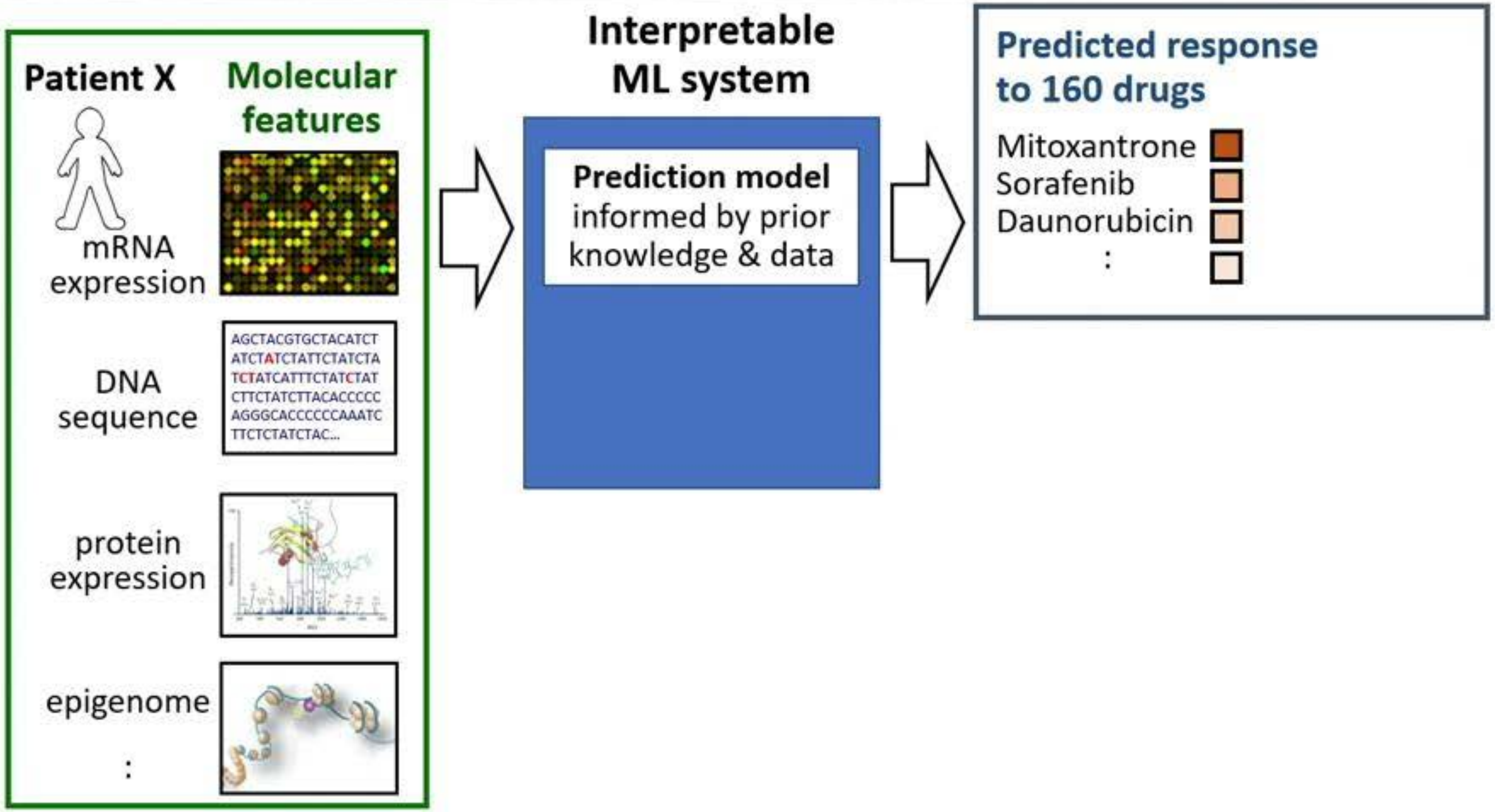

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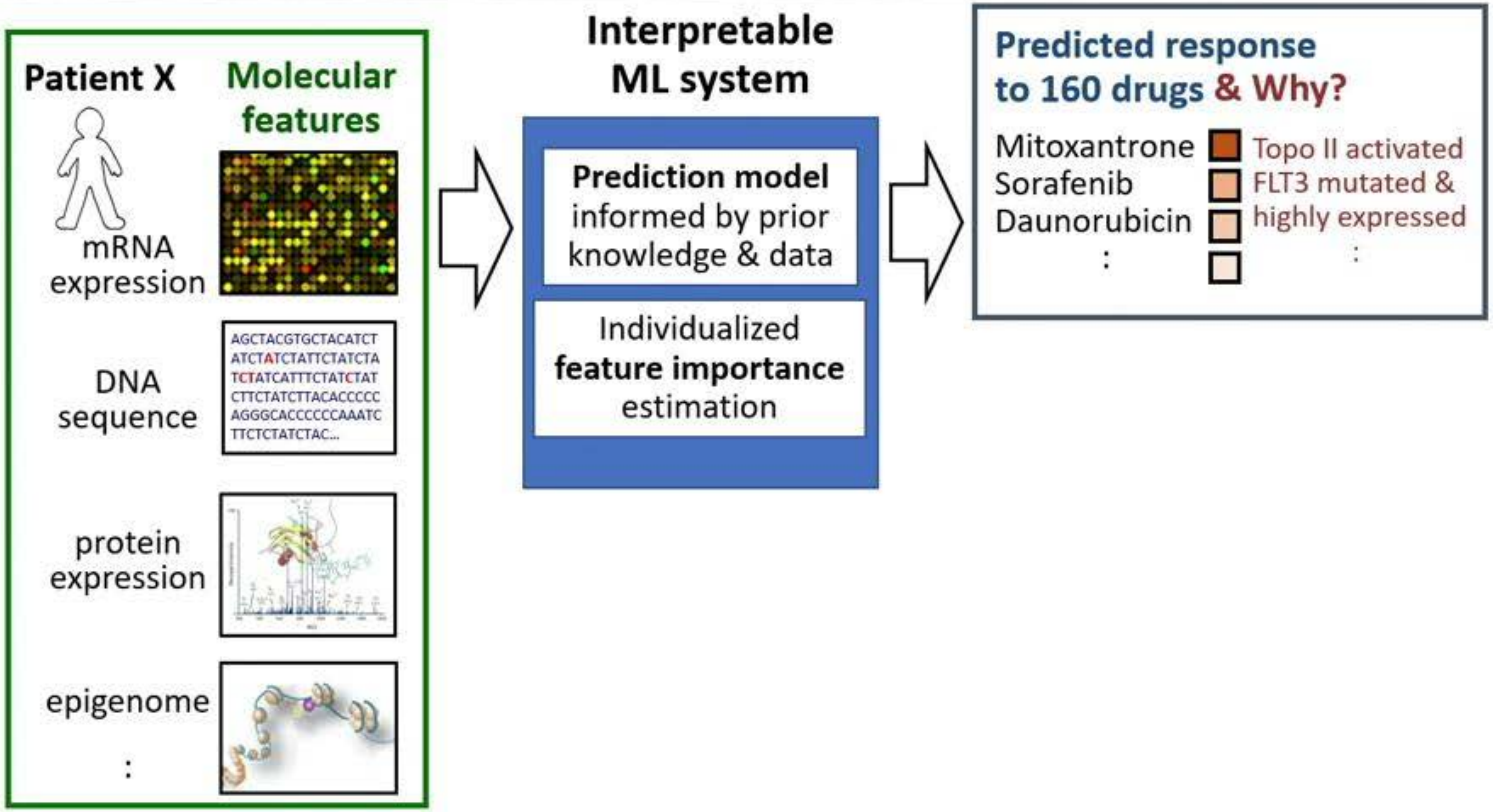

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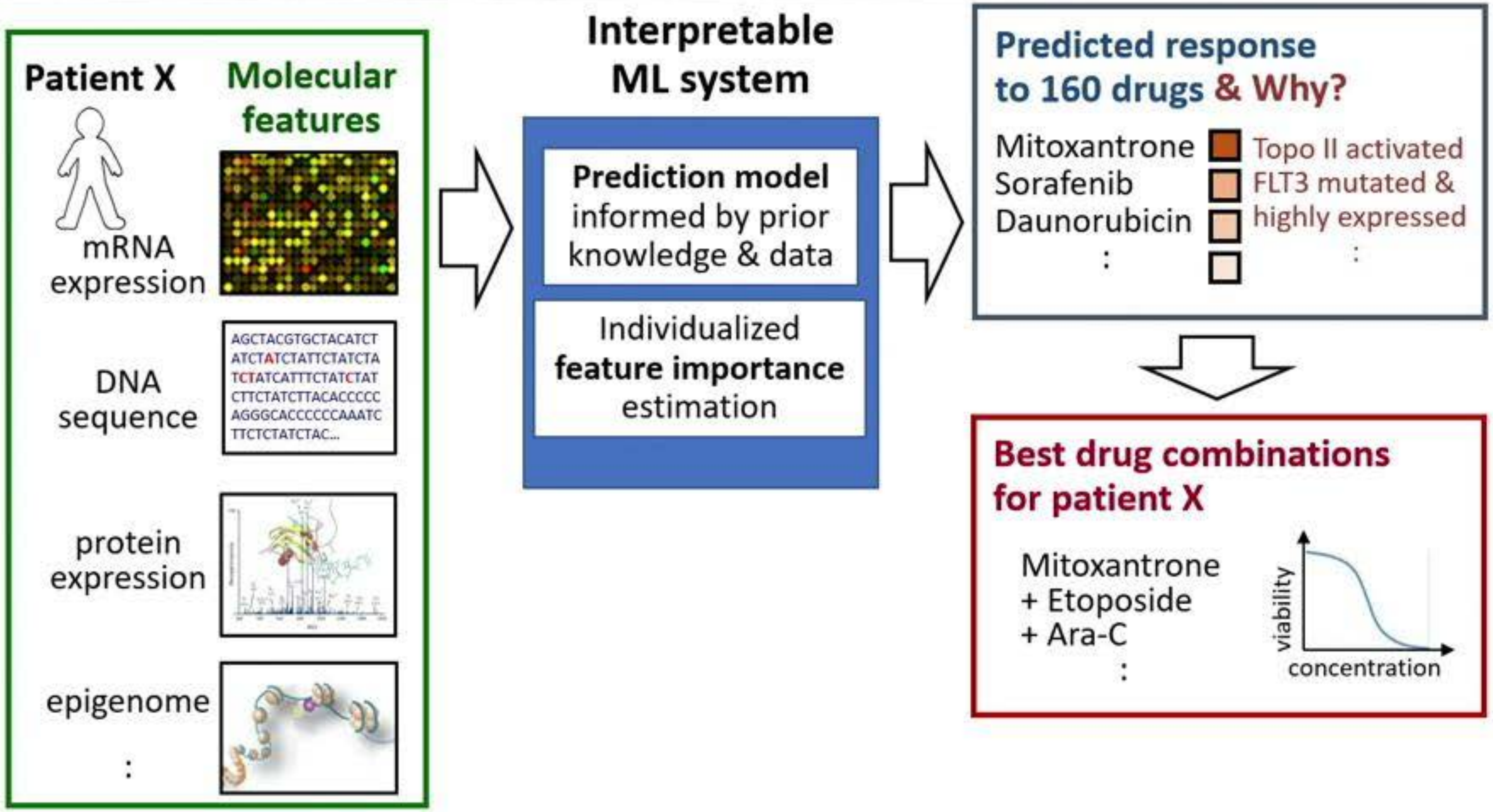

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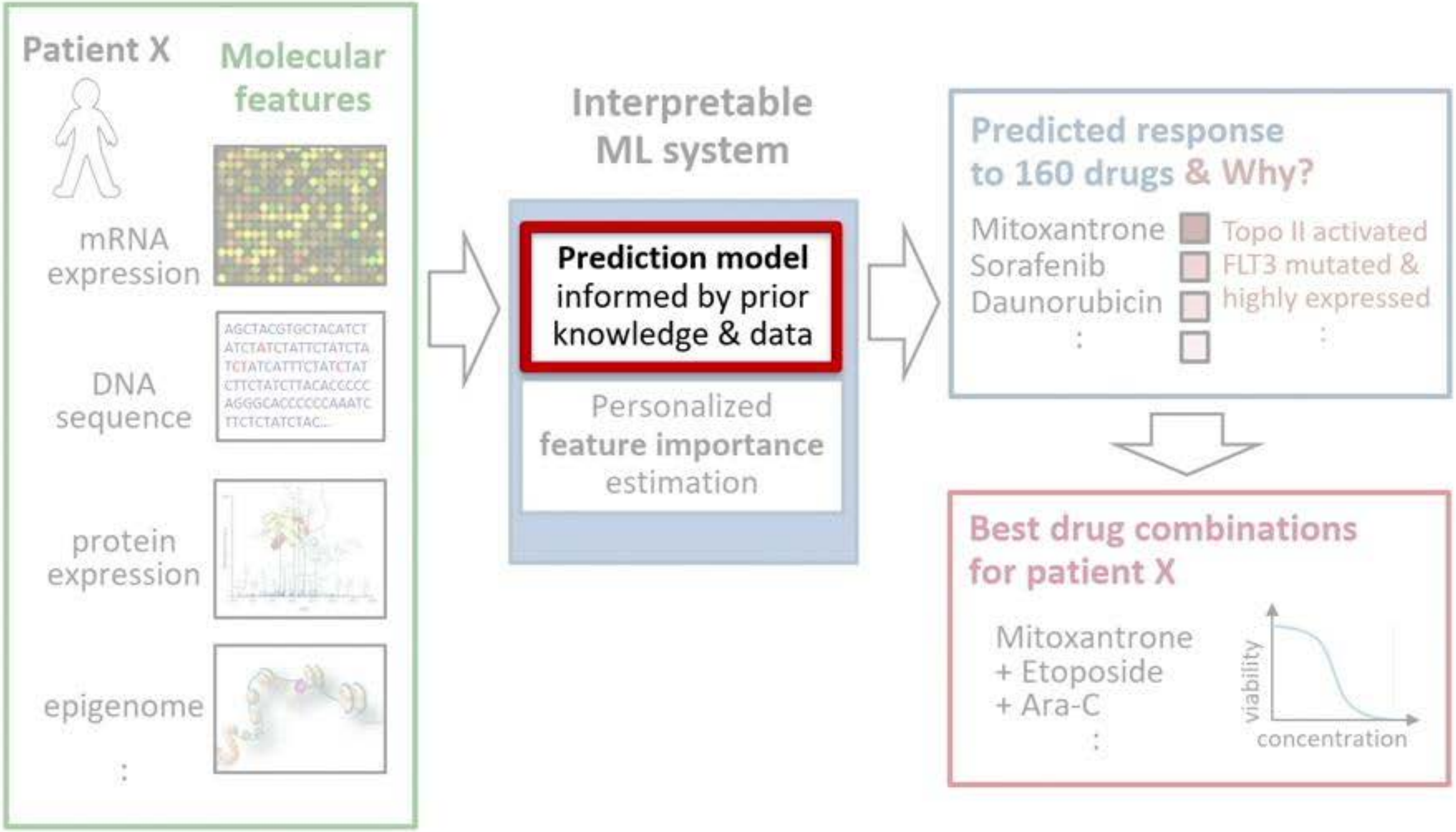
Learn interpretable feature representation



A naïve solution: Supervised learning approach

Safiye

Training Data

Each patient

A naïve solution: Supervised learning approach

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Training Data

<u>Each patient</u>

Hematology

Drs. Pam Becker Tony Blau

A naïve solution: Supervised learning approach

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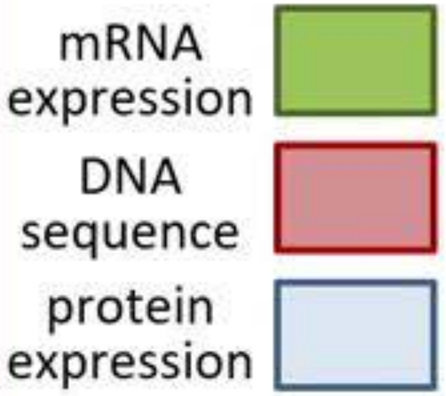
Each patient

Molecular profiling



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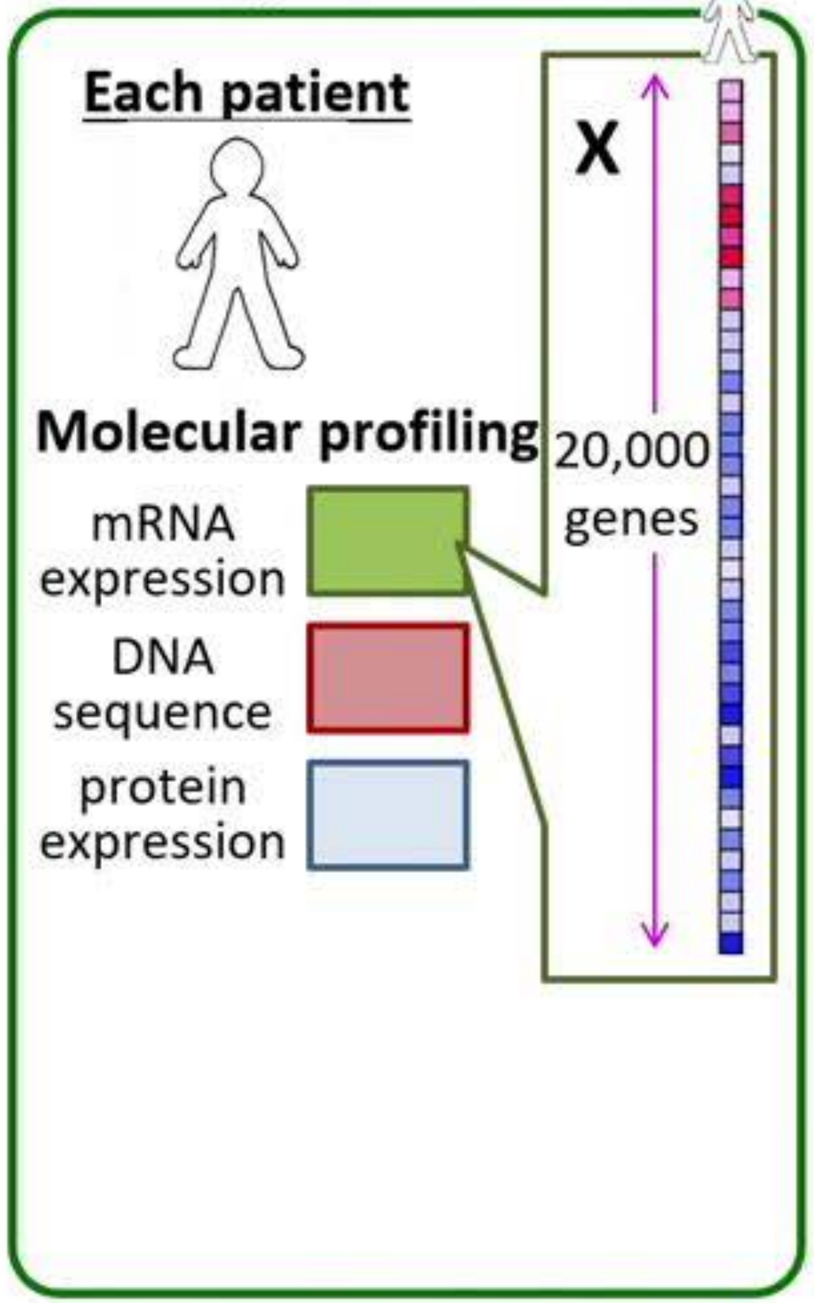

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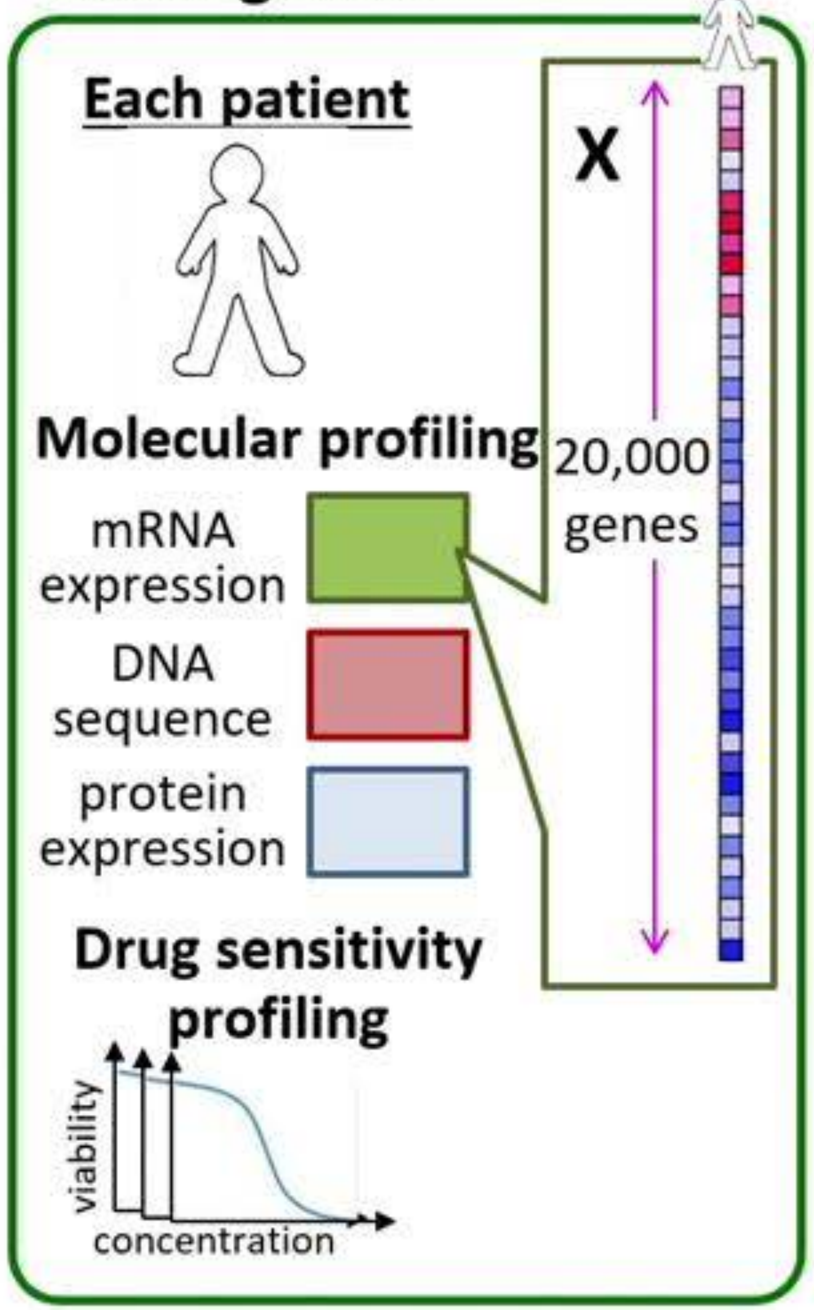

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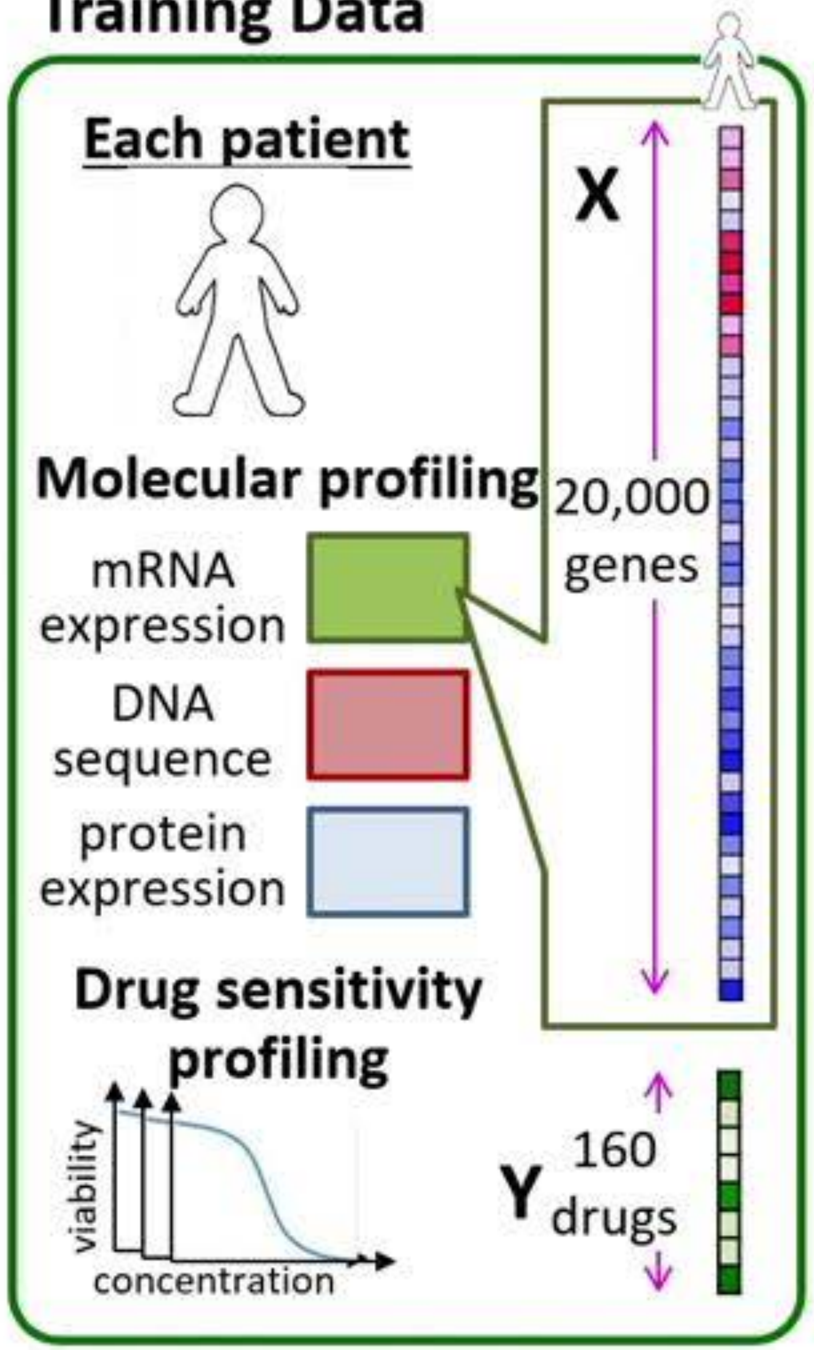

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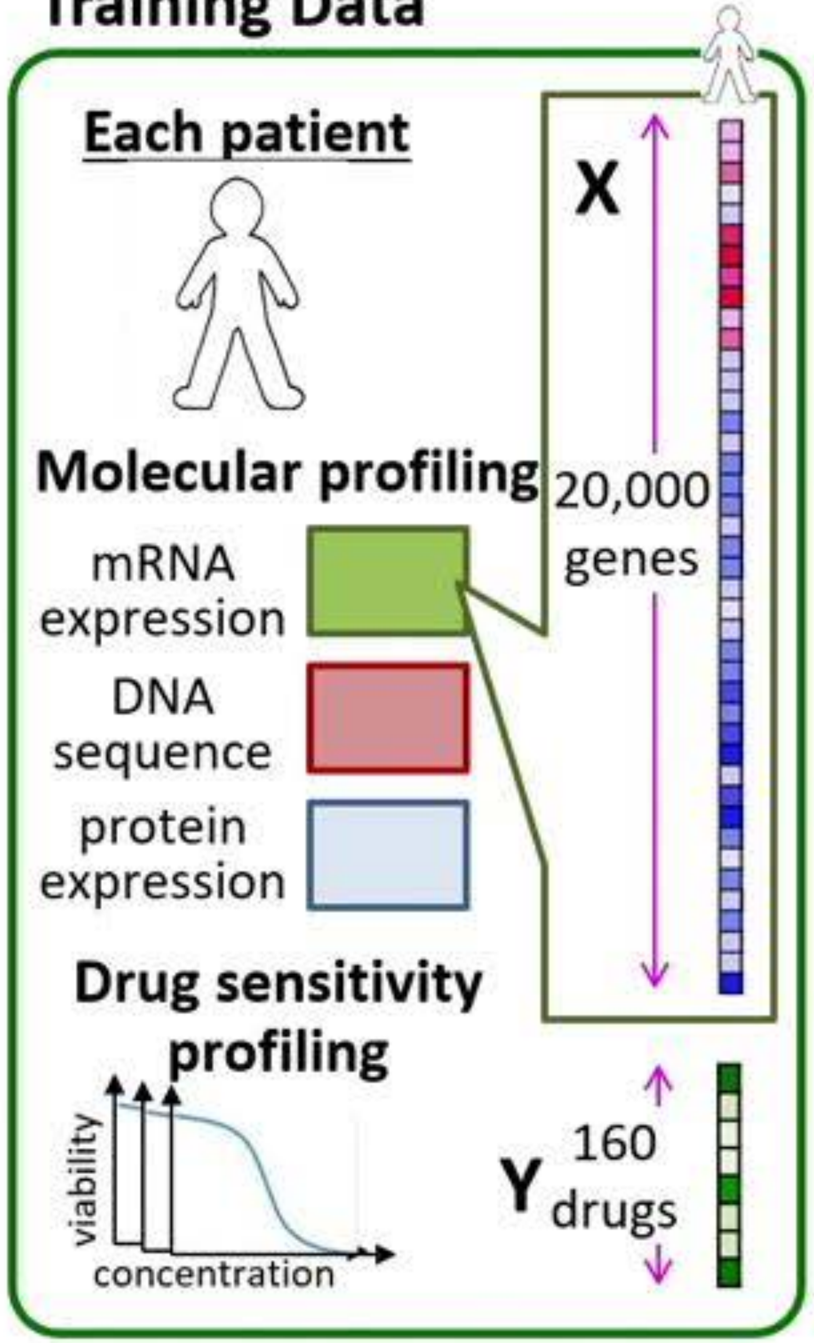
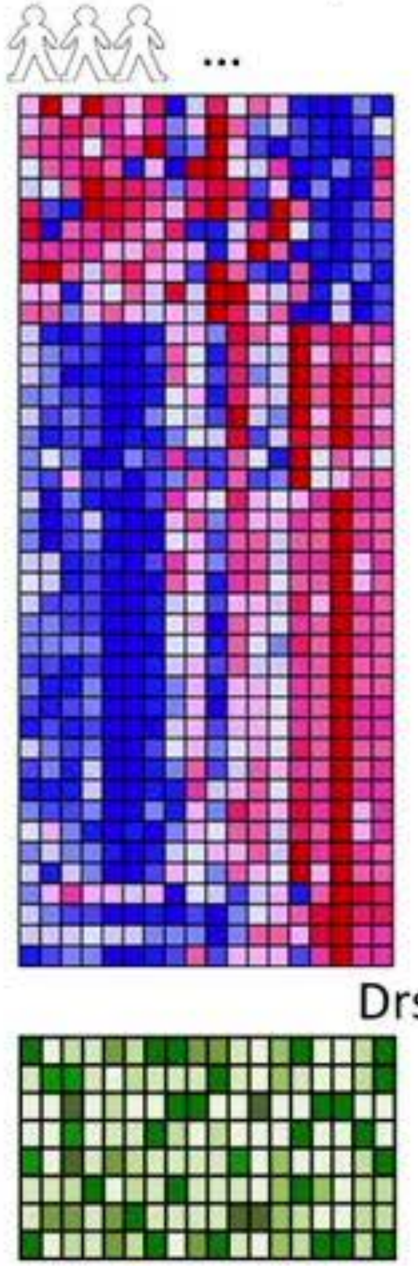


Samples: 200 AML patients



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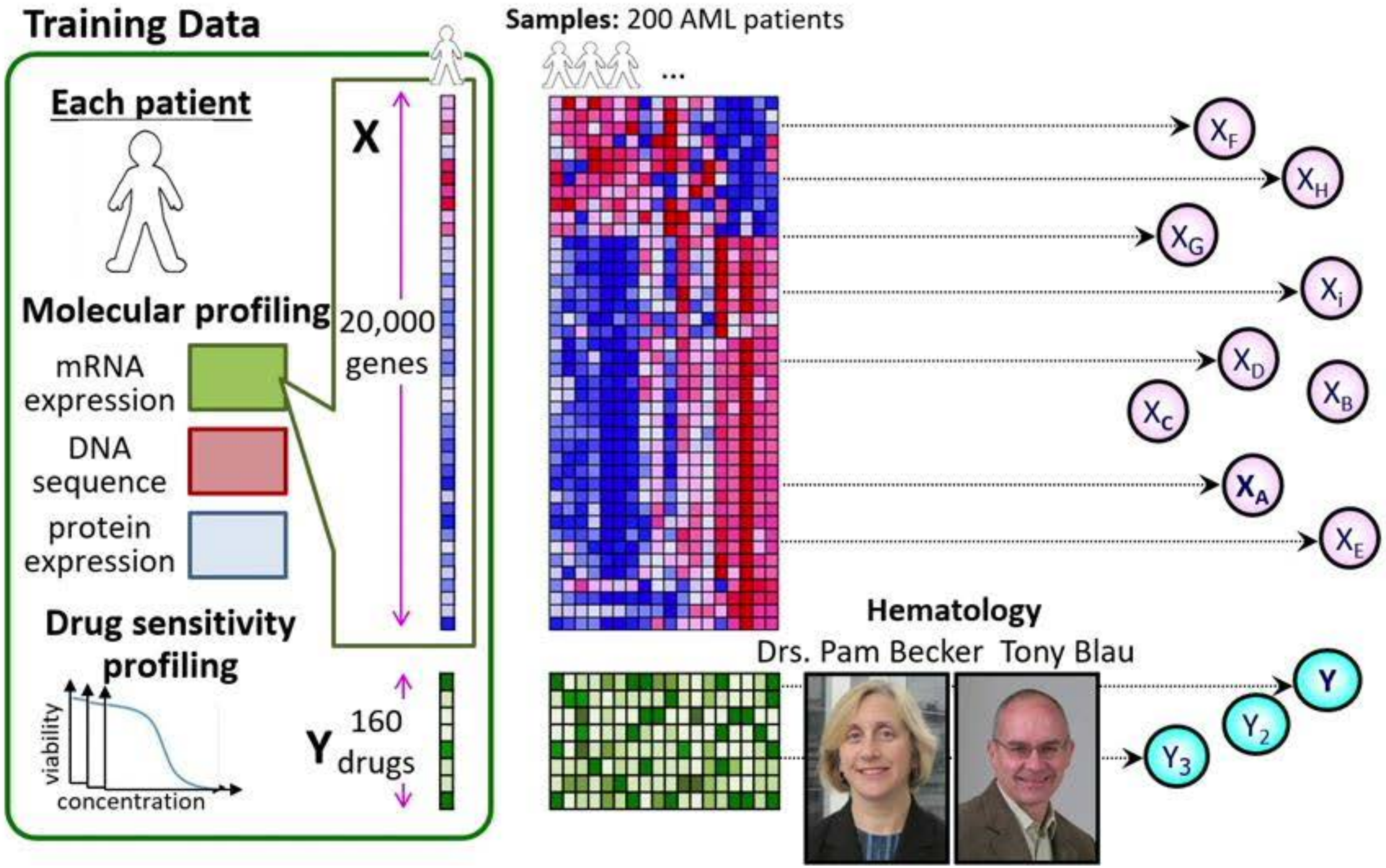

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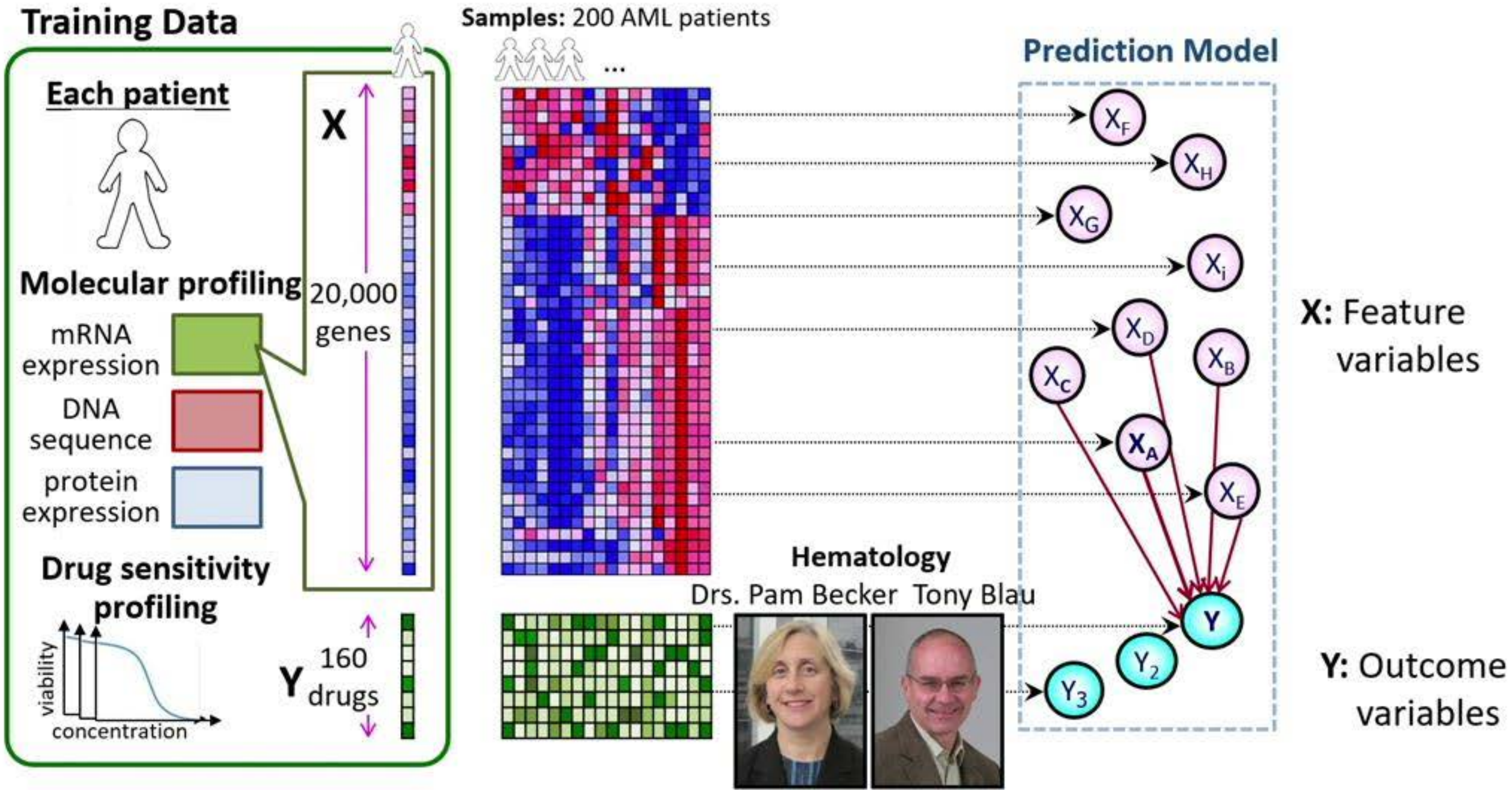

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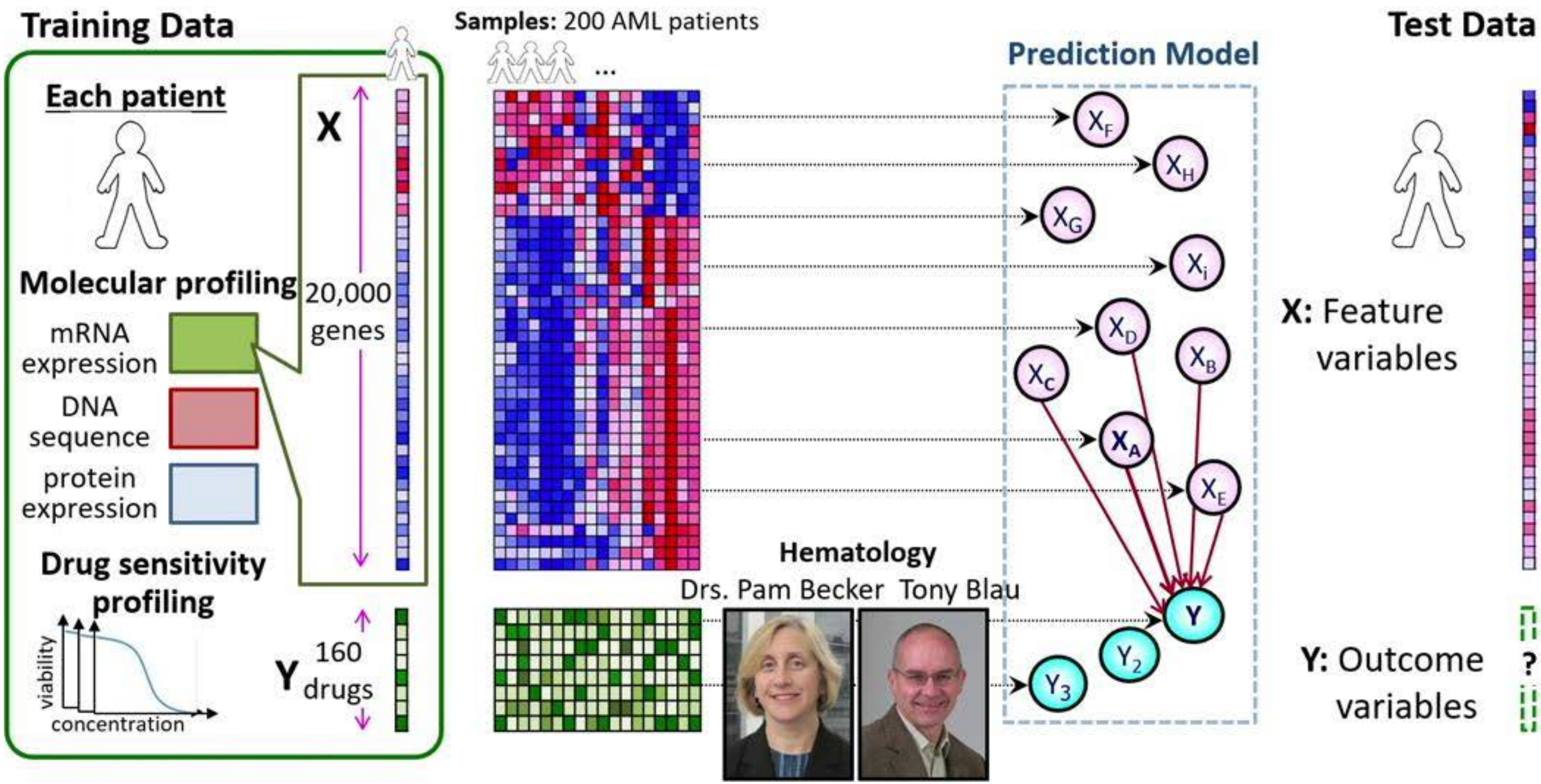

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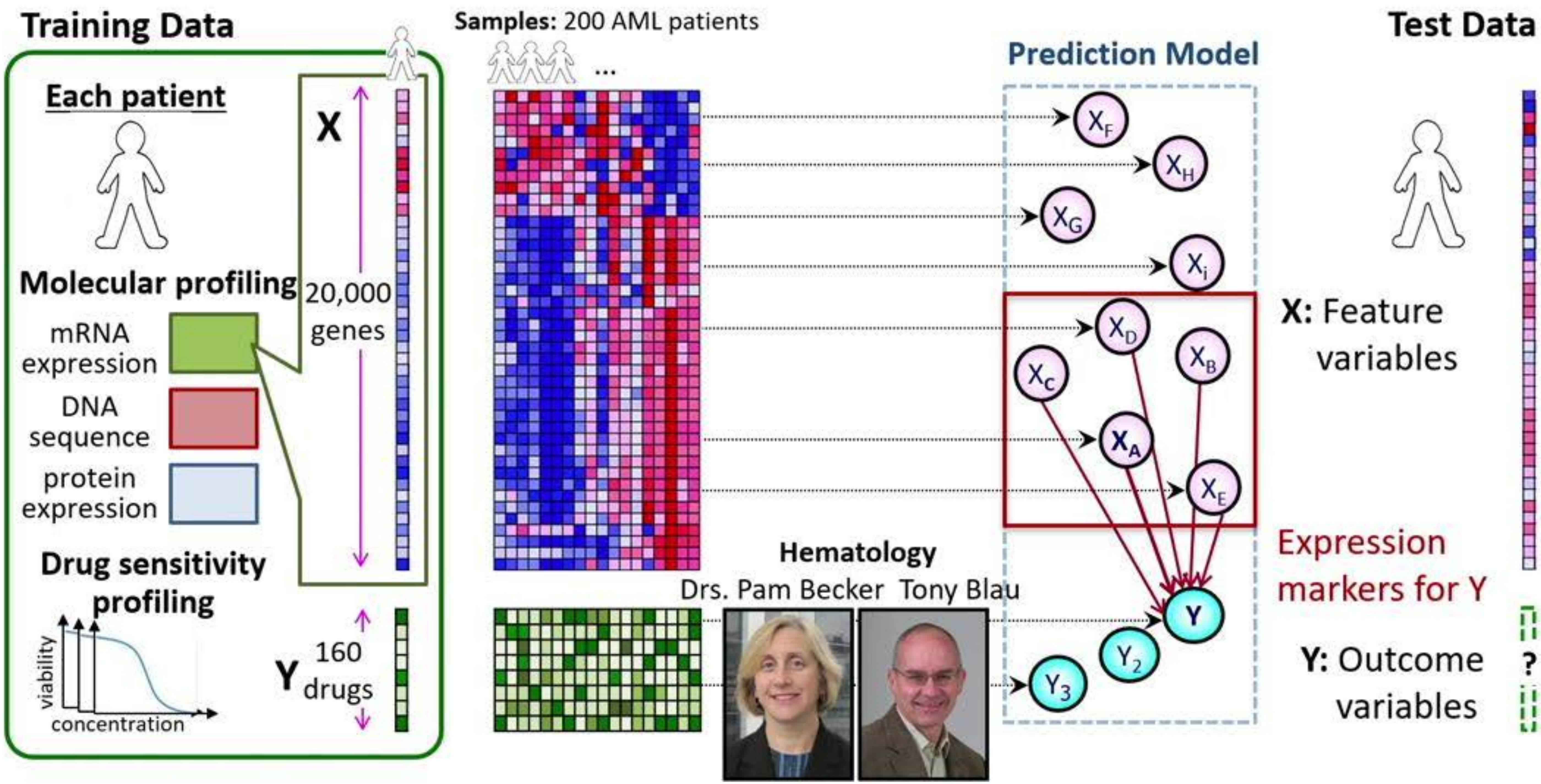

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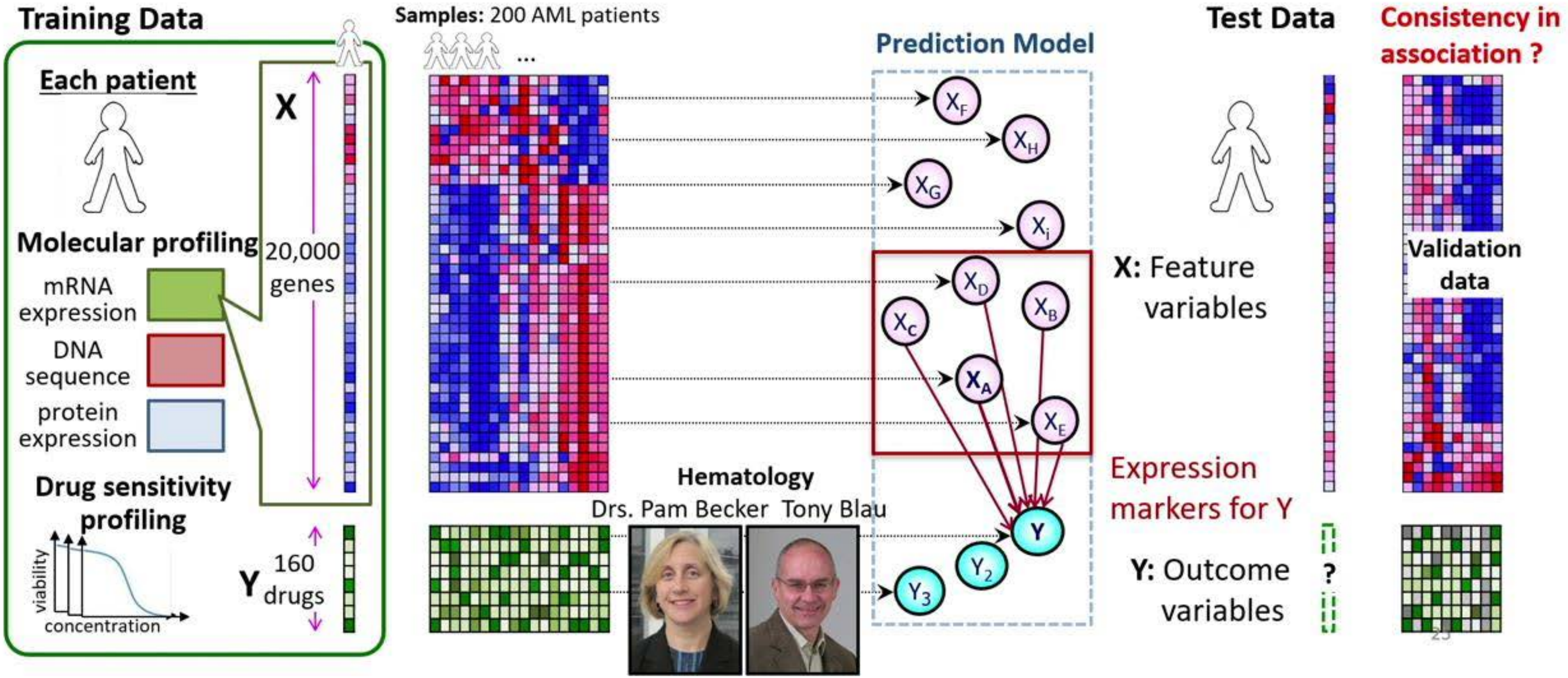
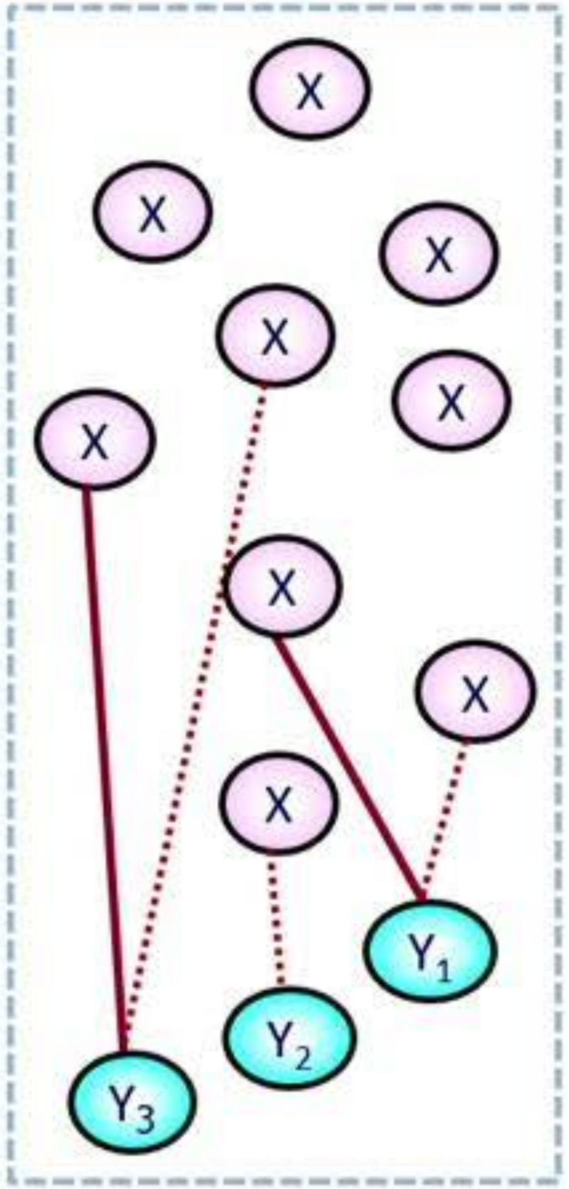


Only a small fraction of significant gene-drug associations are replicated in validation data

Safiye

Validation data



$$\text{Consistency rate (True Discovery Rate)} = \frac{\text{Number of replicated associations (—)}}{\text{Number of significant associations (— or ····)}}$$

Lee*, Celik*, et al. (2018) *Nature Communications*

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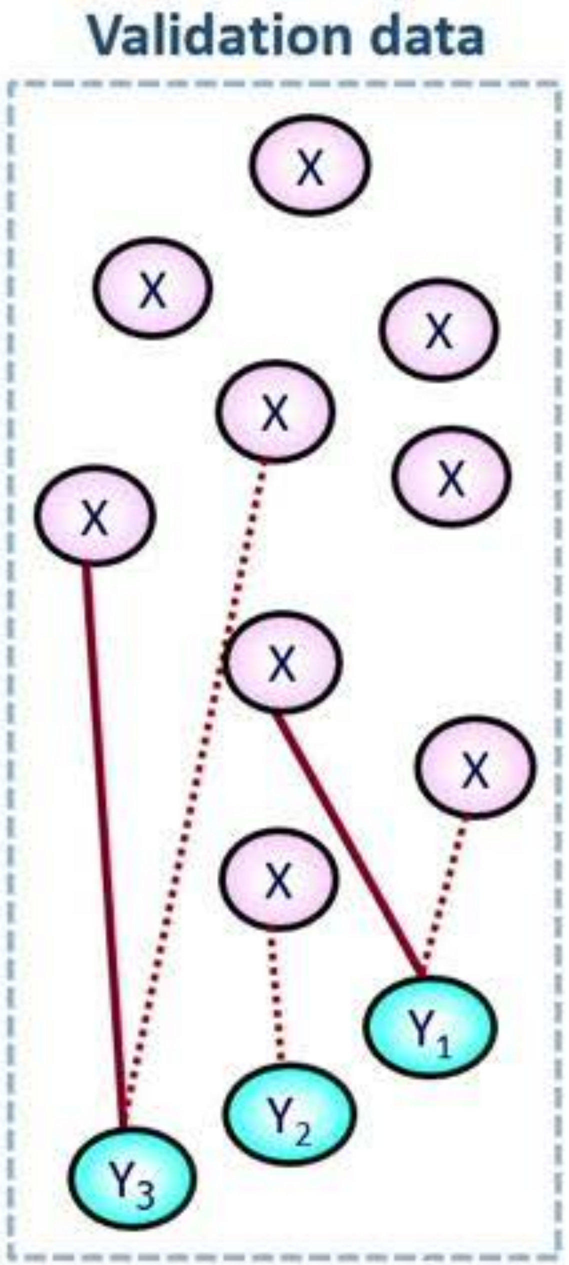

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ordered list of gene-drug pairs based on degrees of associations

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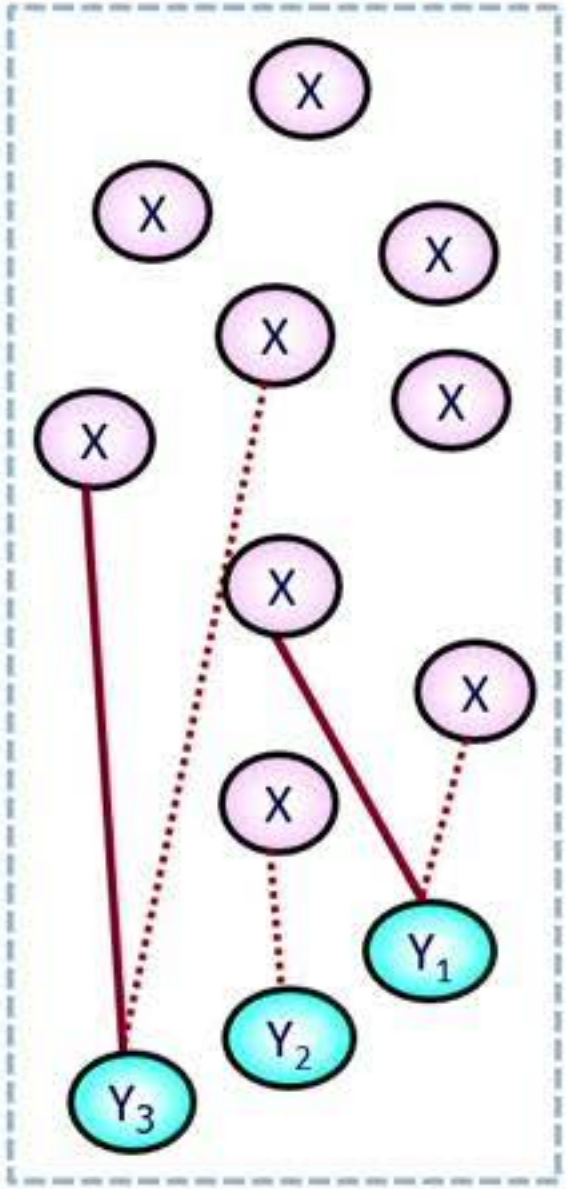

Consistency rate (True Discovery Rate) = **Number of replicated associations** (—) / **Number of significant associations** (— or ···)

ordered list of gene-drug pairs based on degrees of associations

200 400 600 800 1000 1200 1400 1600 1800 2000 2200

average # associations per drug to follow up on

Lee*, Celik*, et al. (2018)
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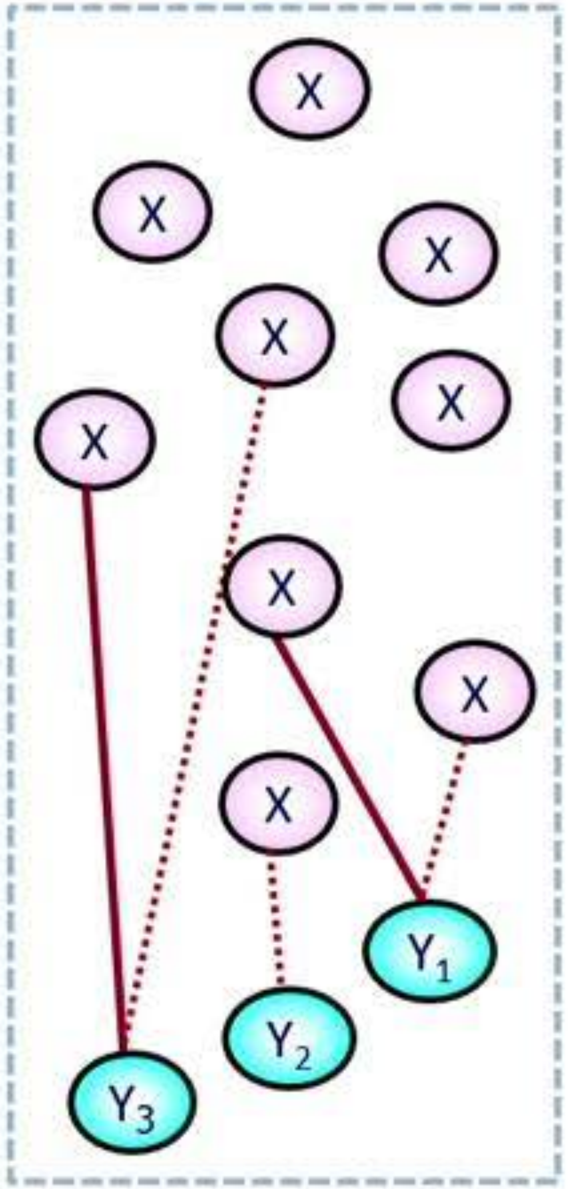

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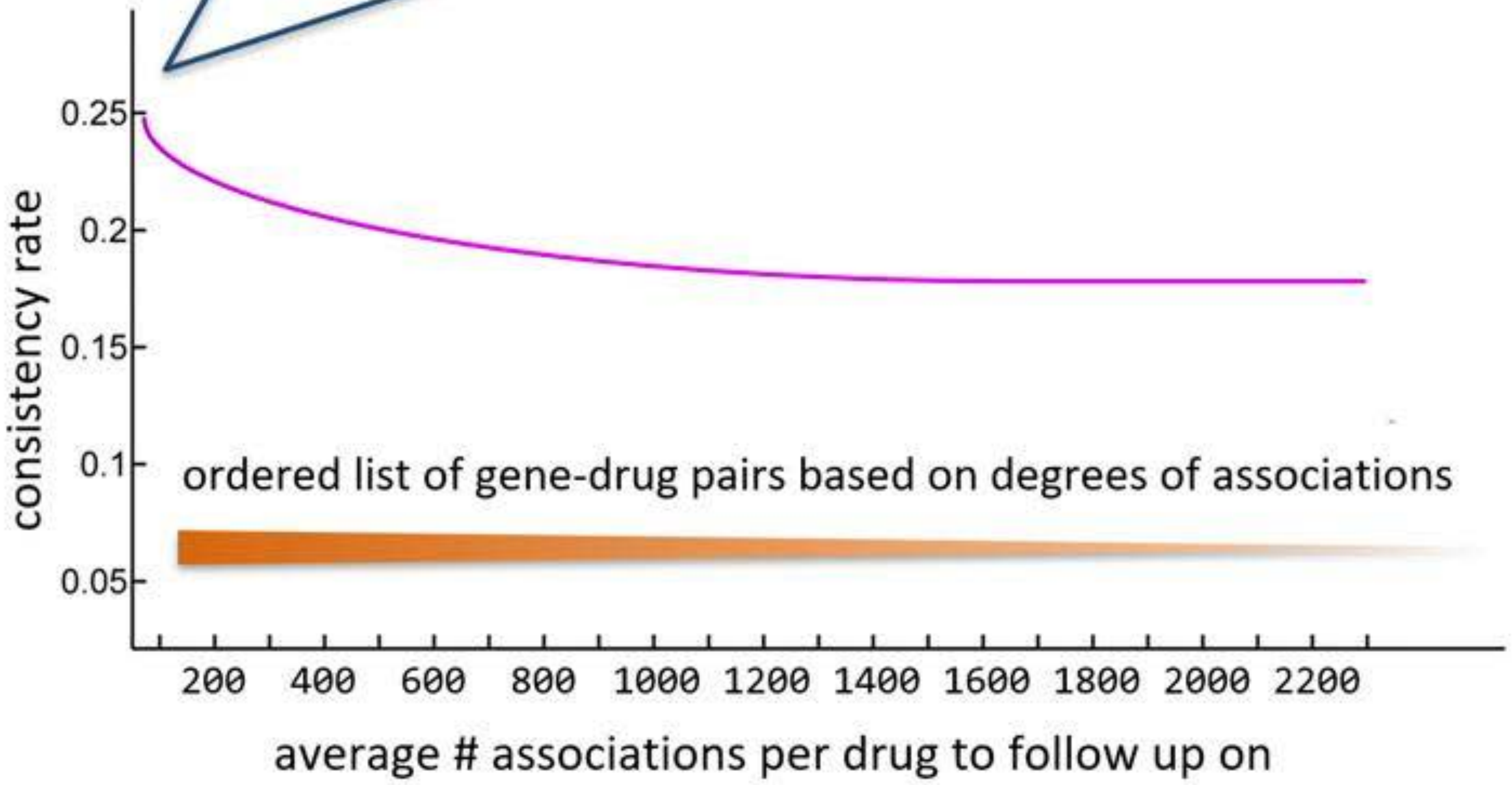

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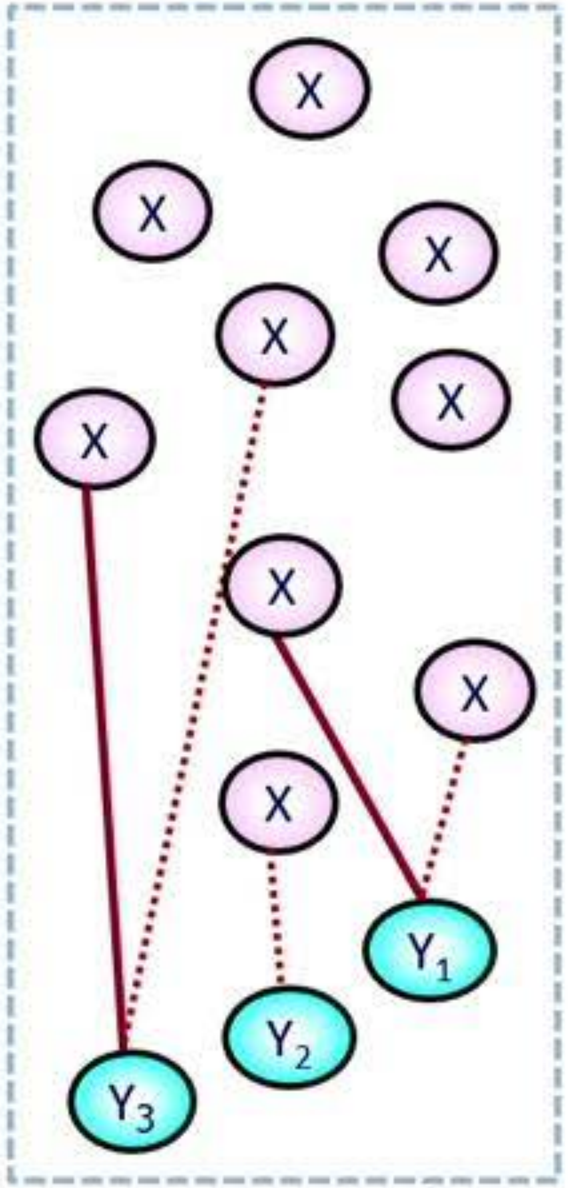

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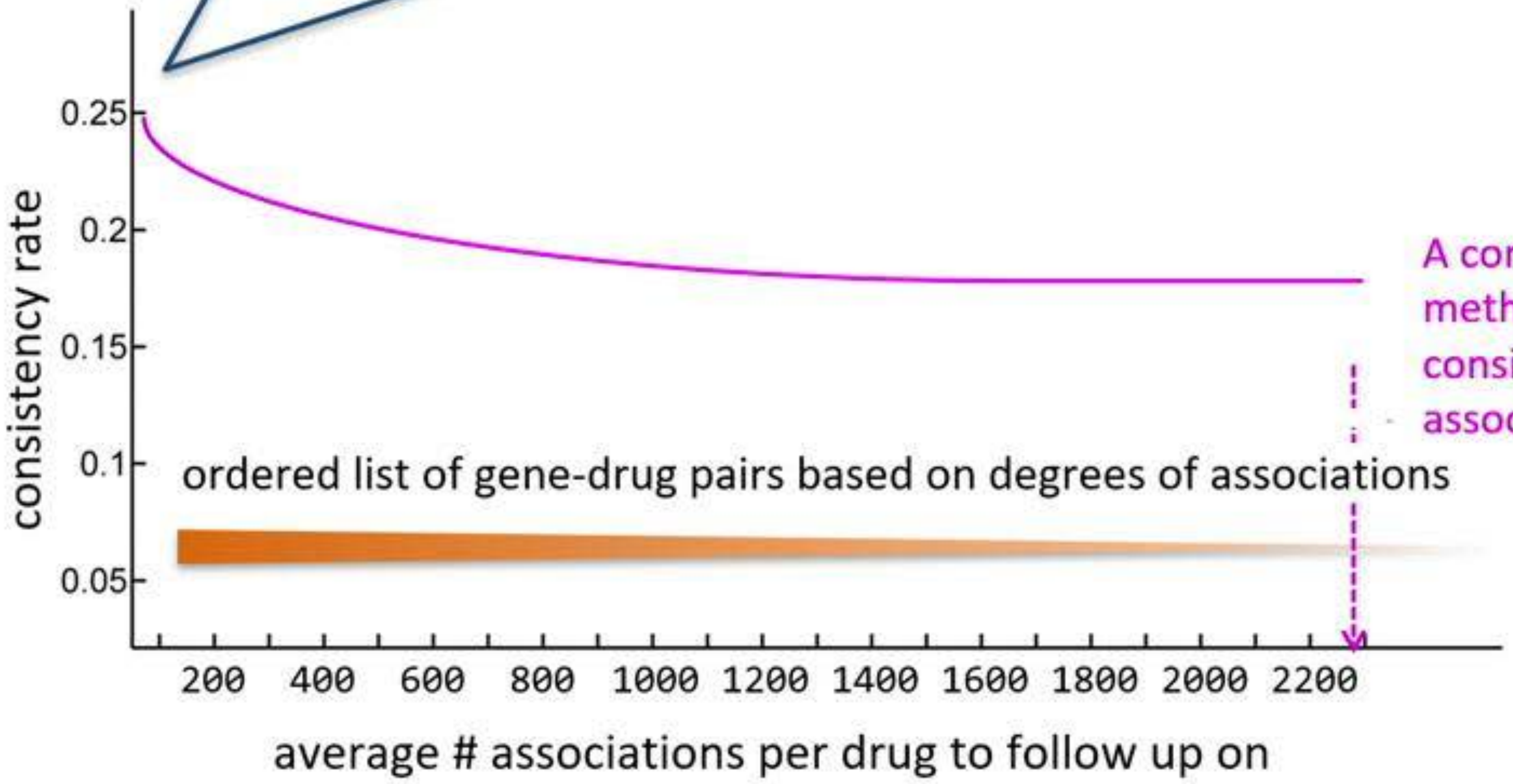

A conventional statistical method suggests to consider the gene-drug associations up to here.

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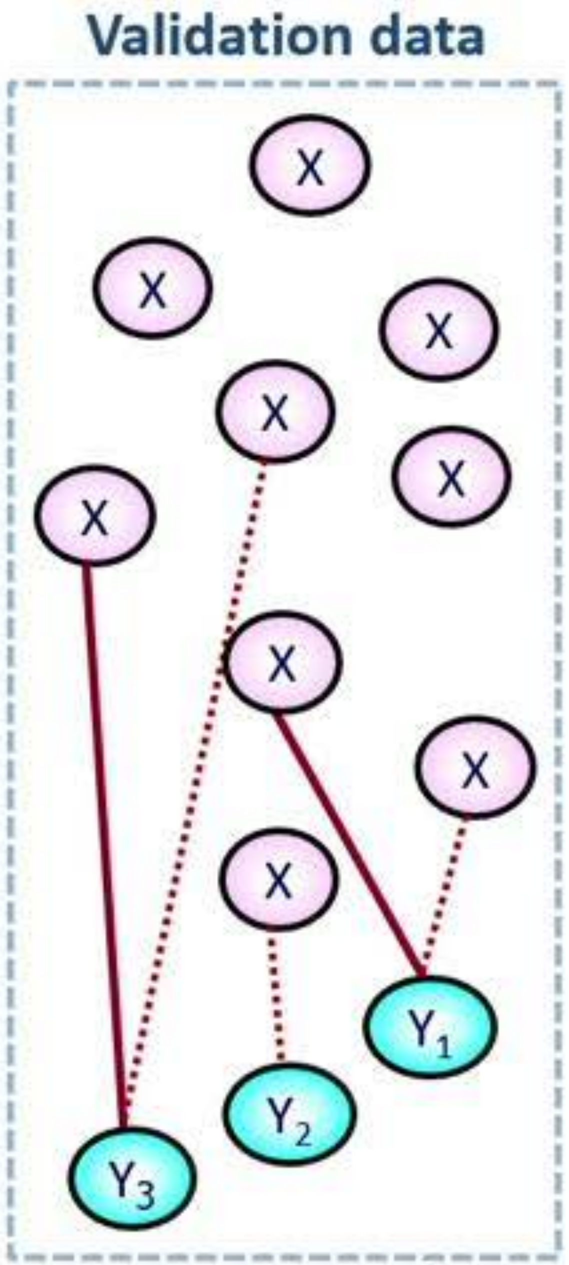

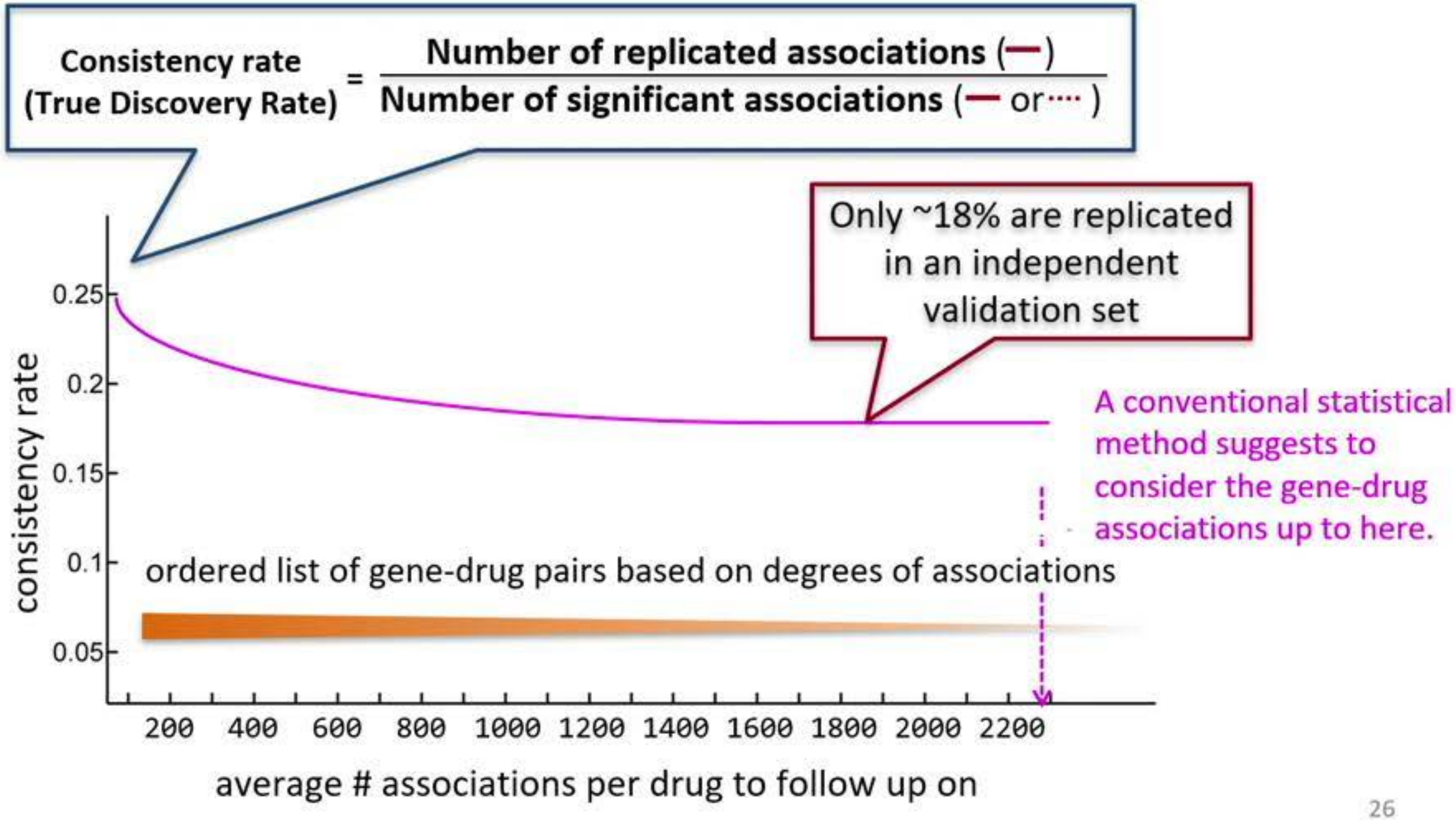

Lee*, Celik*, et al. (2018) *Nature Communications*

Supervised learning approach has serious drawbacks

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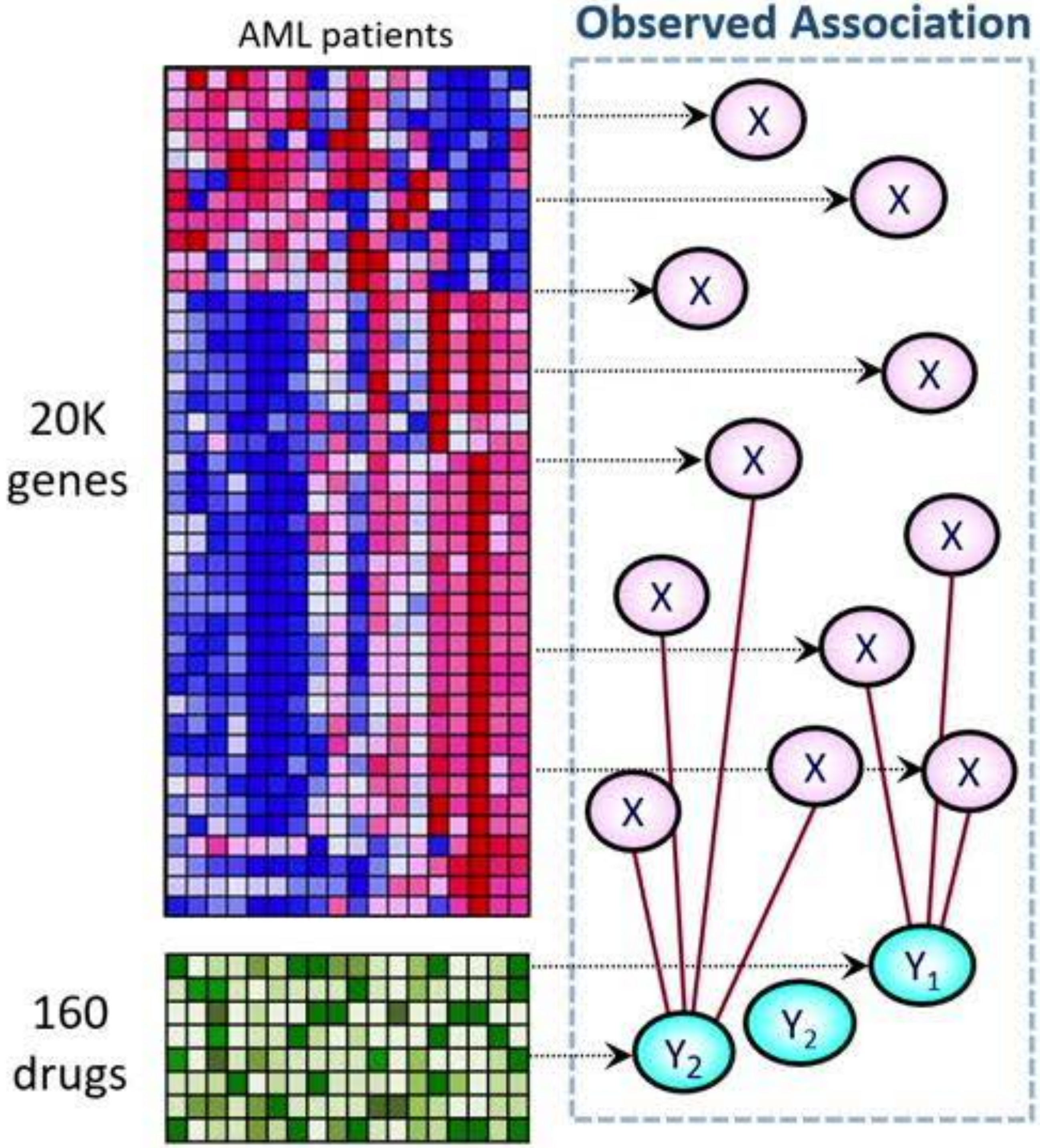

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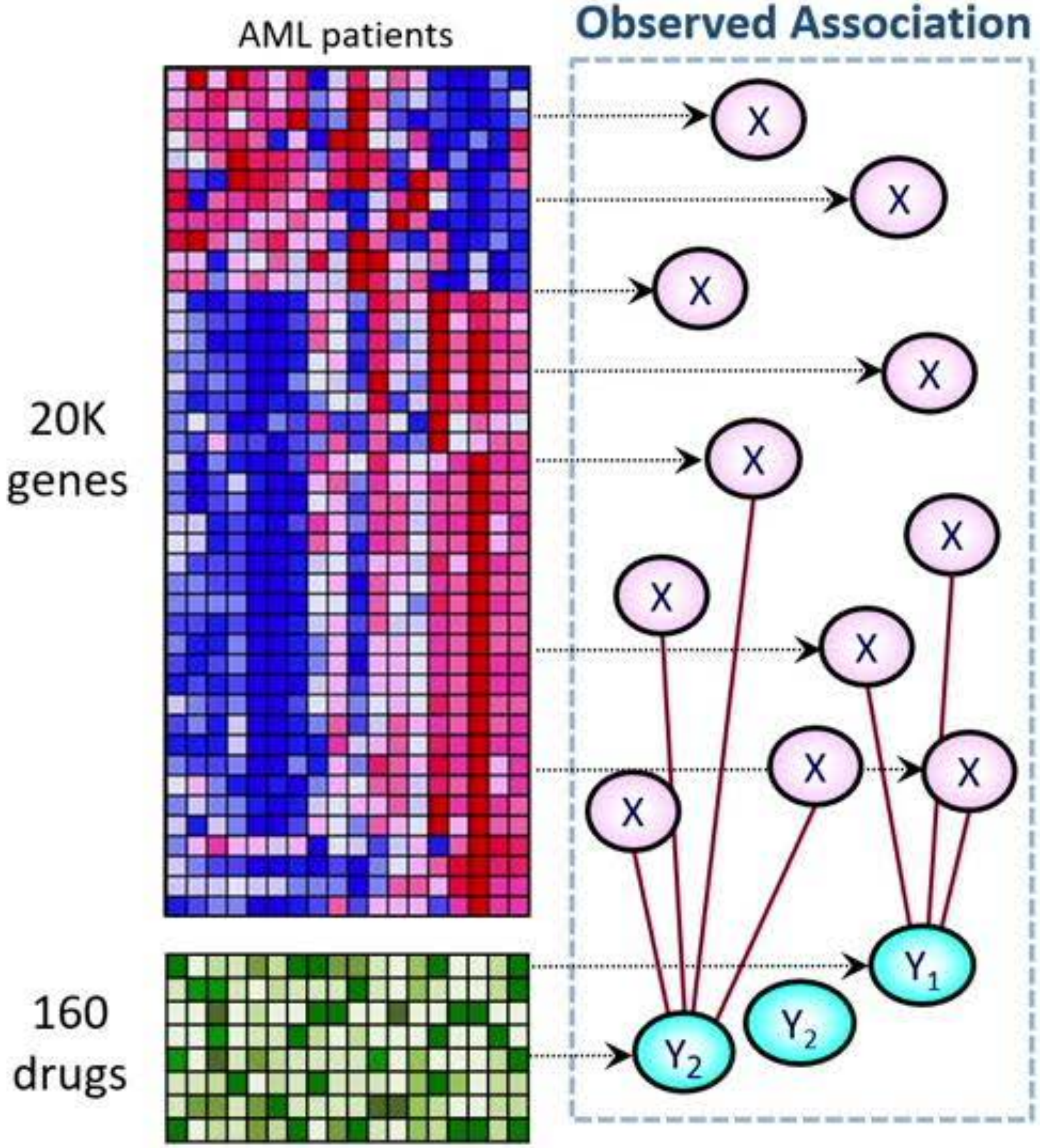

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  - # of (genes x drugs) ≫ # of patients

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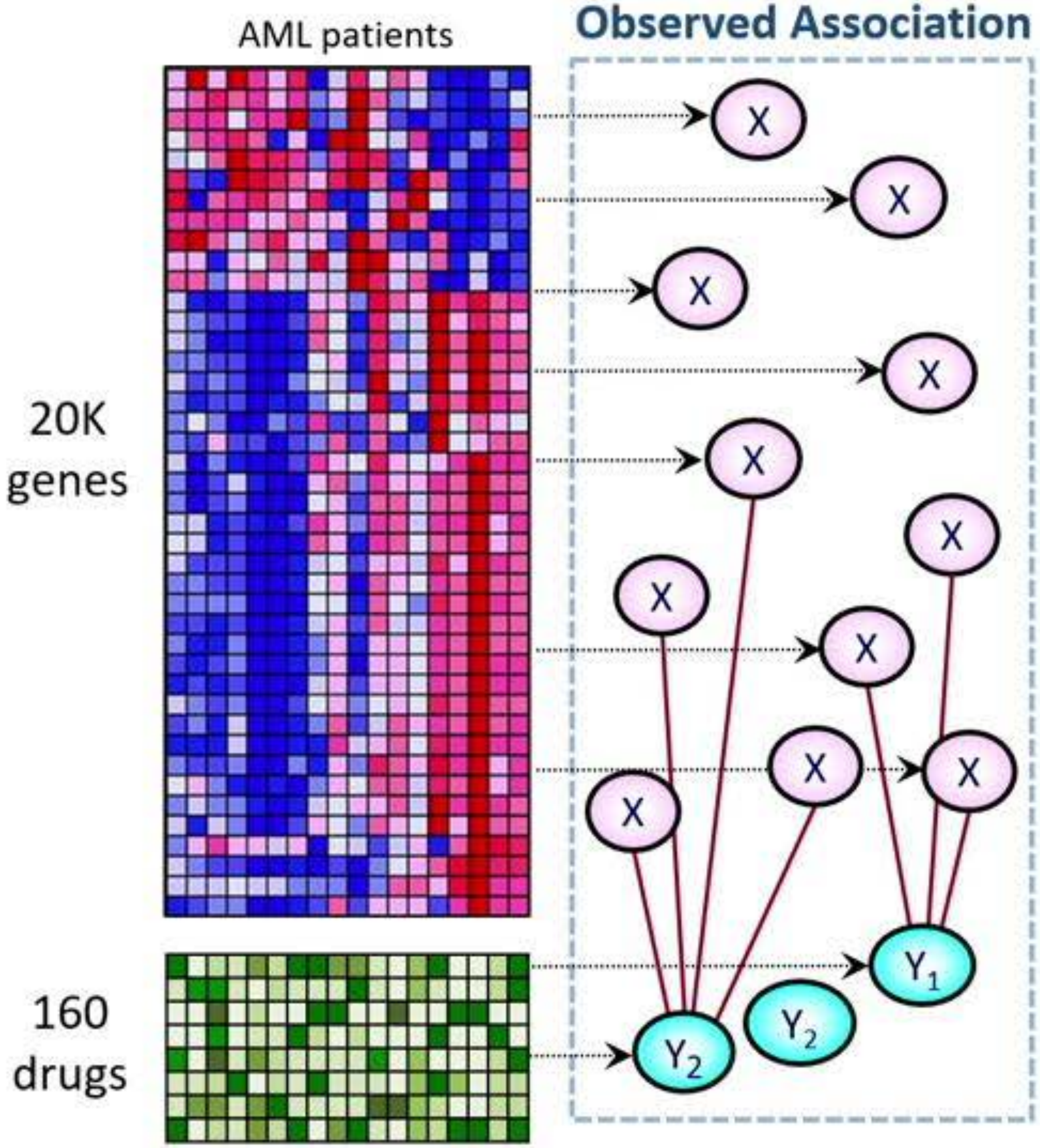

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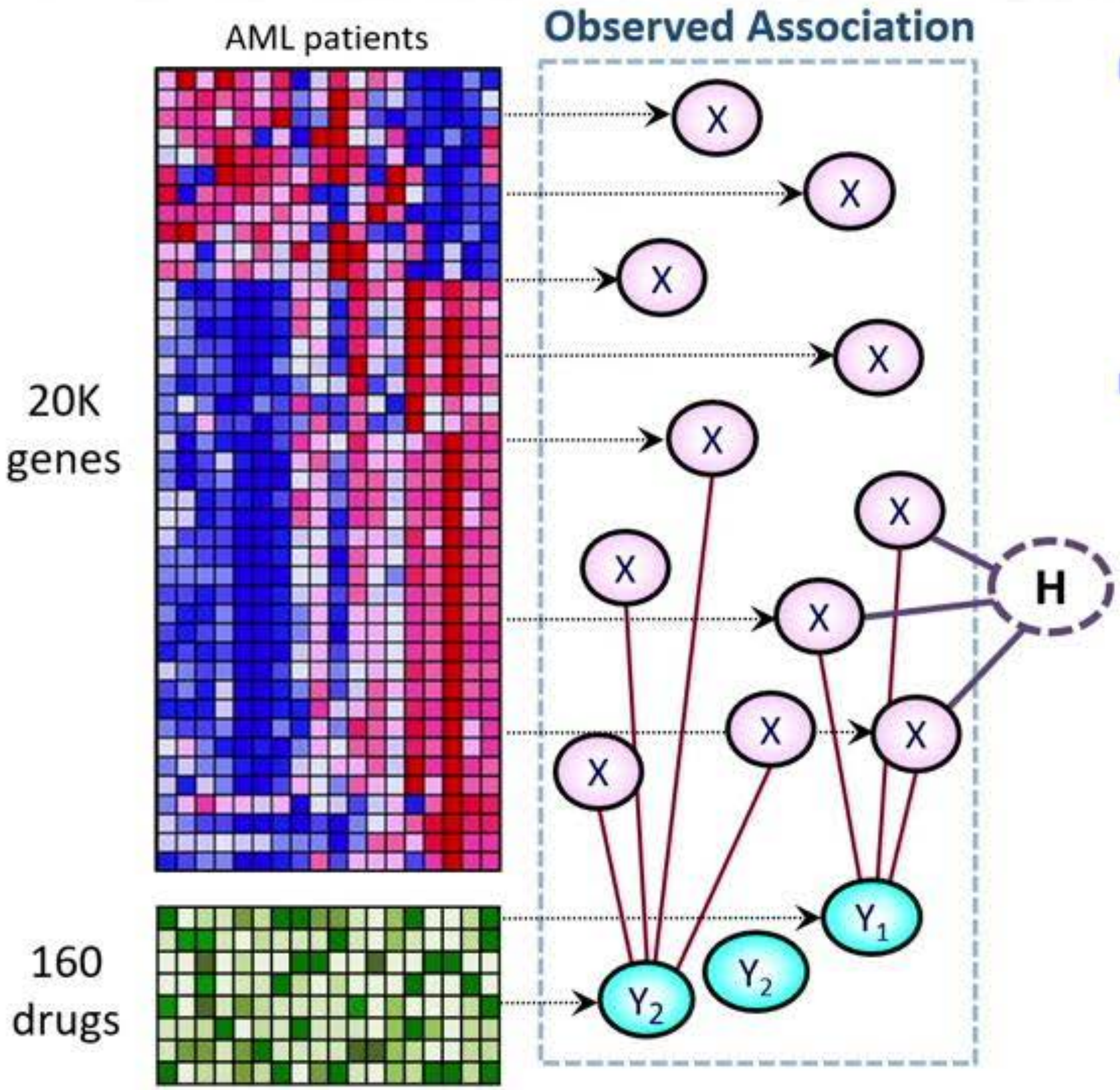

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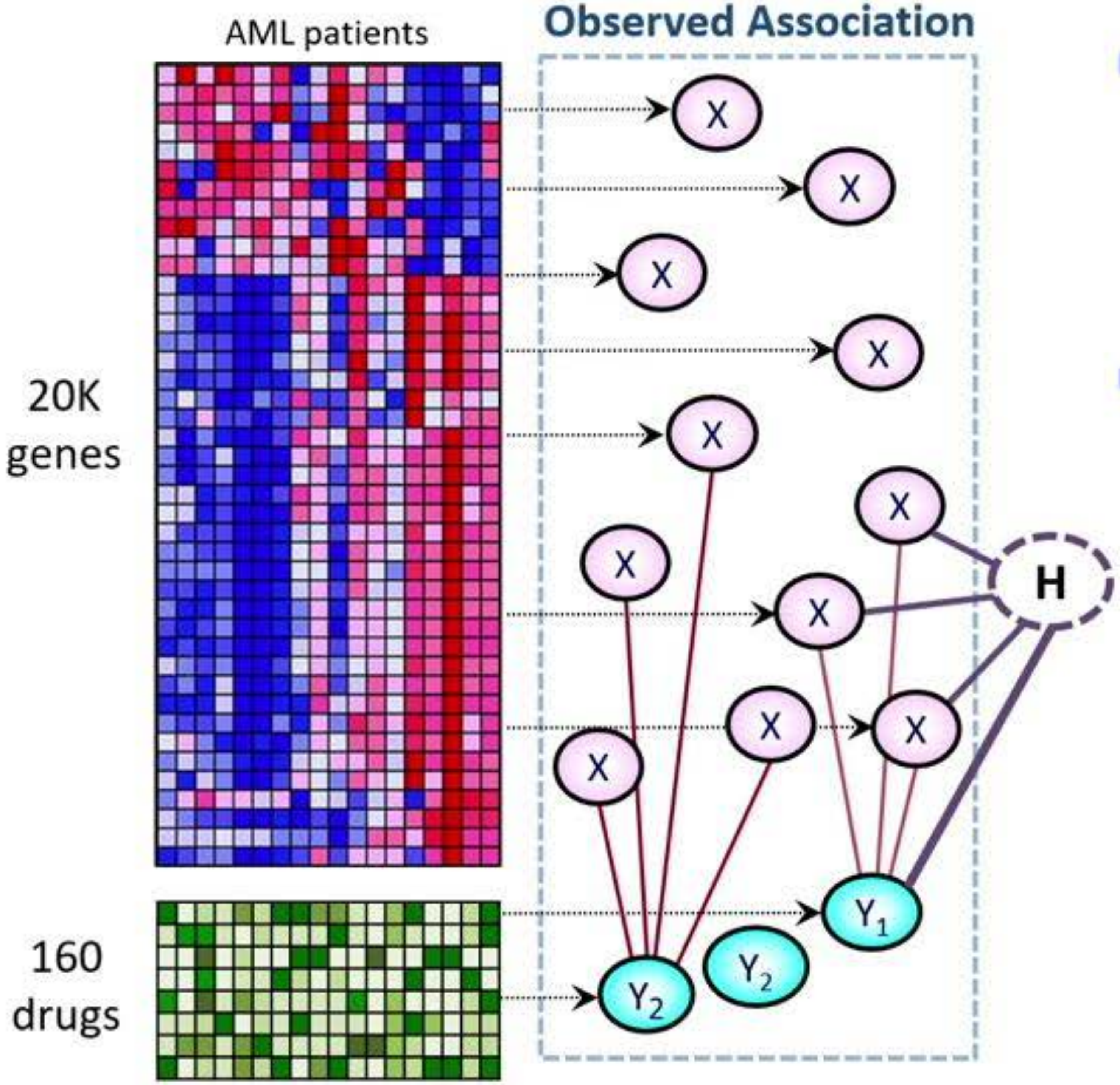

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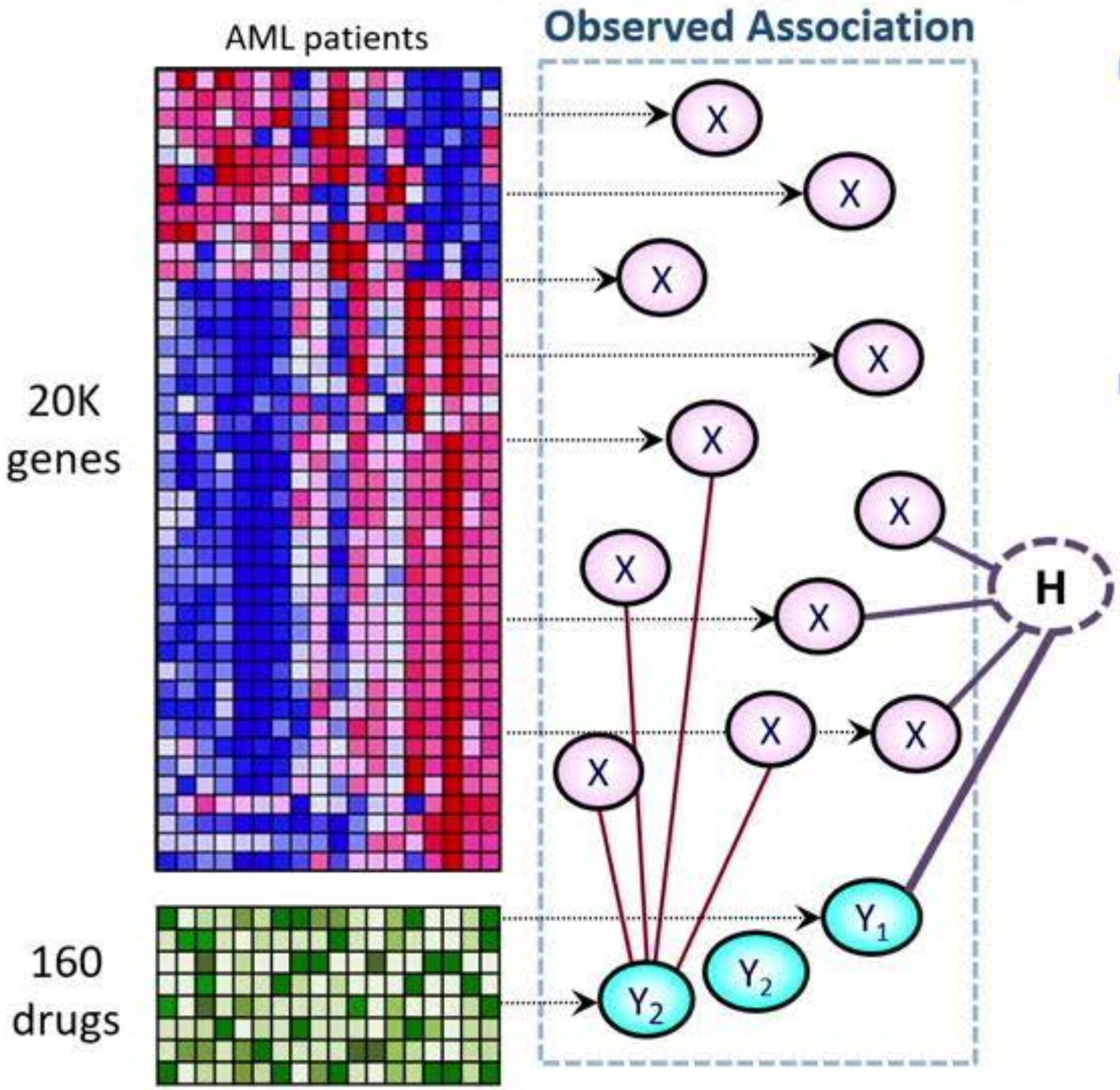

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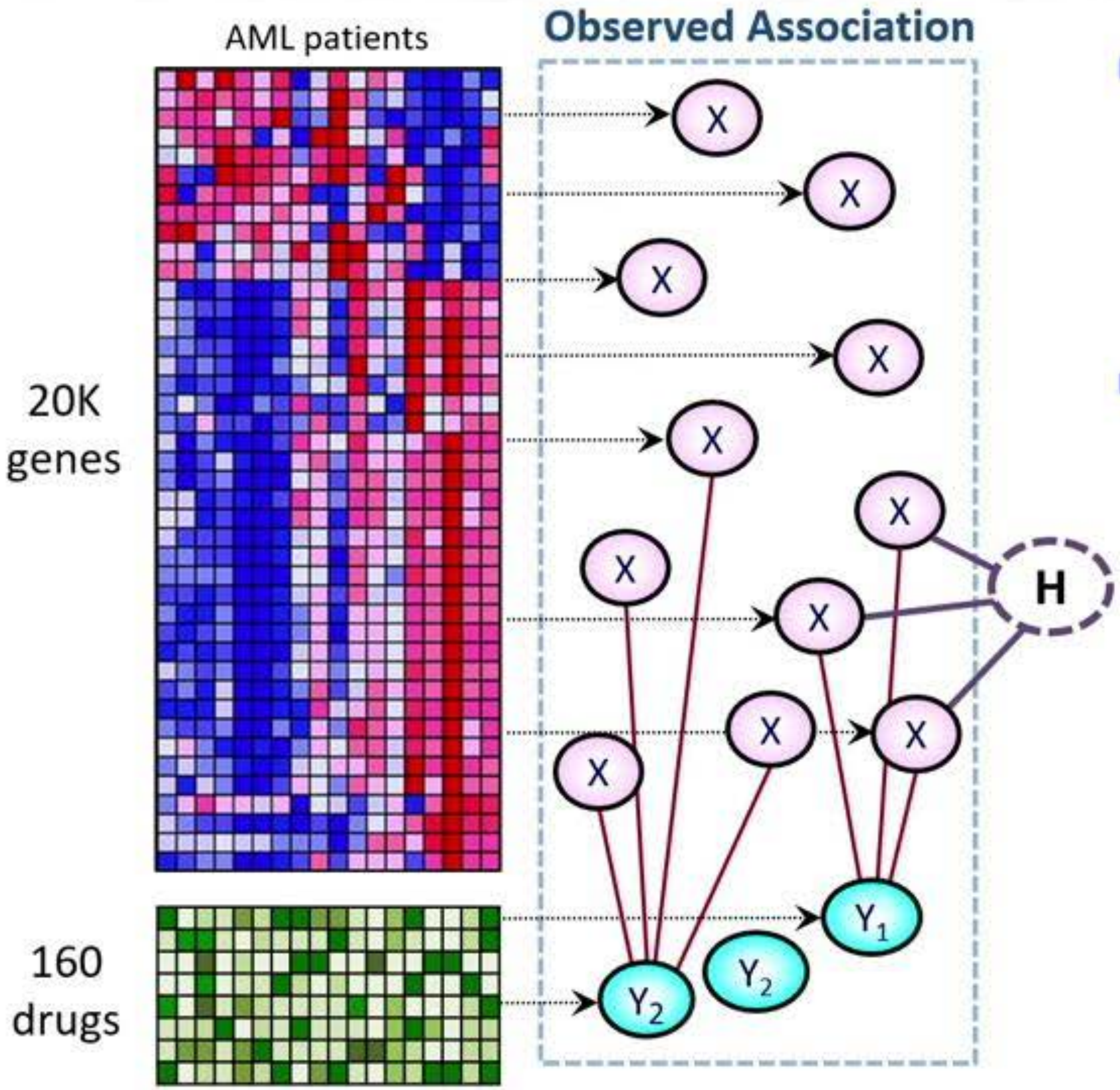

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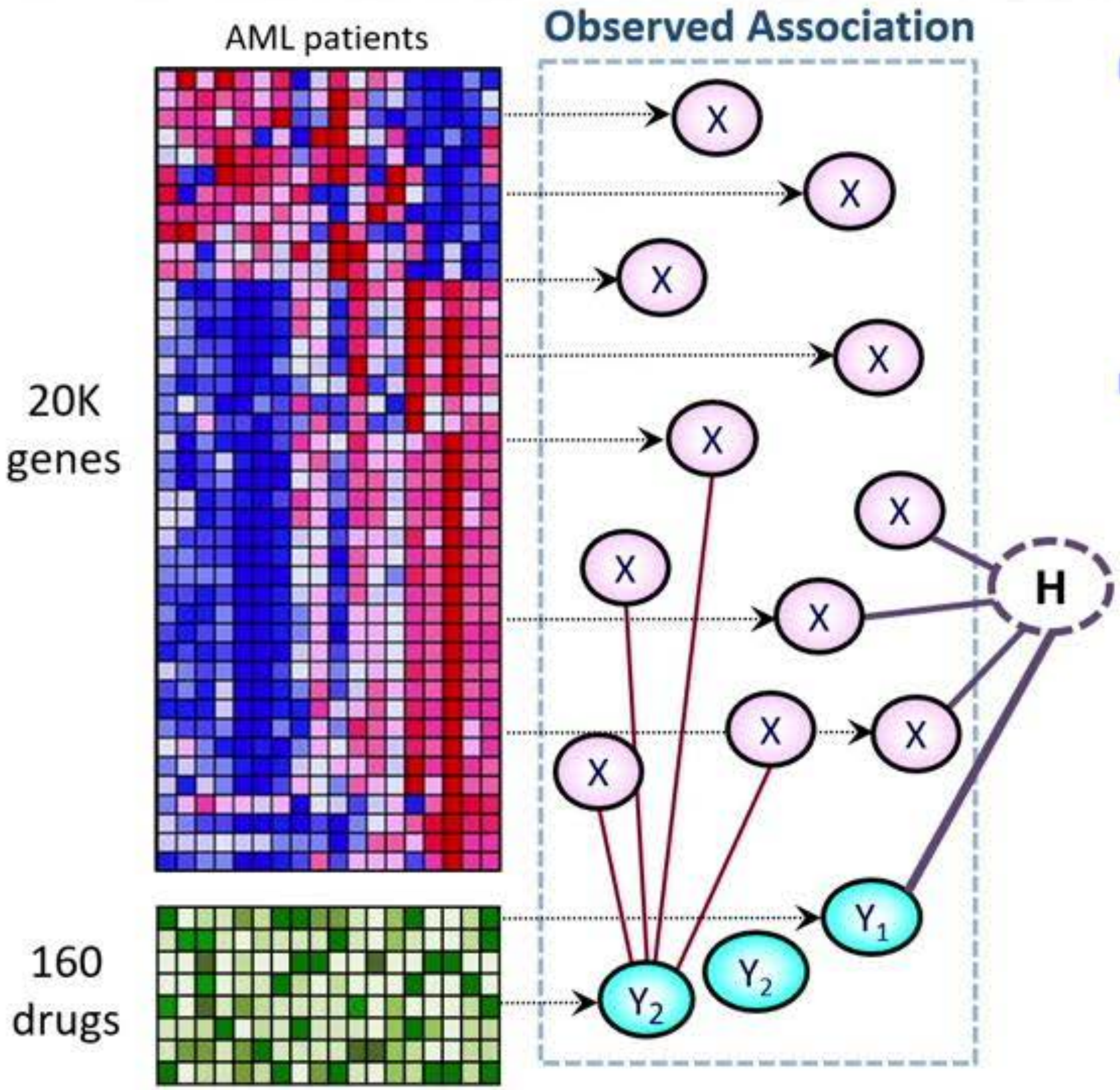

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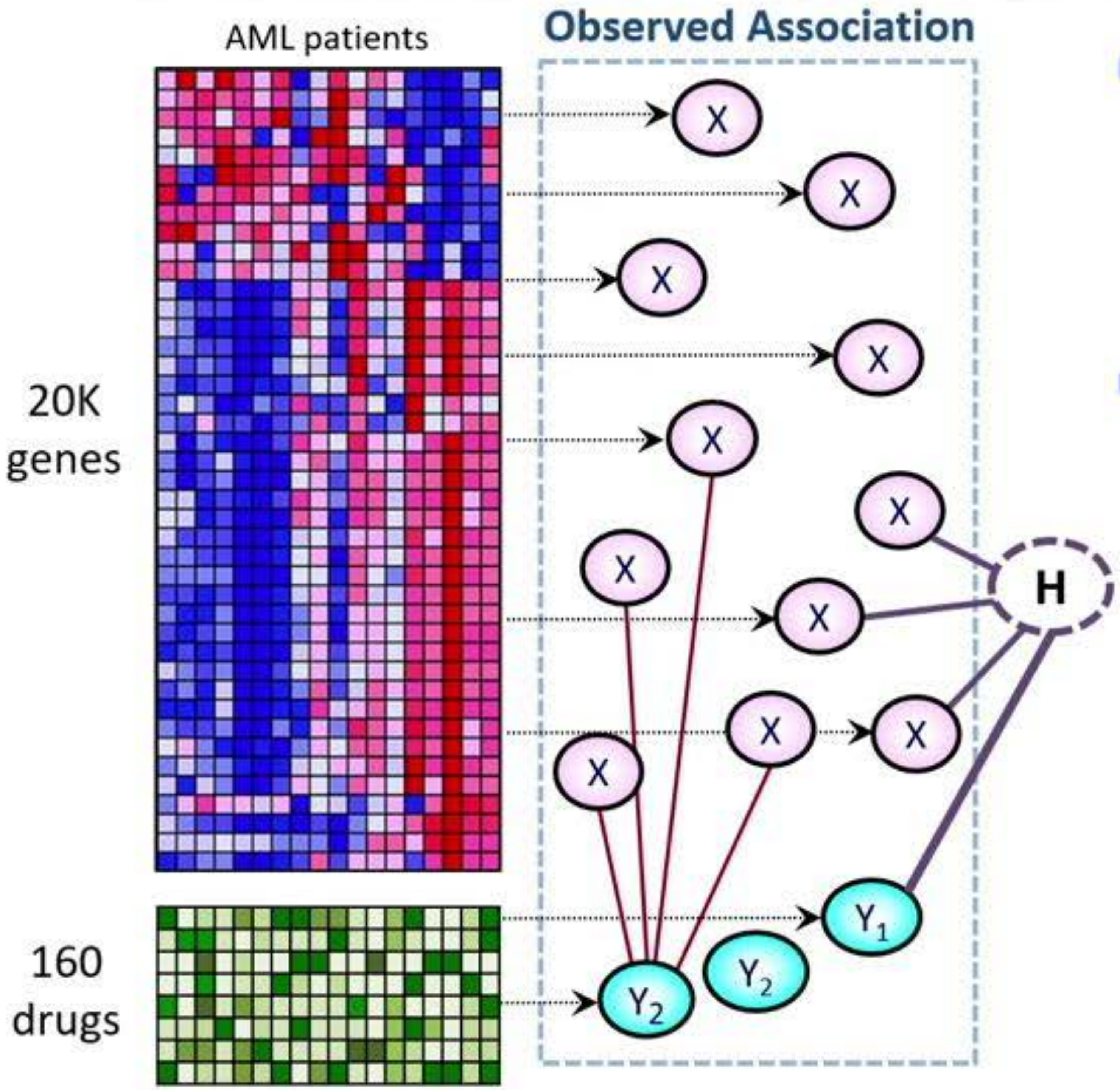

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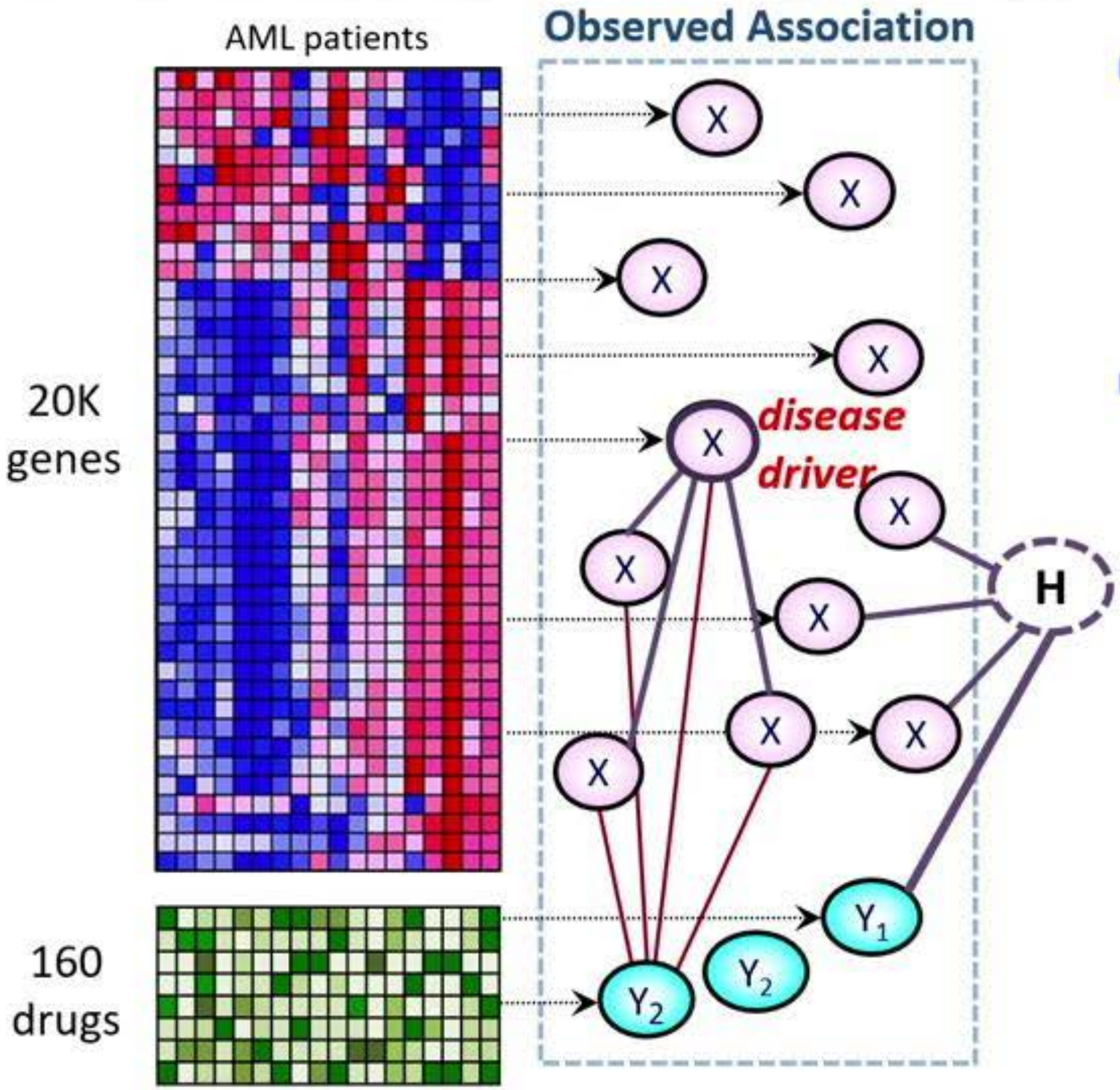

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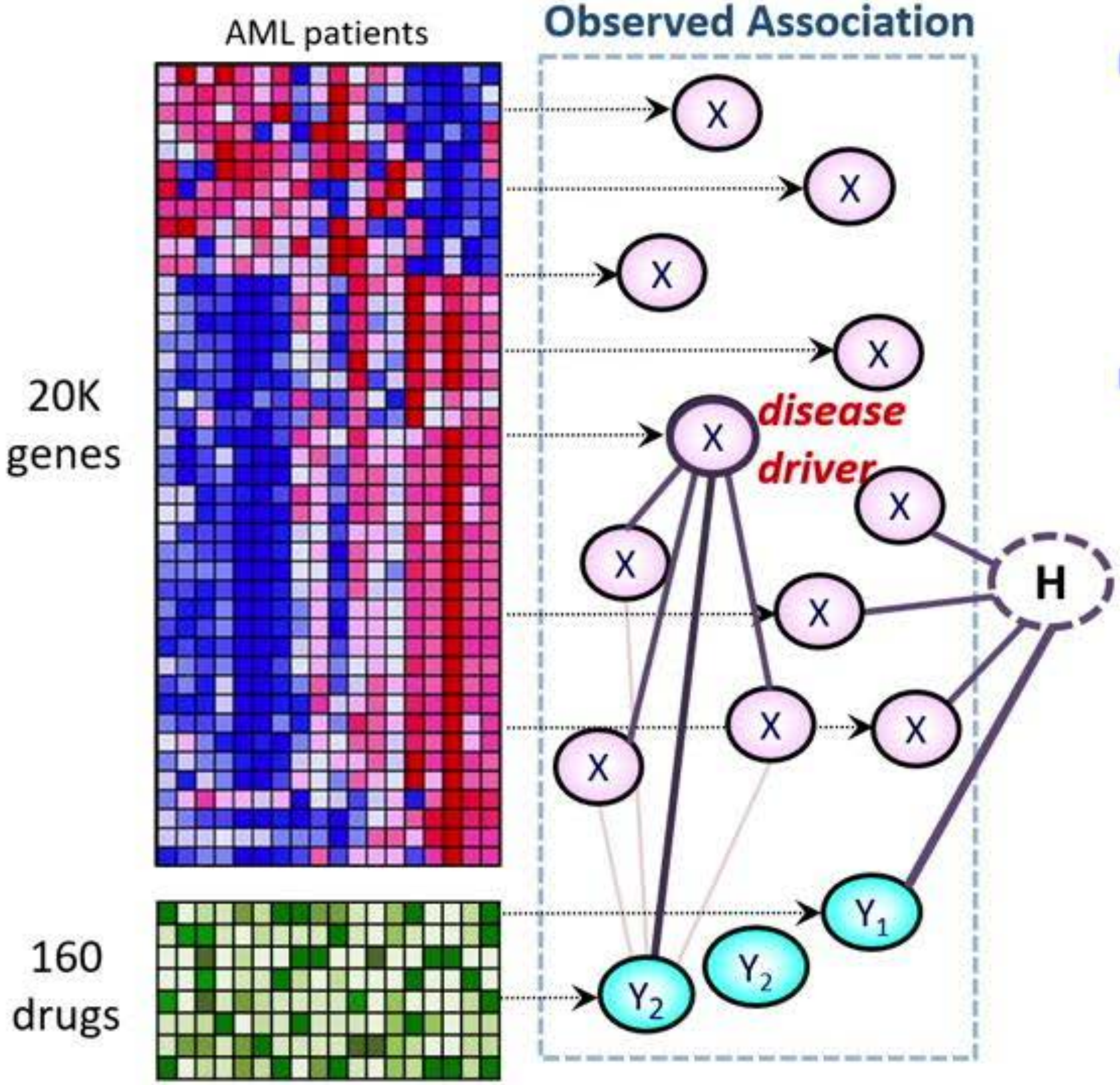

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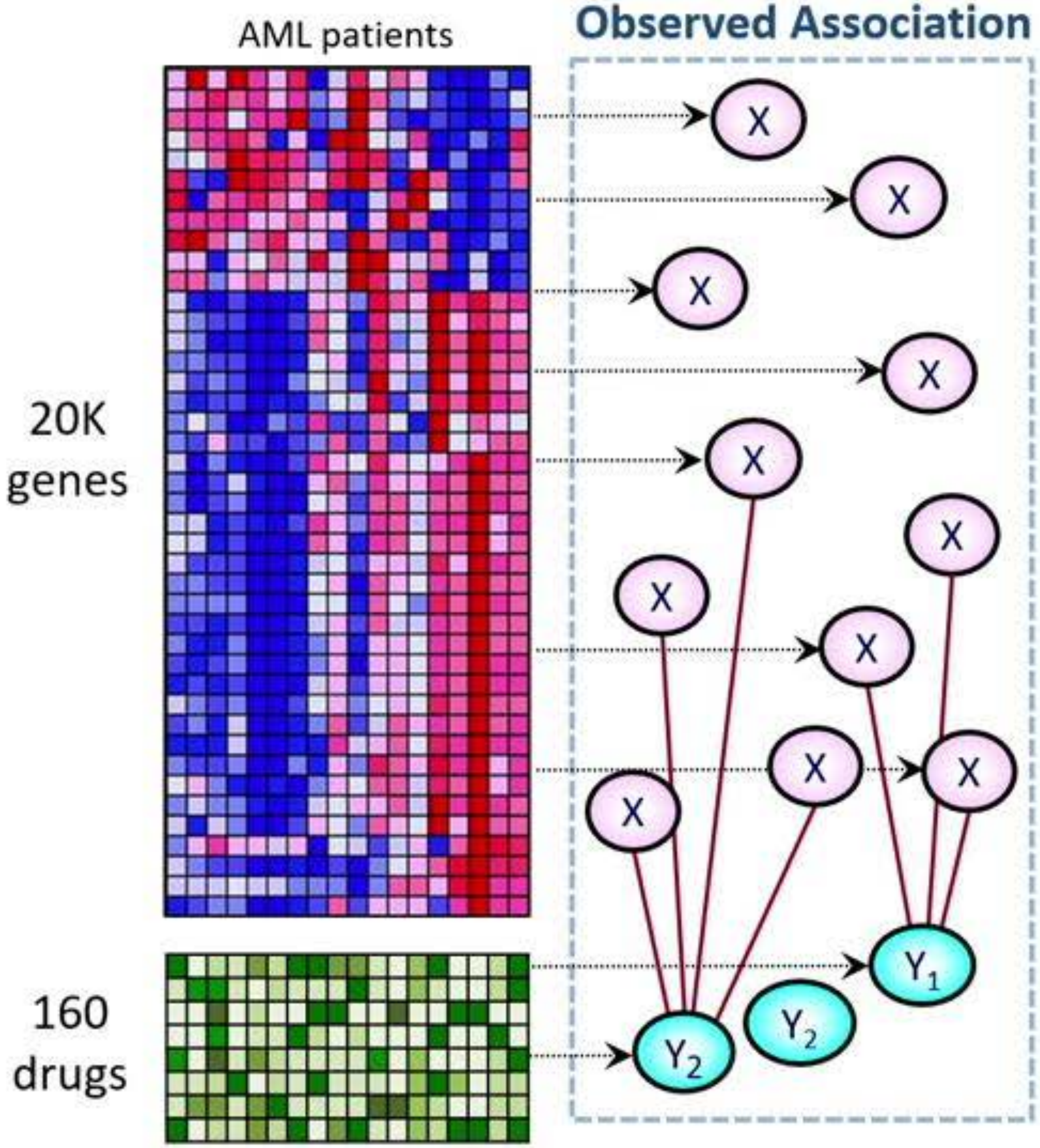

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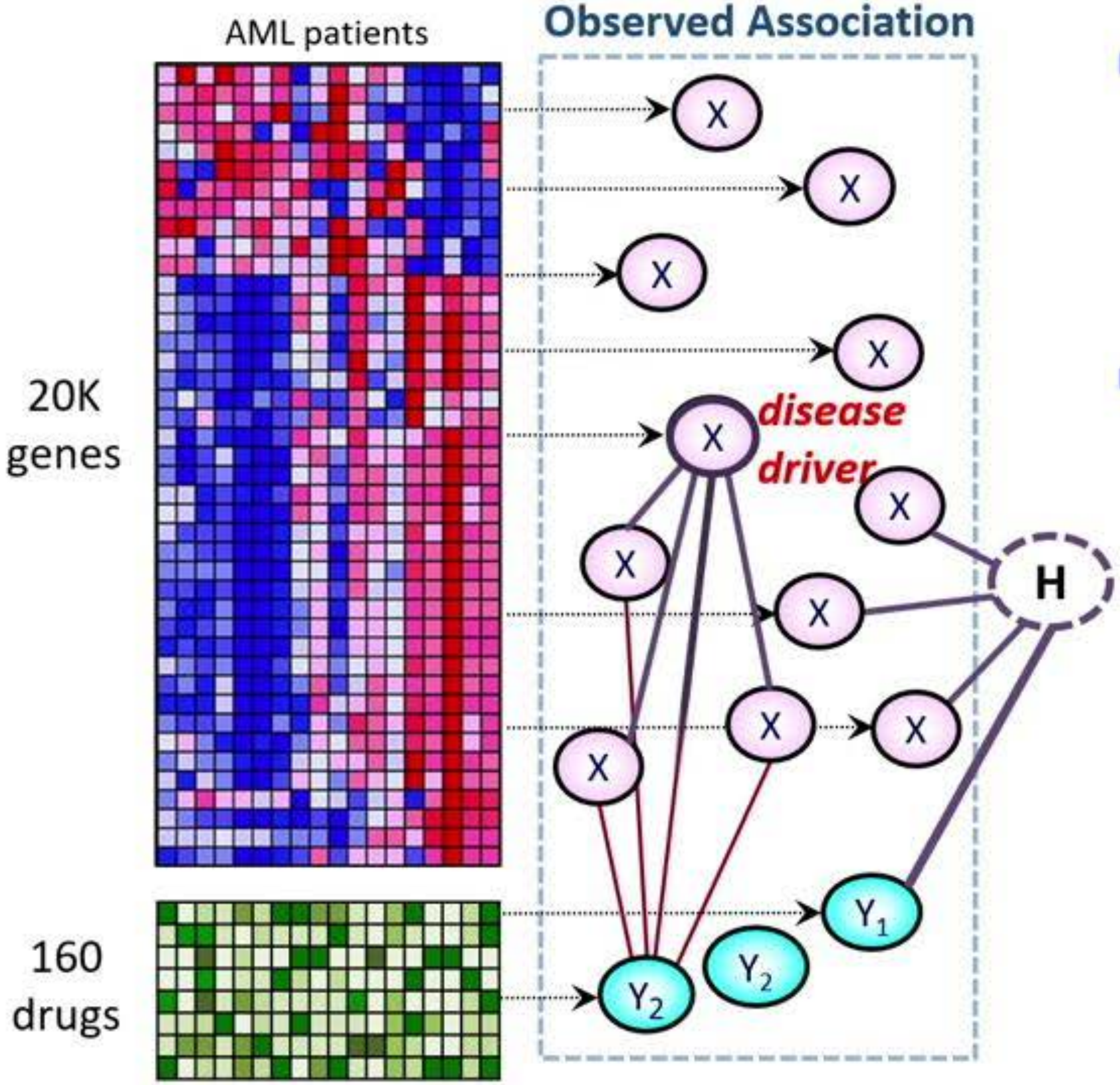
Supervised learning approach has serious drawbacks


Safiye



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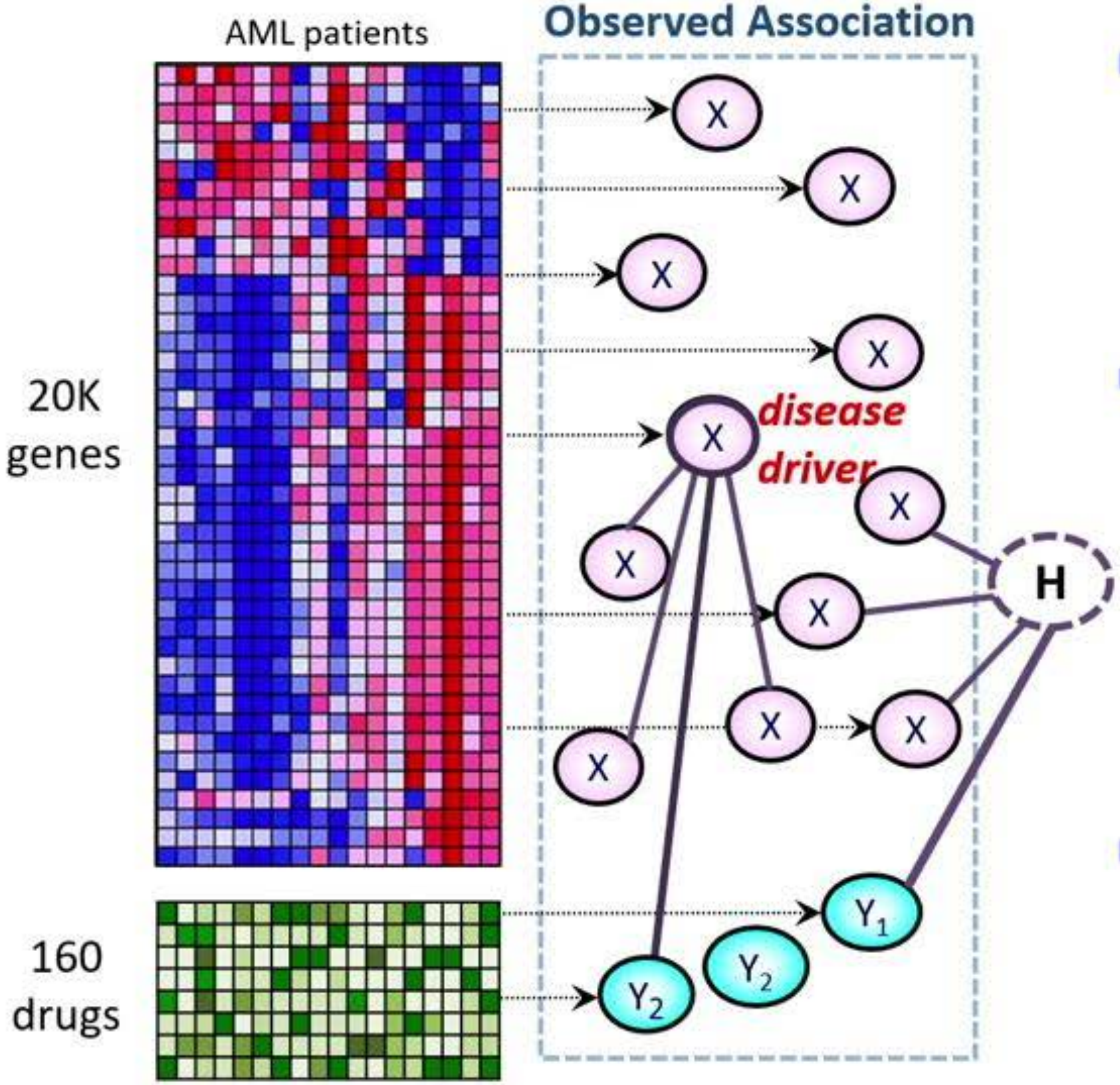

- **High-dimensionality**
  - # of (genes x drugs) ≫ # of patients
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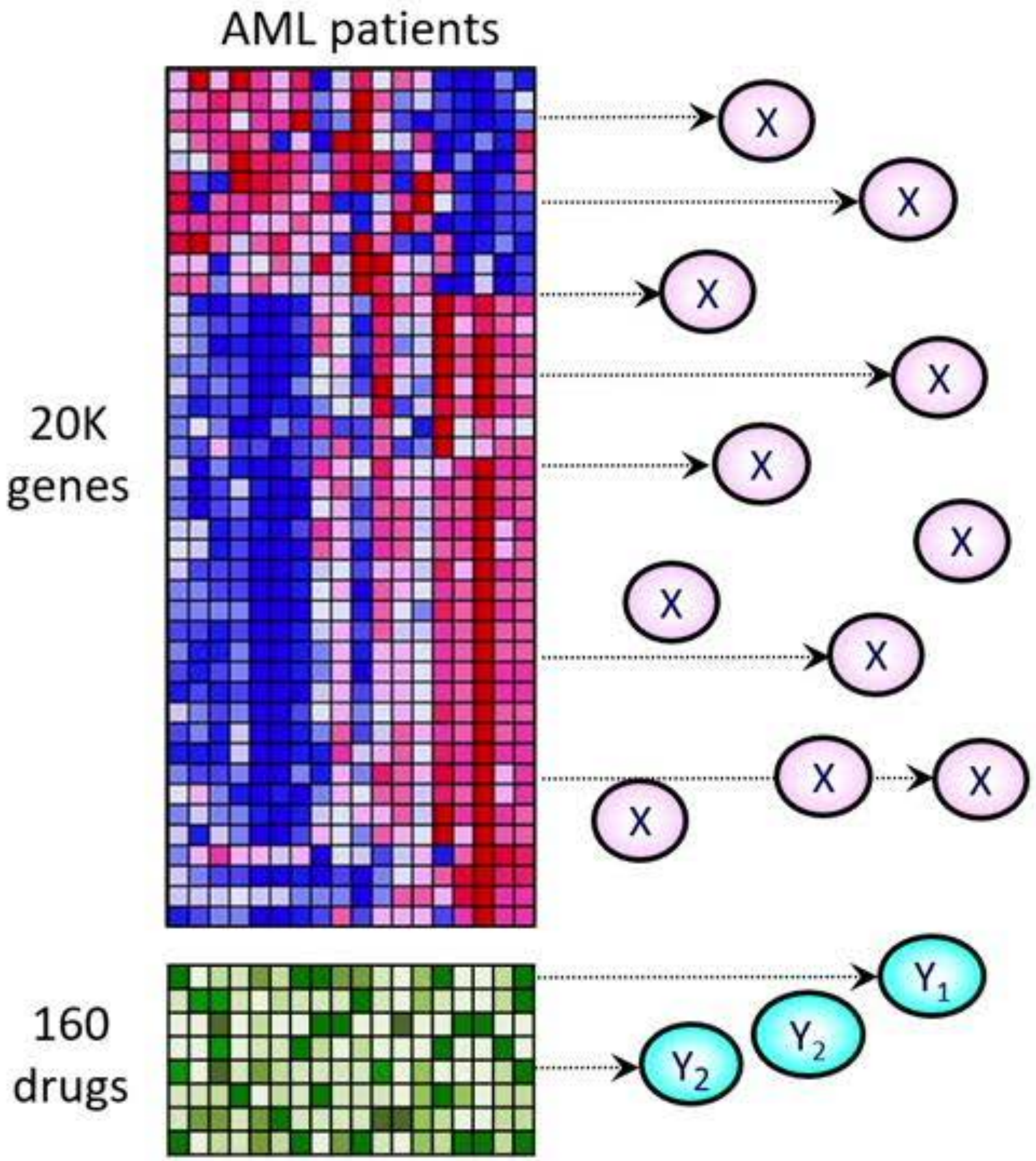
- **Our solution –** Unsupervised feature learning to select genes likely to explain associations.

MERGE: Machine learning approach to integrate big data to select robust expression markers



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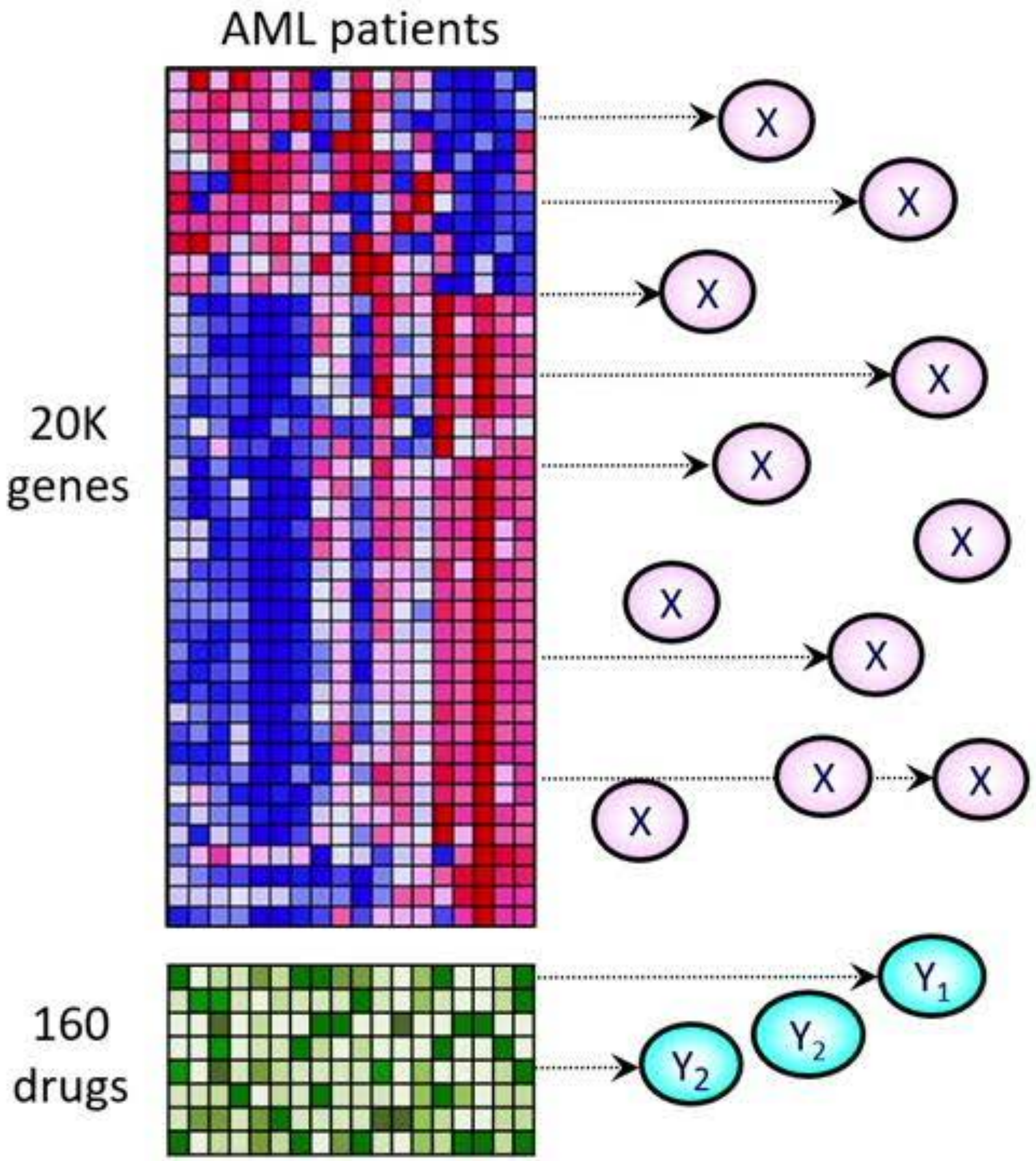

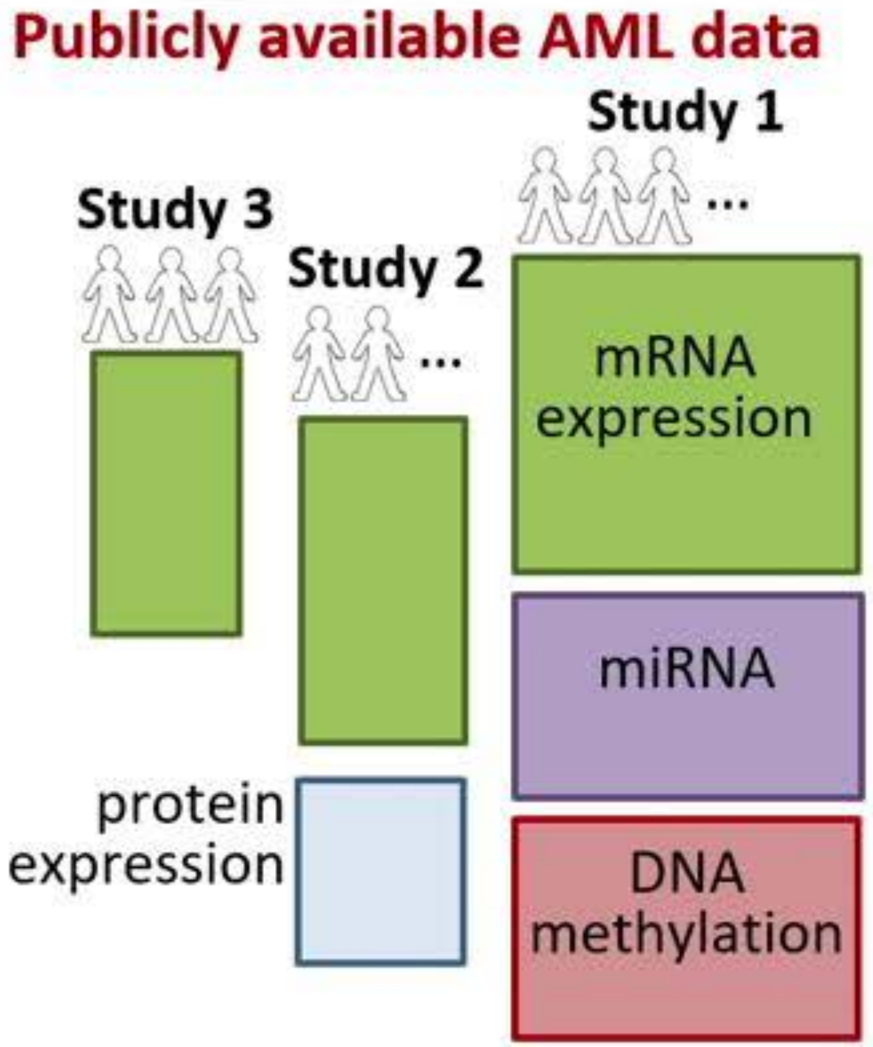

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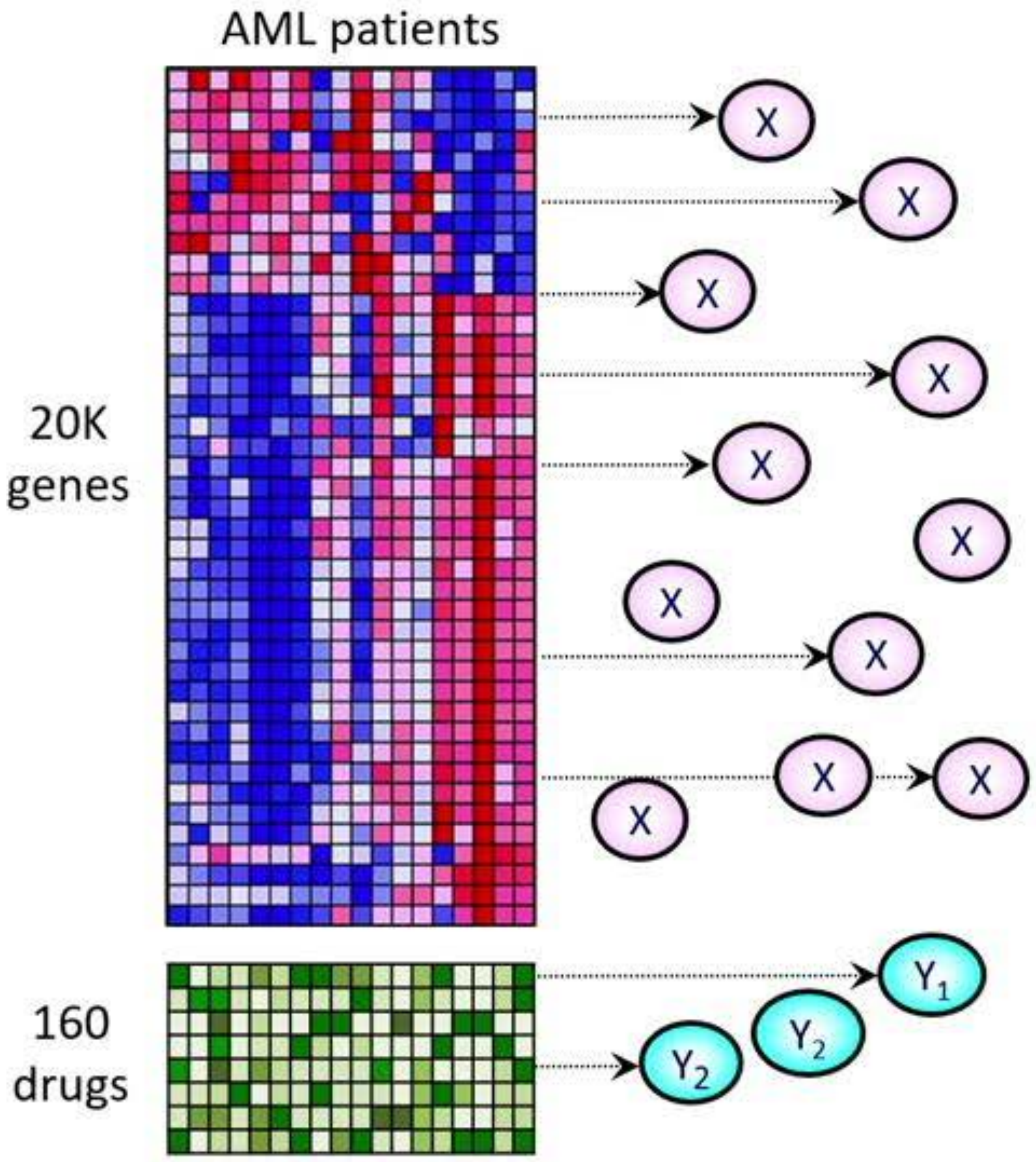

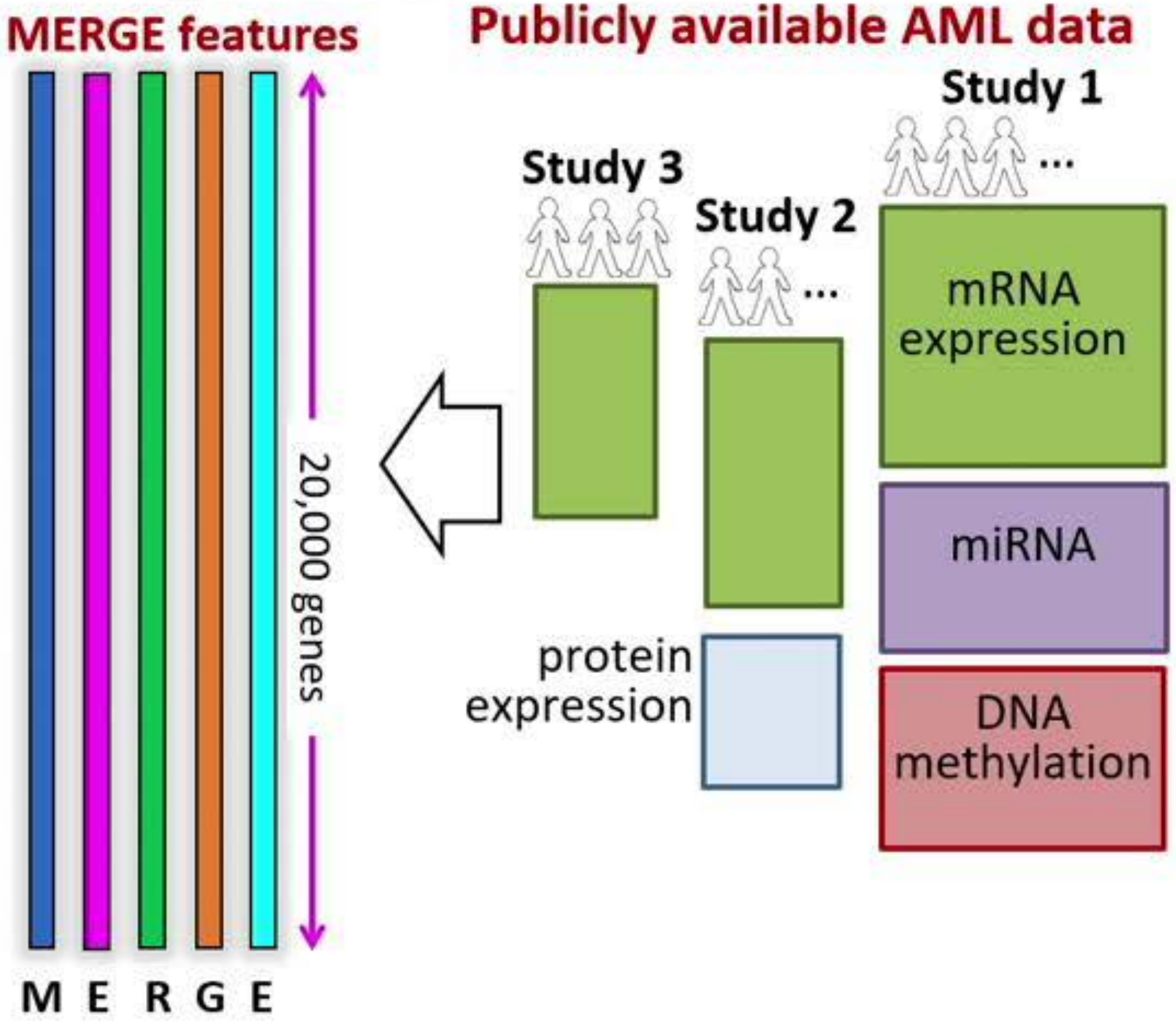

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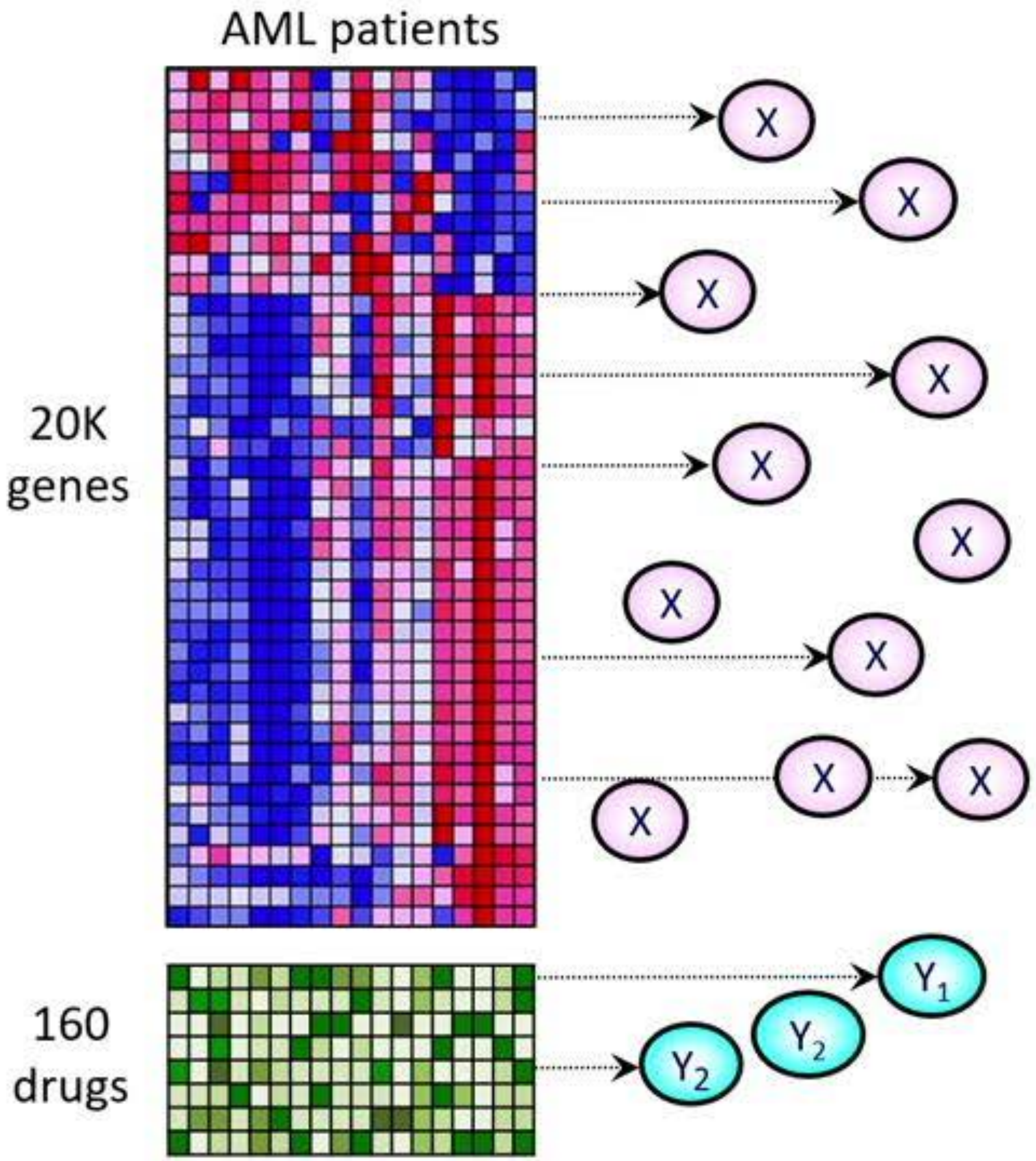

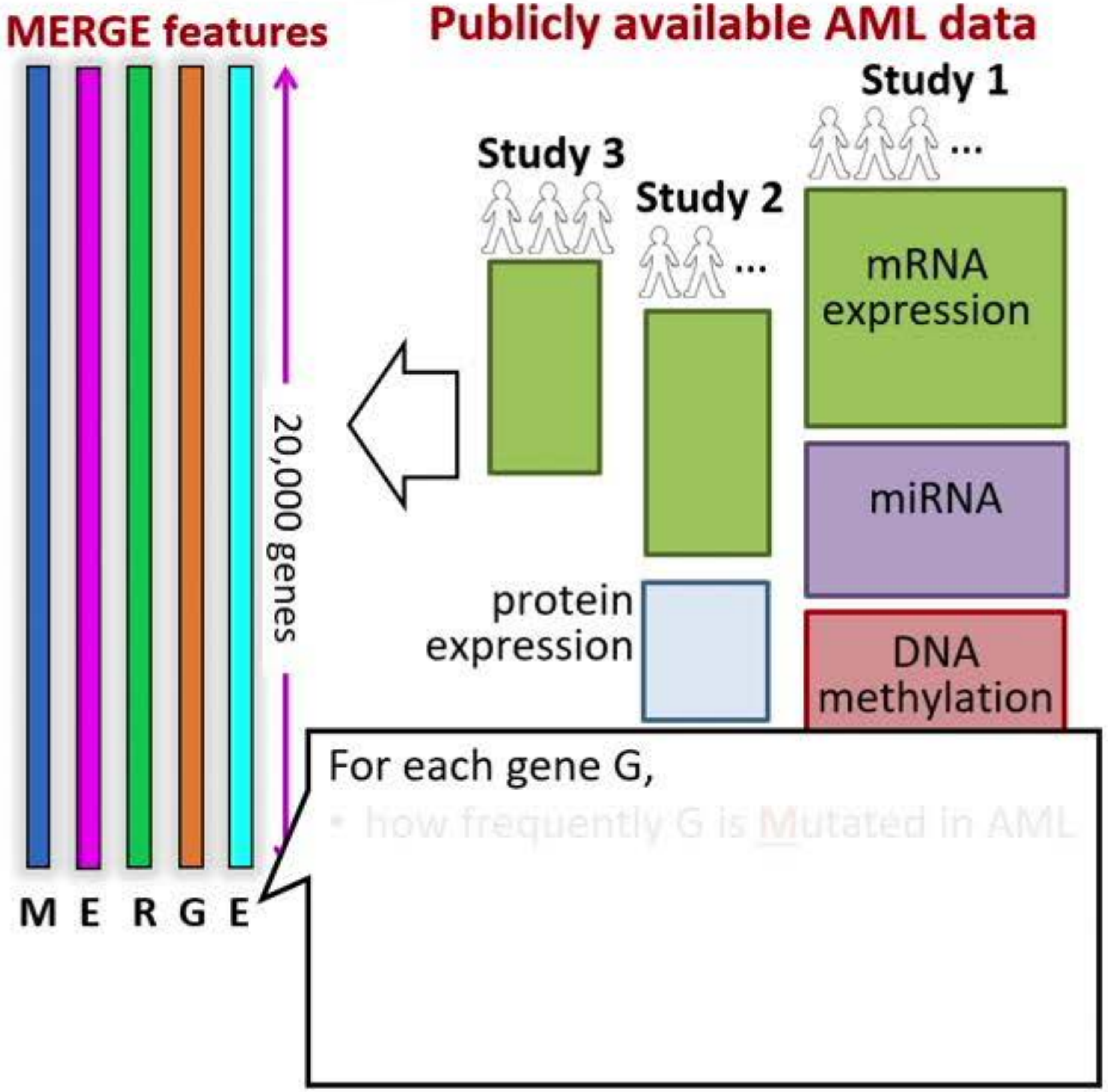

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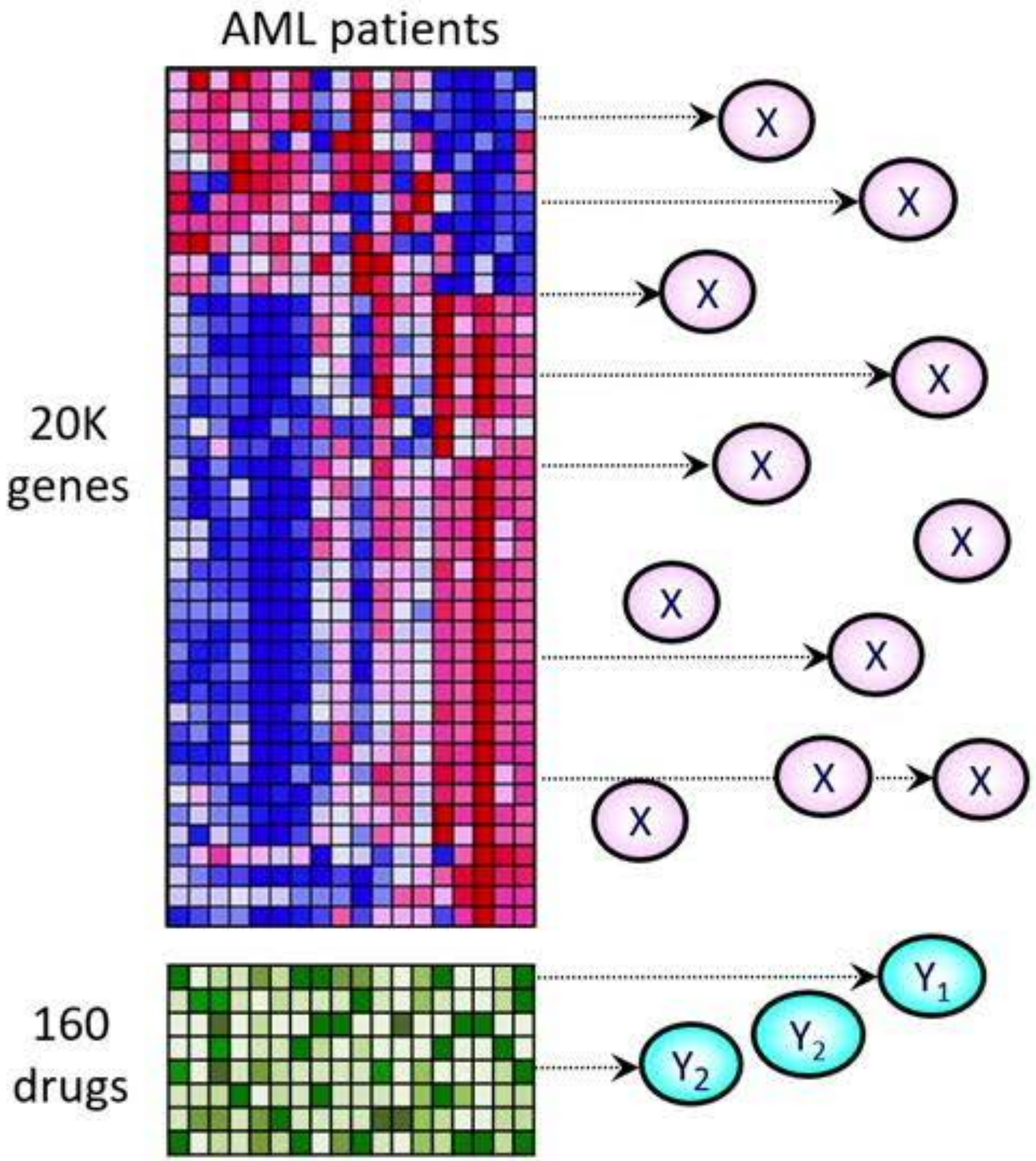

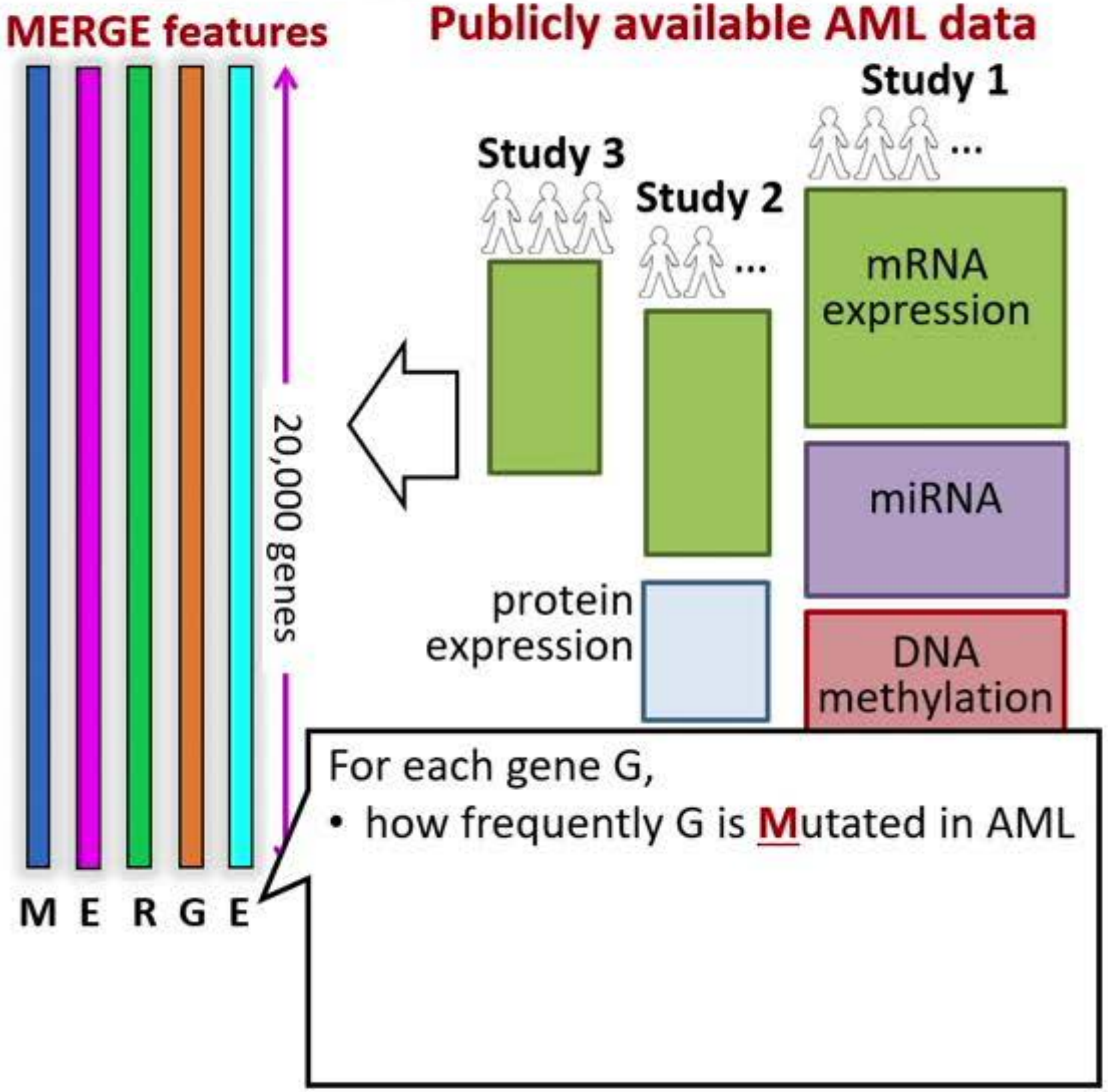

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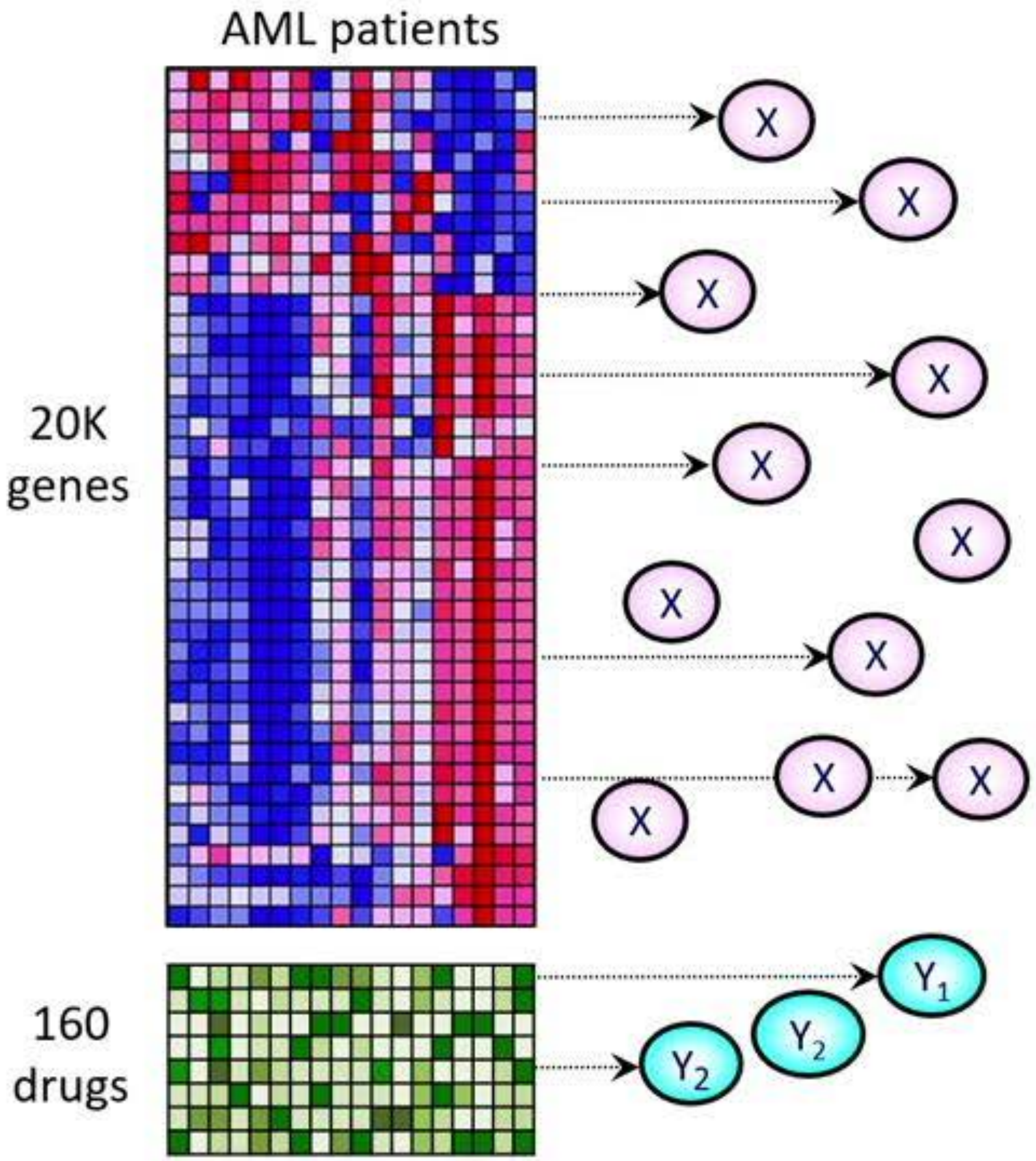

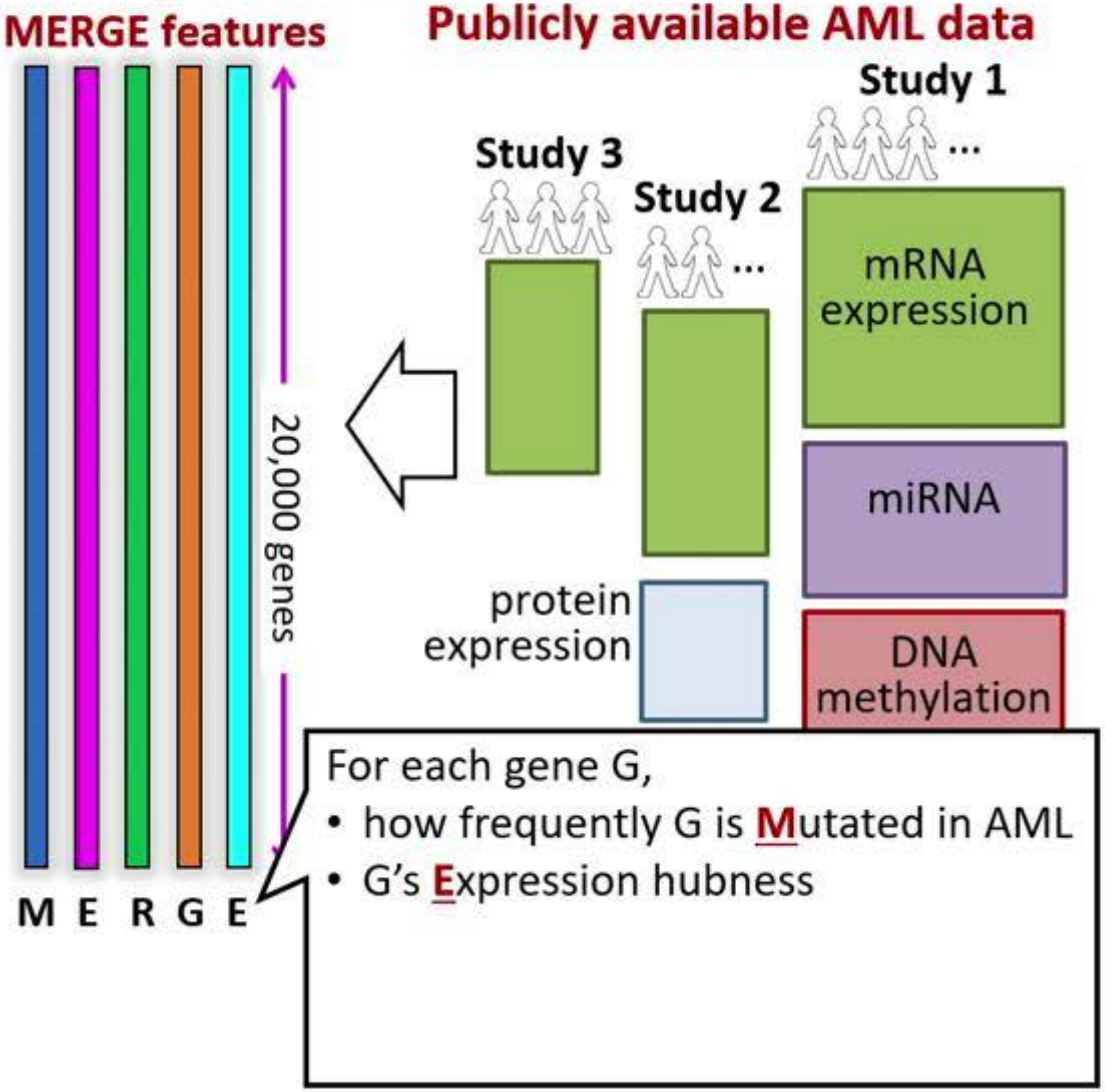

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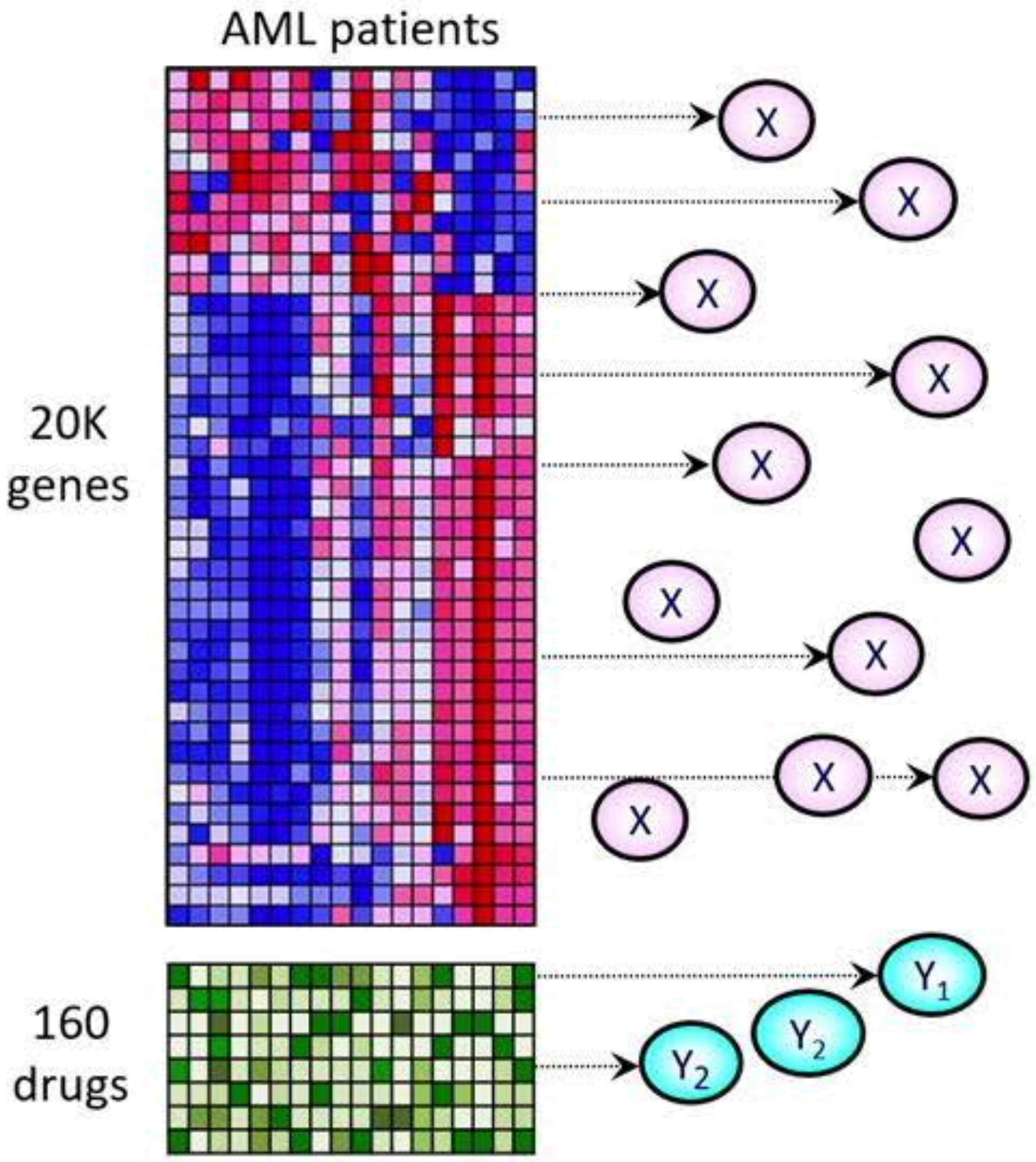

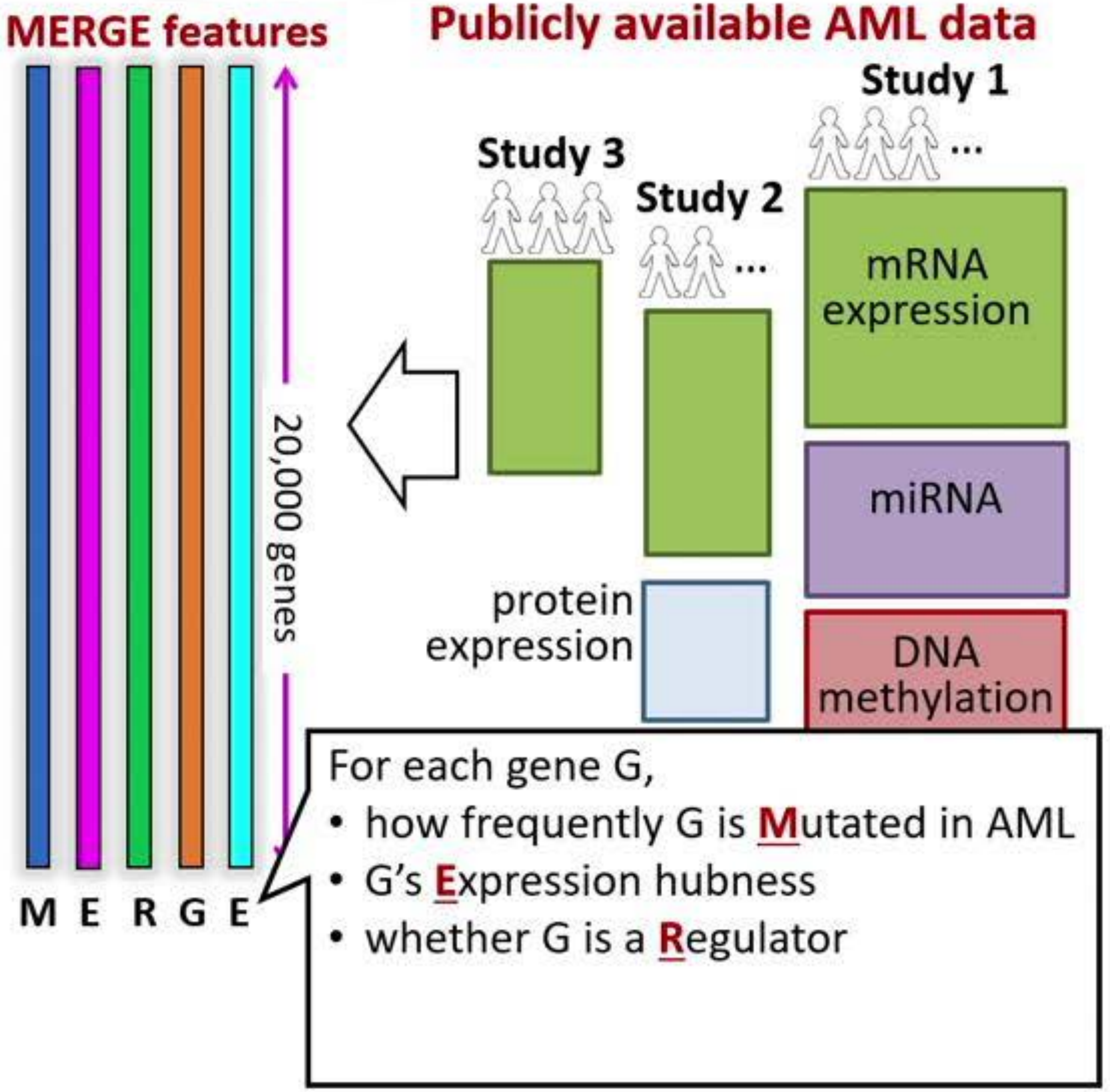

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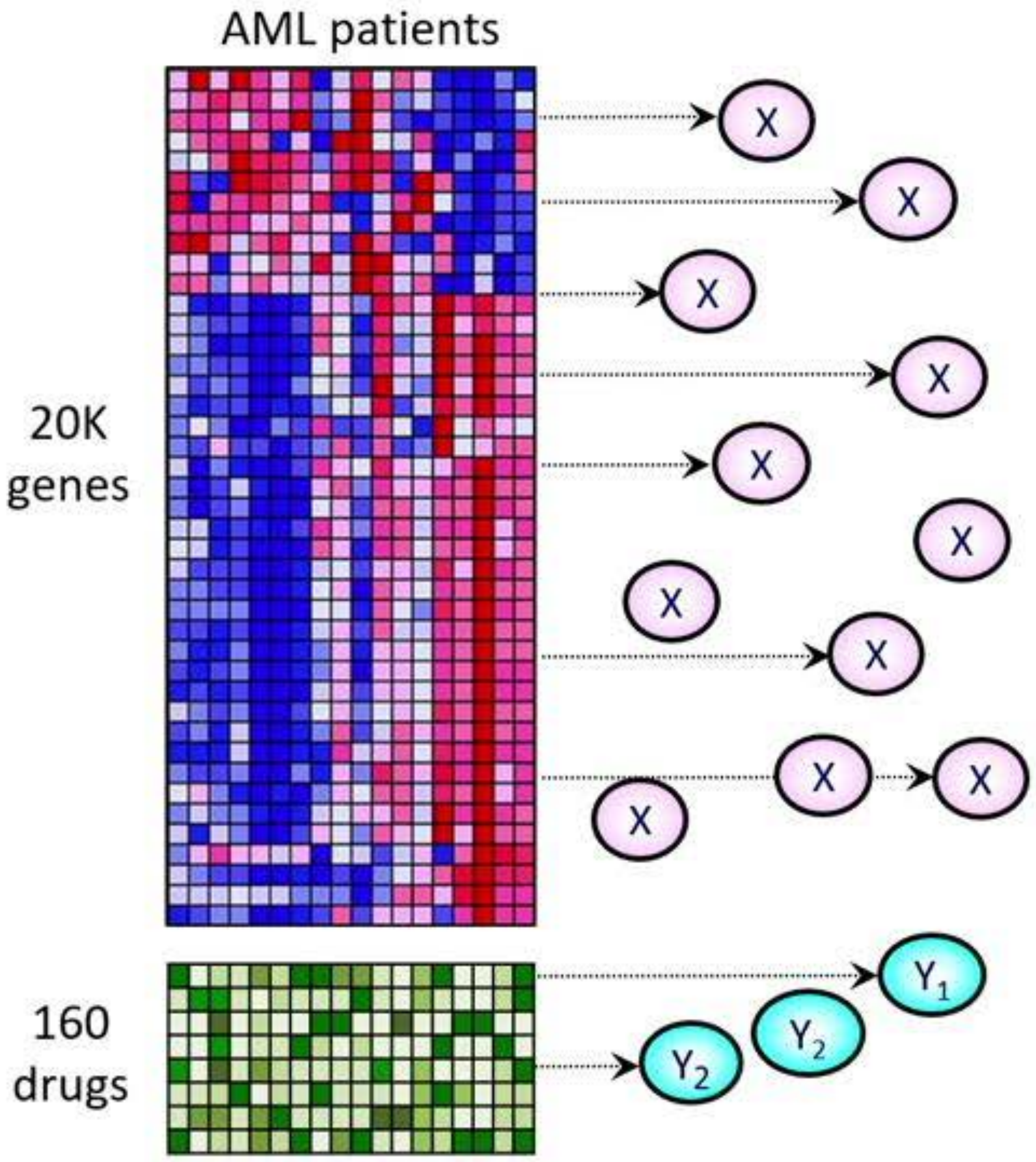

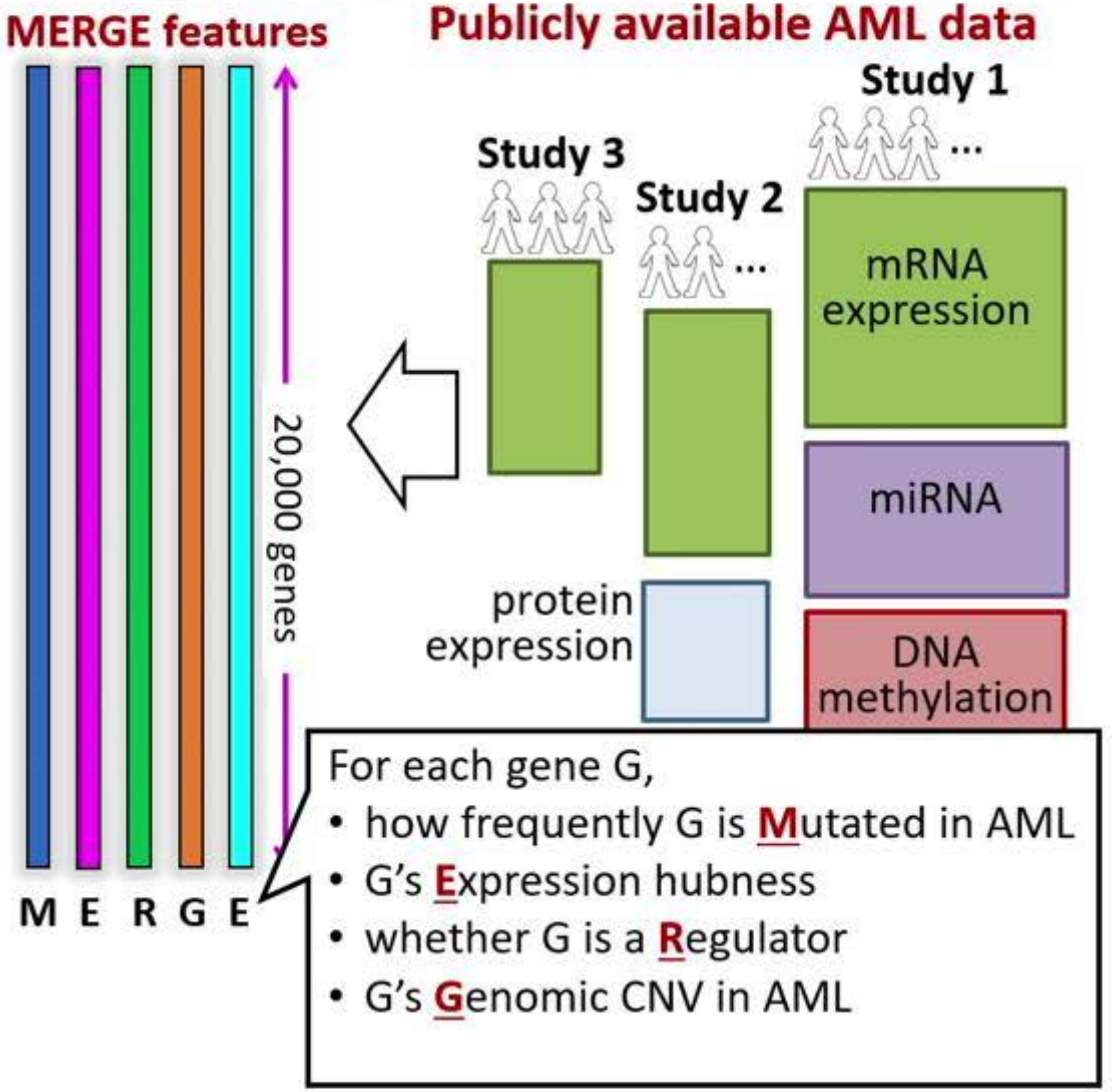

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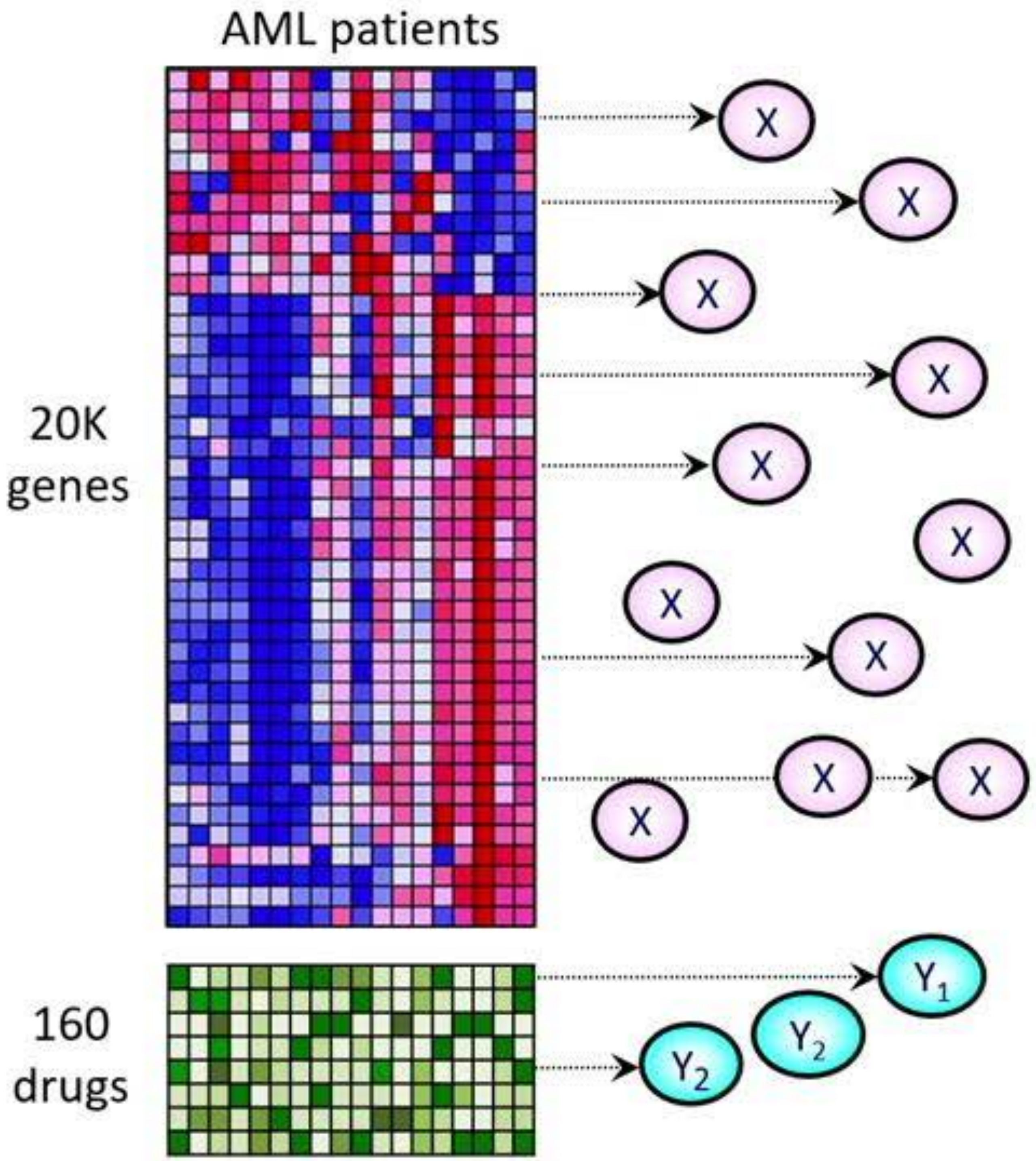

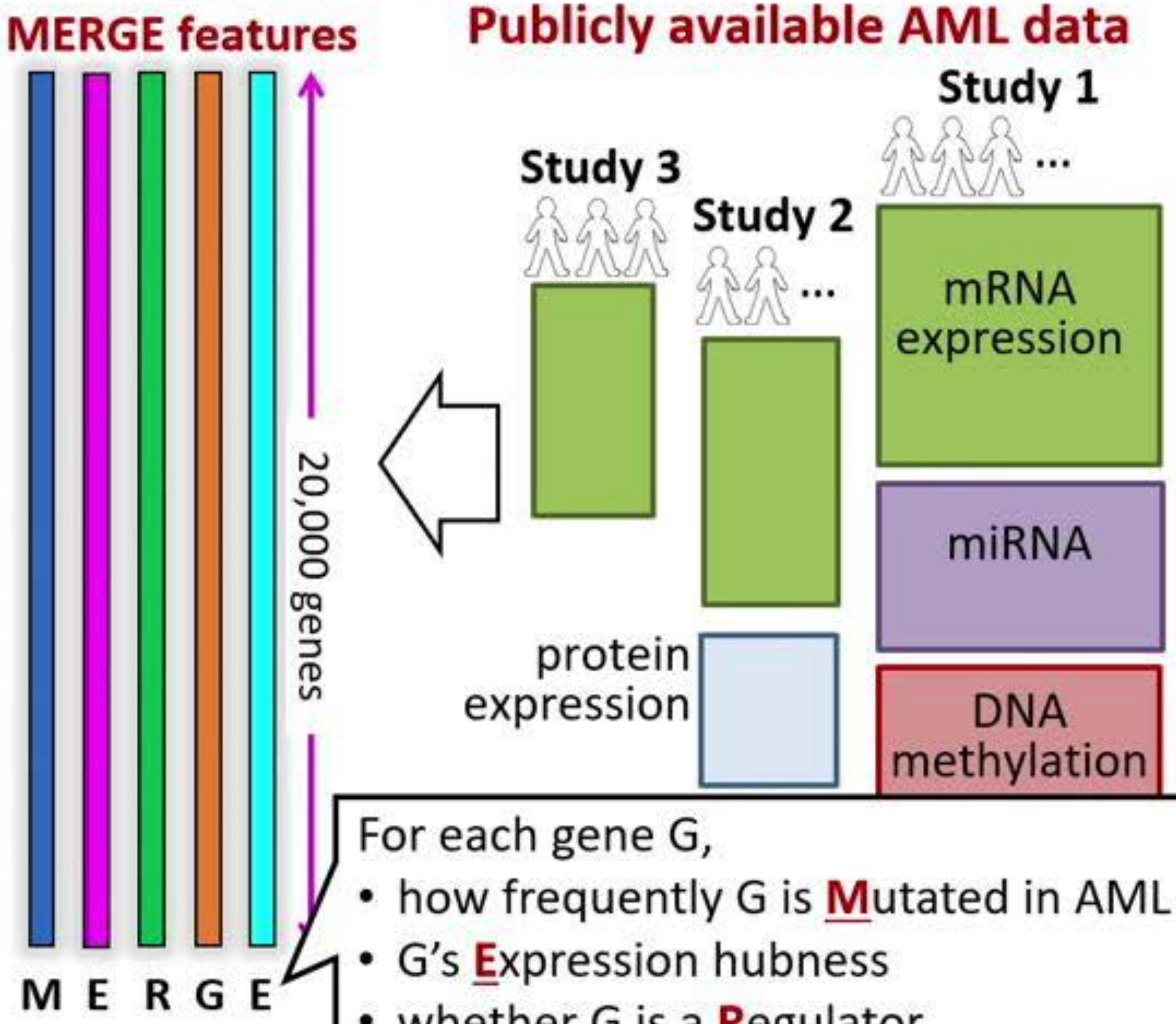

For each gene G,

- how frequently G is **M**utated in AML
- G's **E**xpression hubness
- whether G is a **R**egulator
- G's **G**enomic CNV in AML
- G's m**E**thylation status in AML

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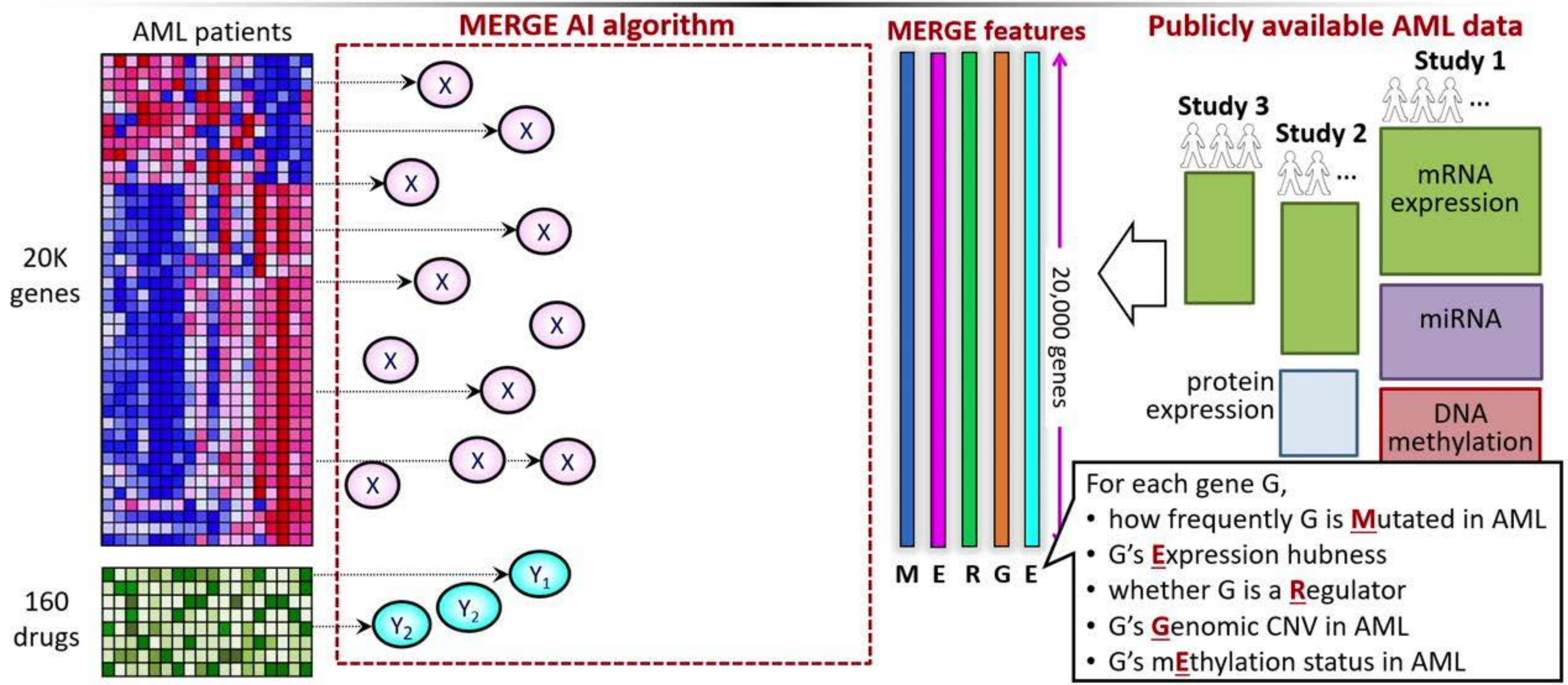

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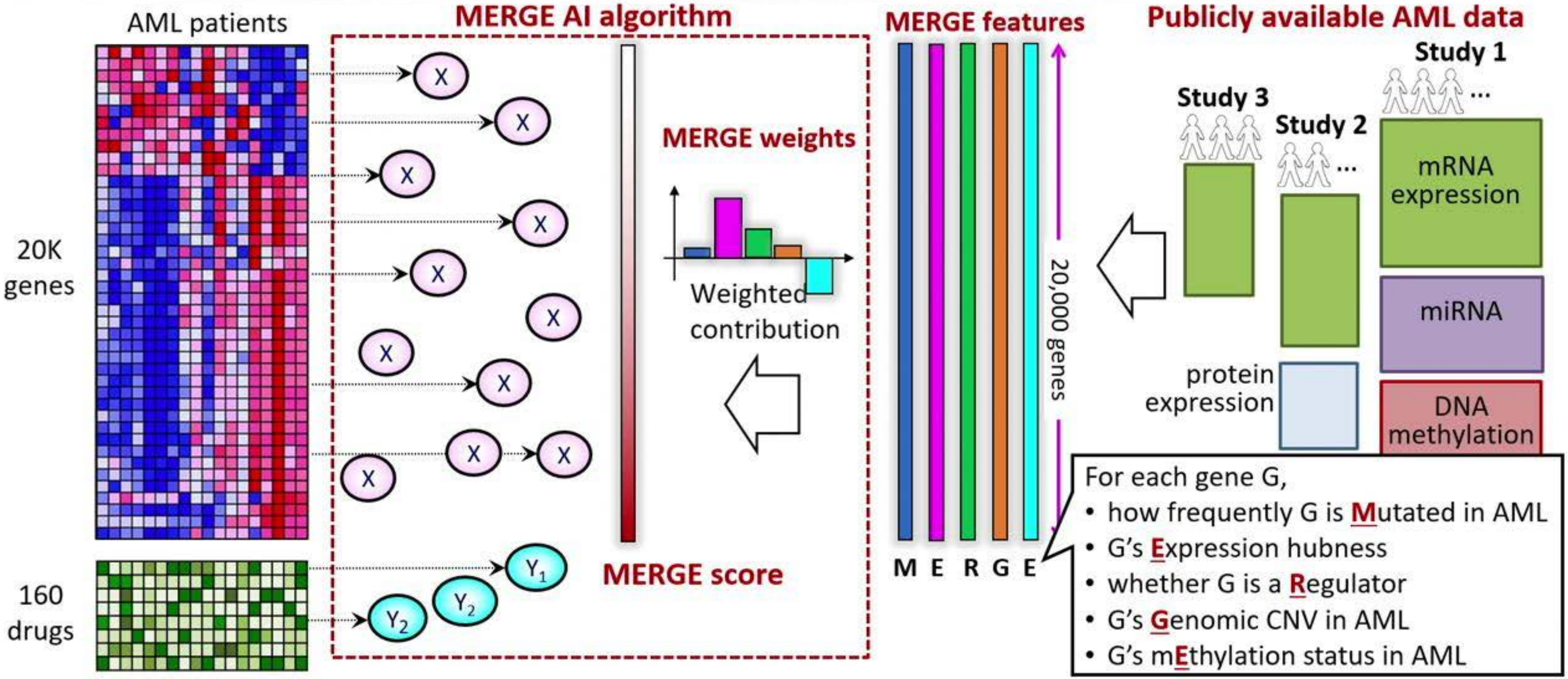

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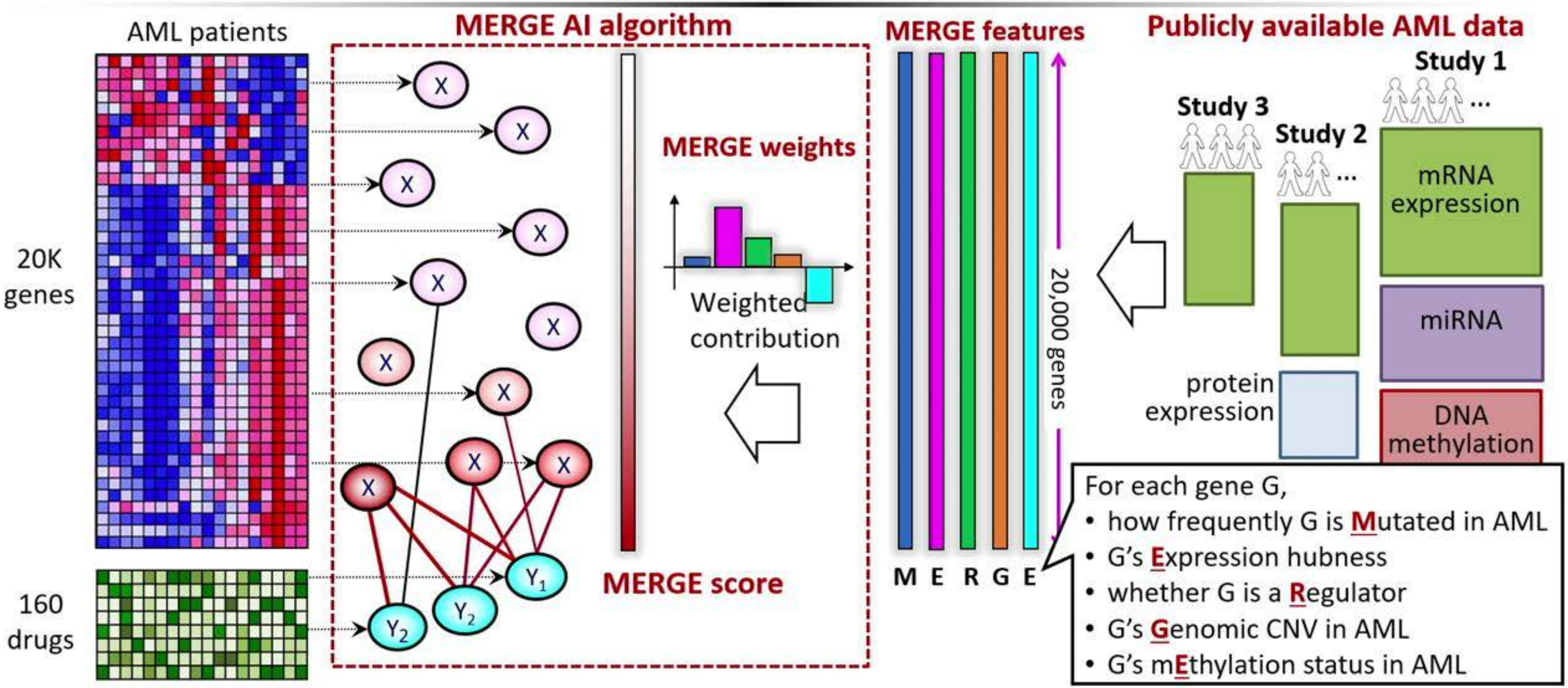

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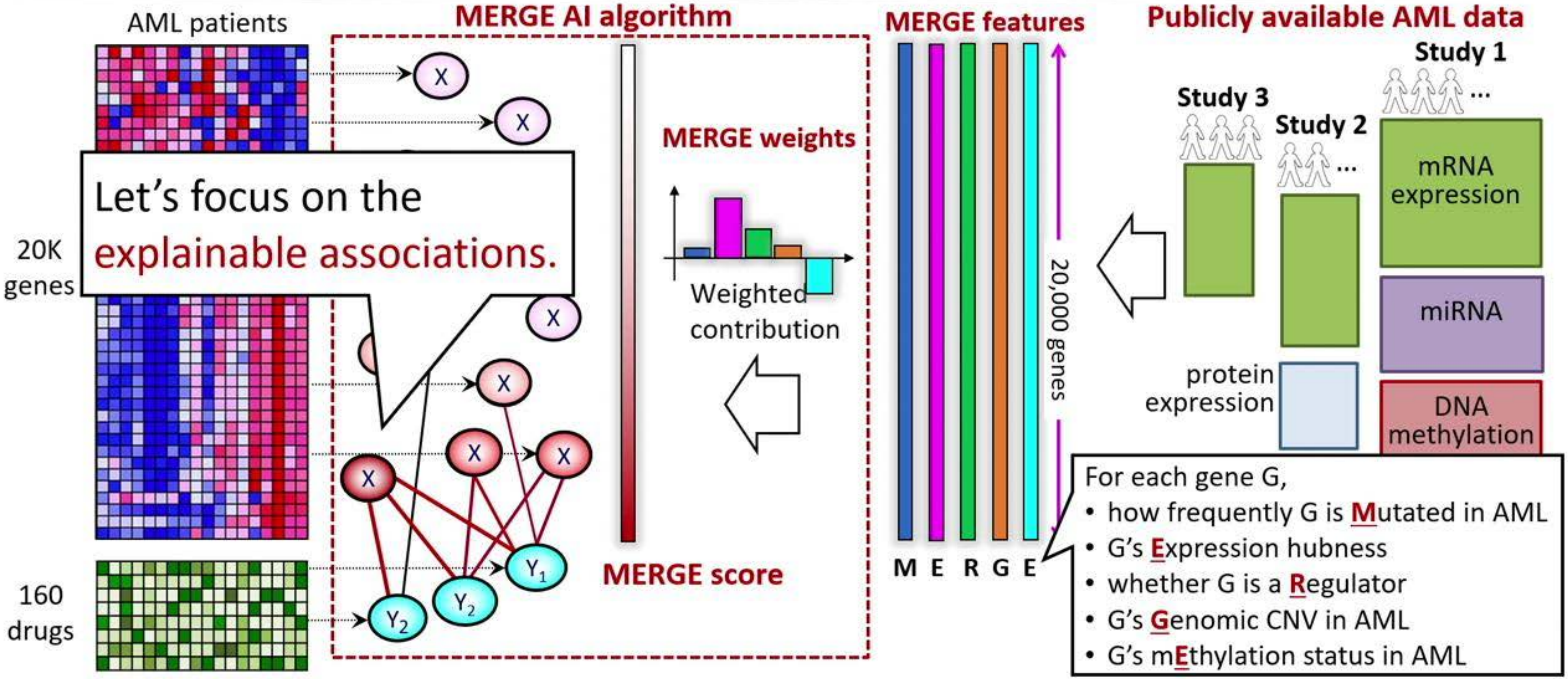

MERGE outperforms its competitors on consistency rate and drug sensitivity prediction accuracy


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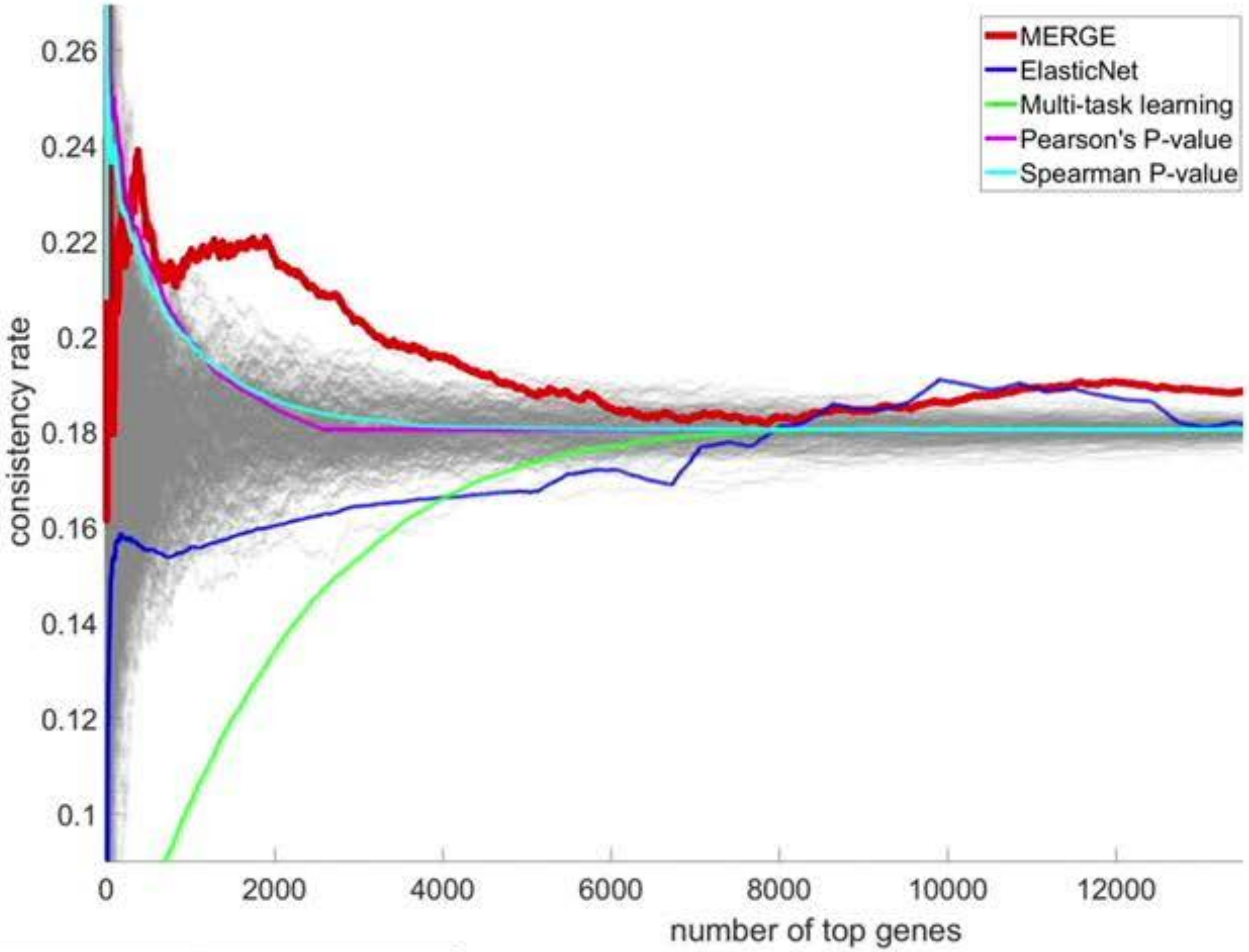

Lee*, Celik*, et al. (2018)
Nature Communications

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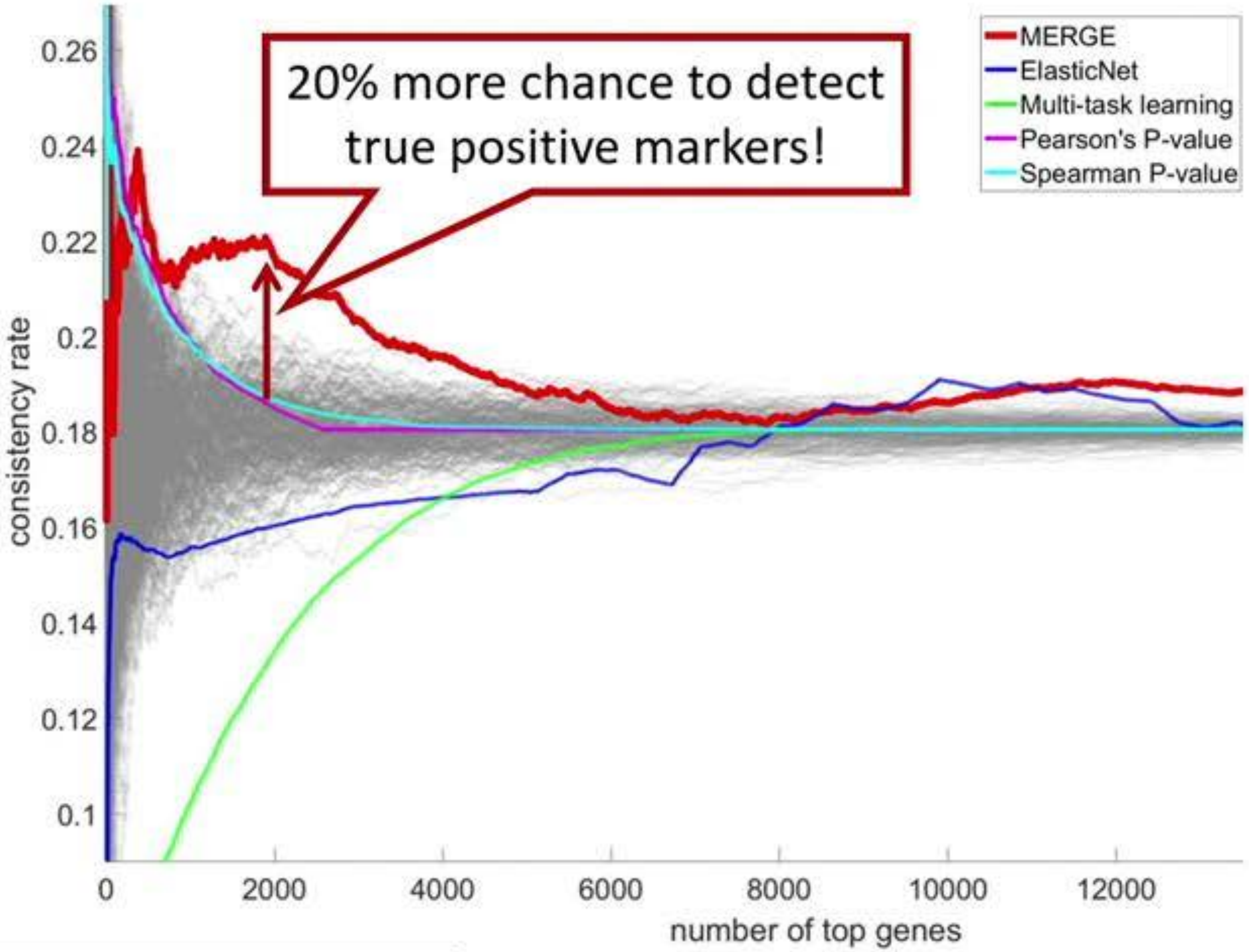

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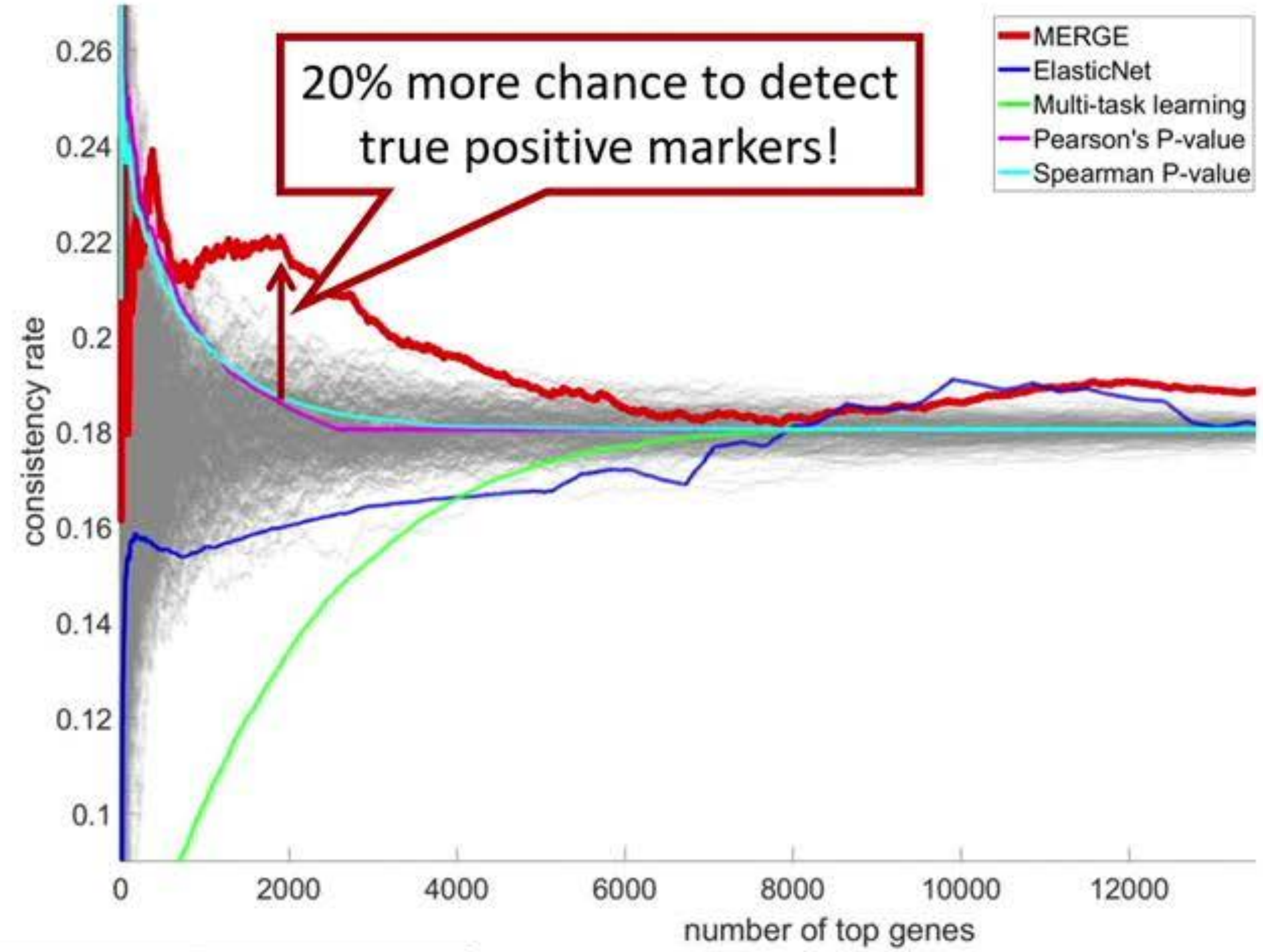

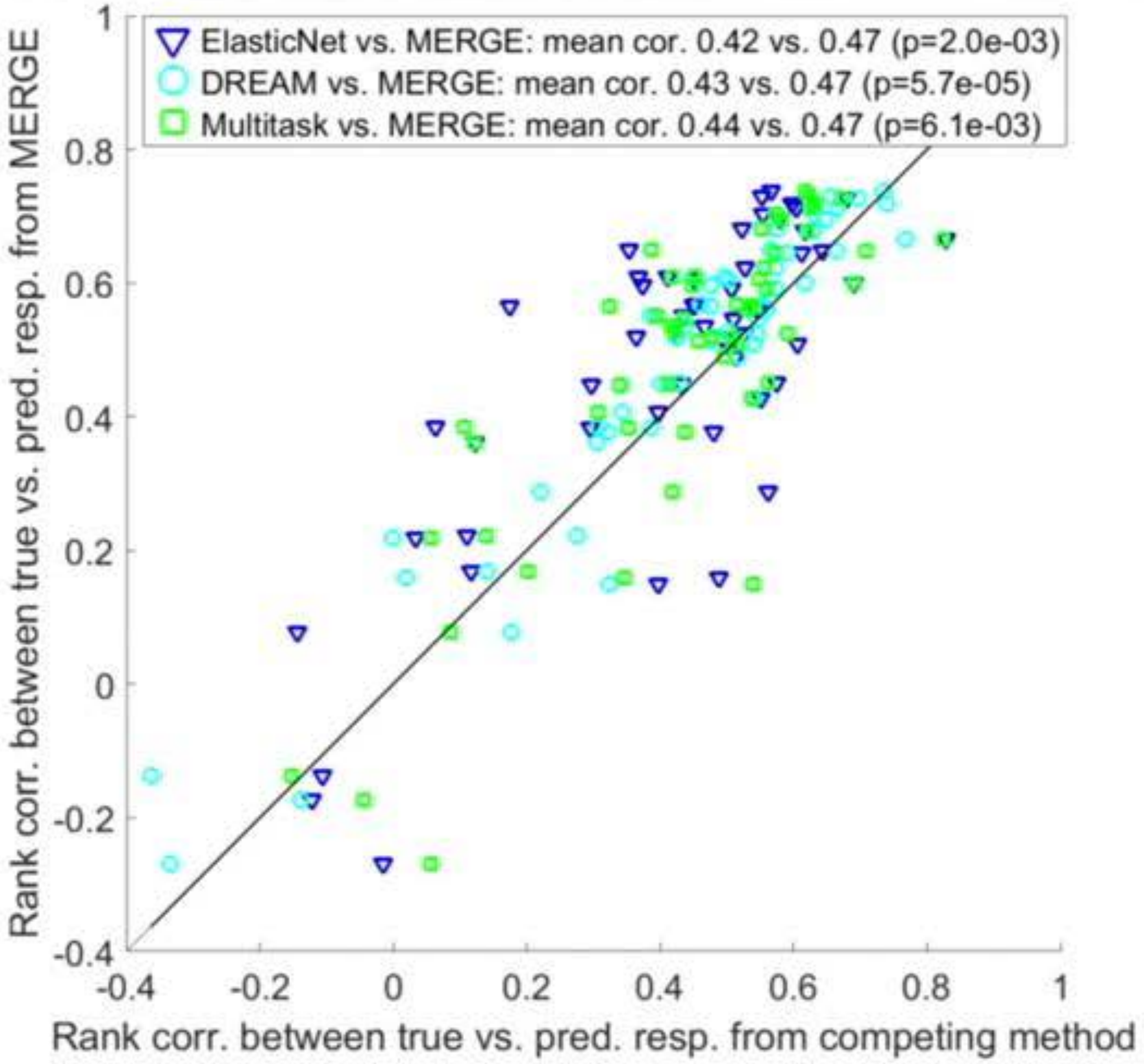

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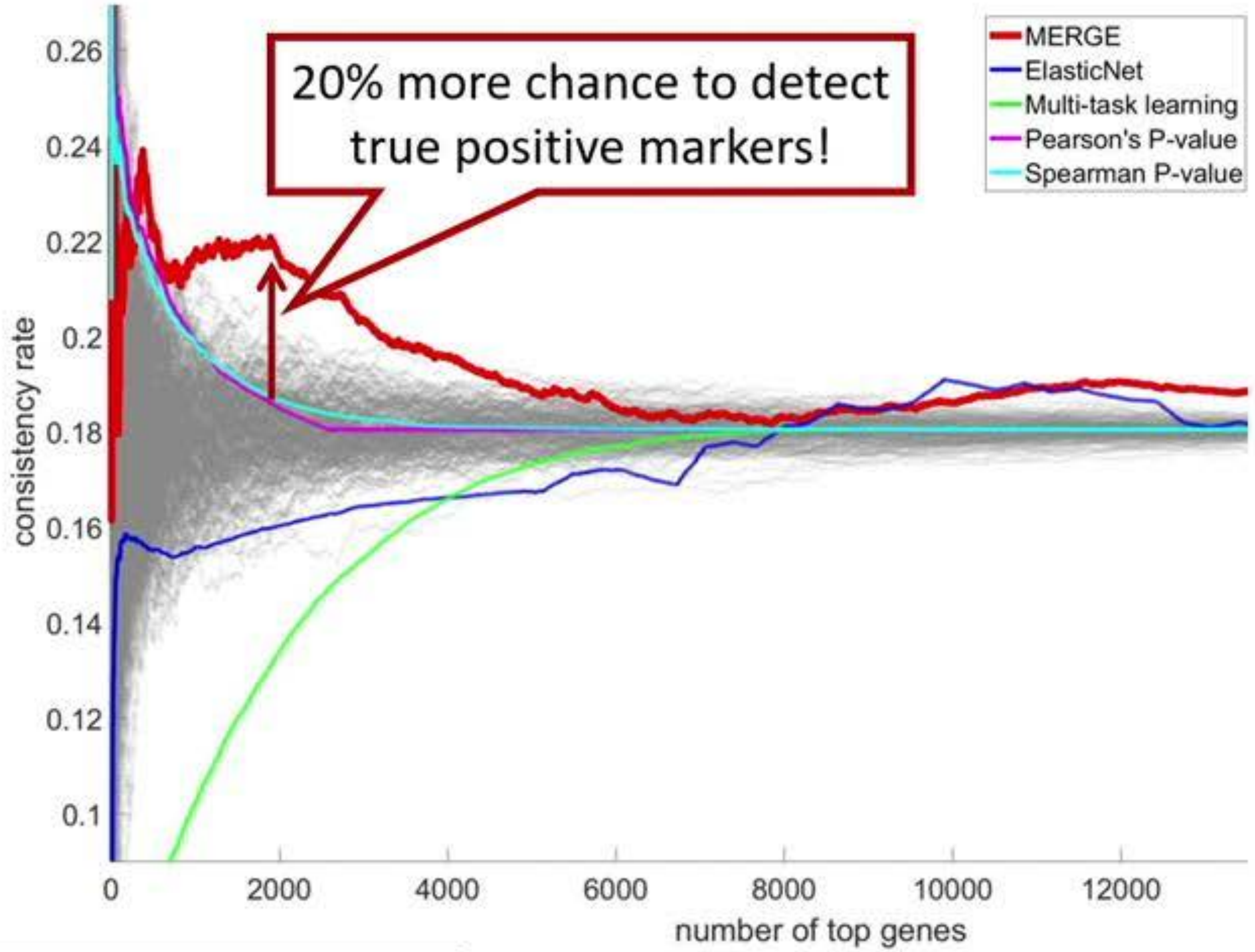

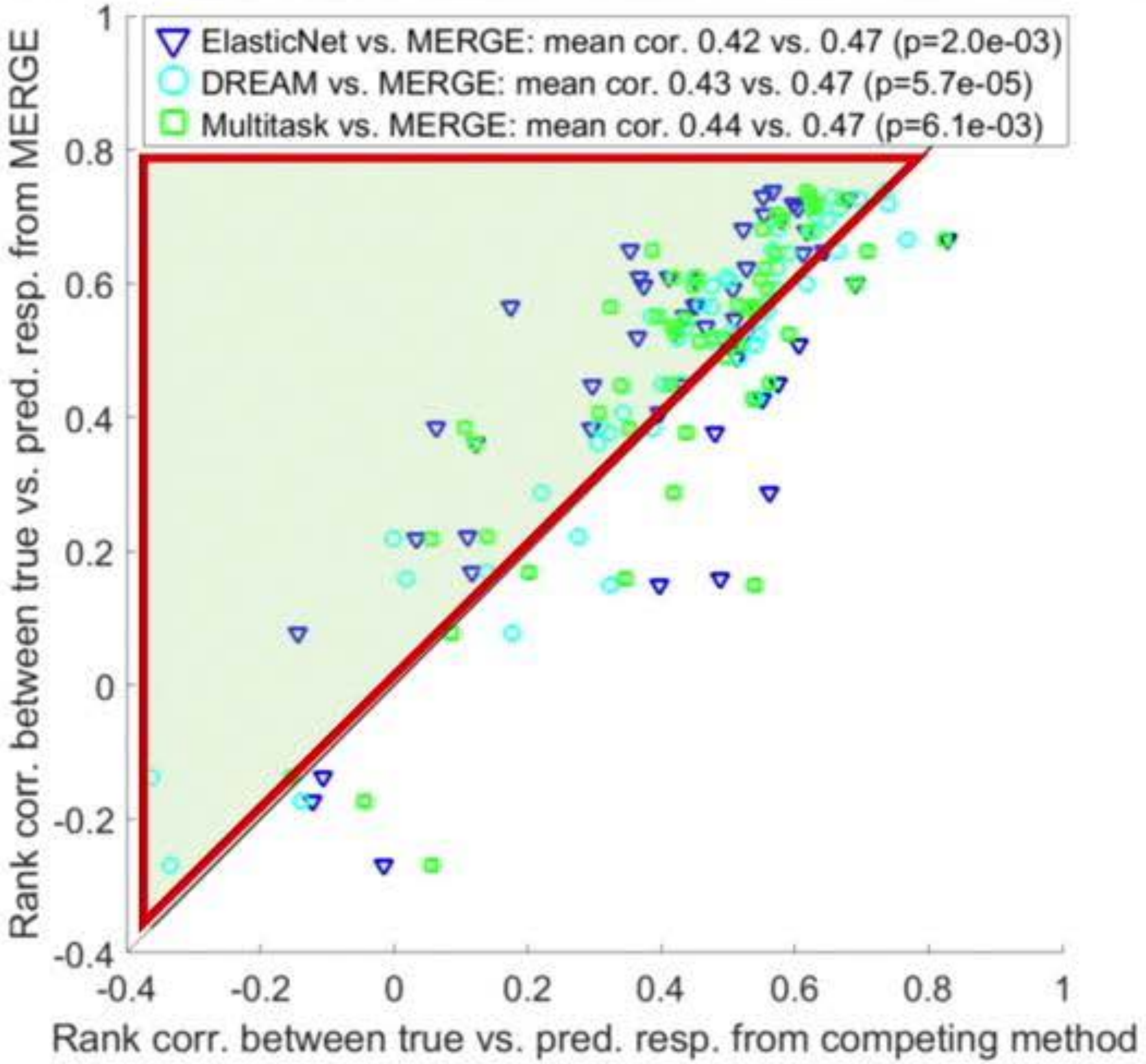

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Example novel gene-drug associations captured by the learned marker potential

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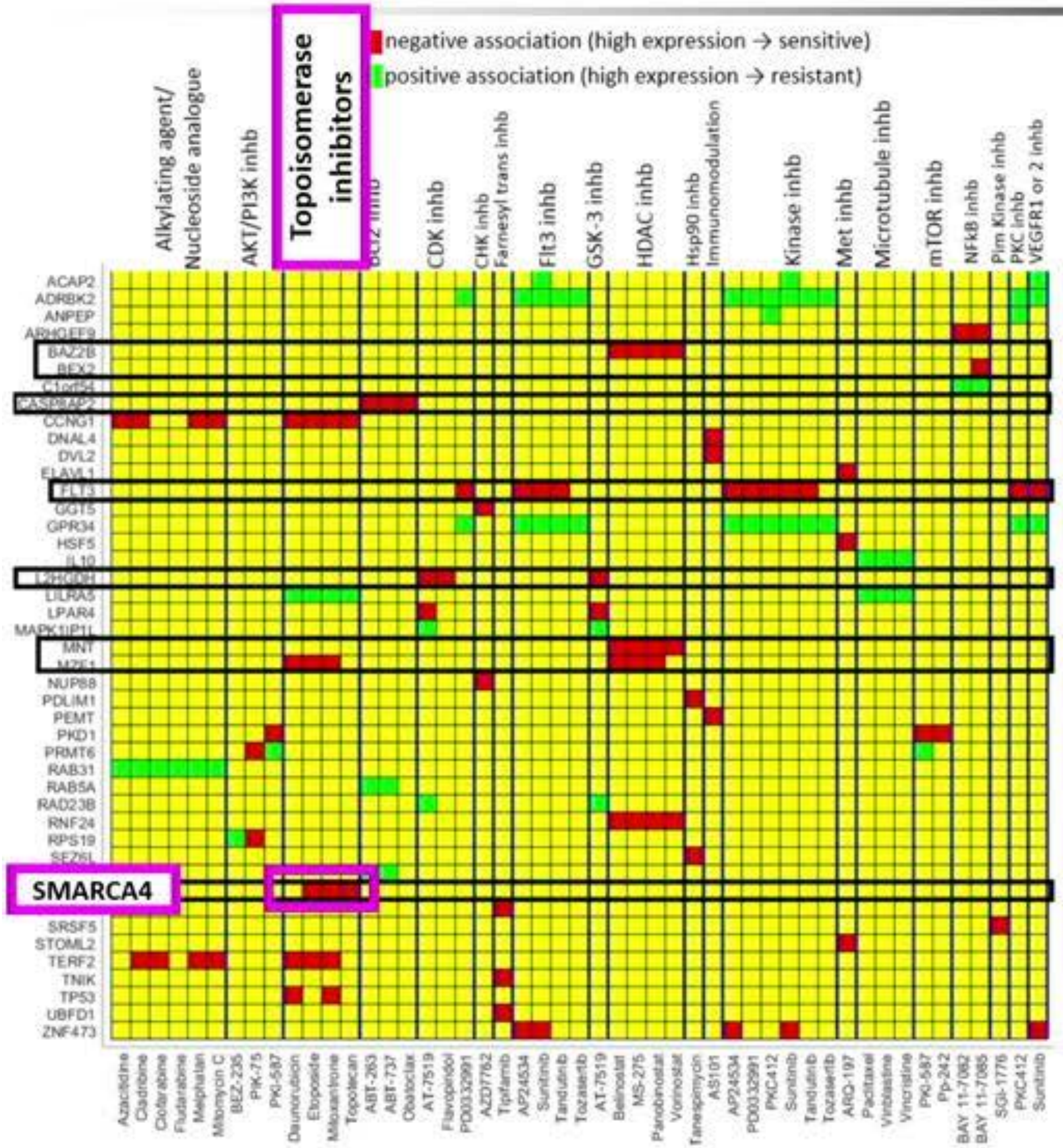

- High expression of *SMARCA4* is associated with increased sensitivity of *mitoxantrone* and *etoposide*

Hematology
Dr. Pamela Becker

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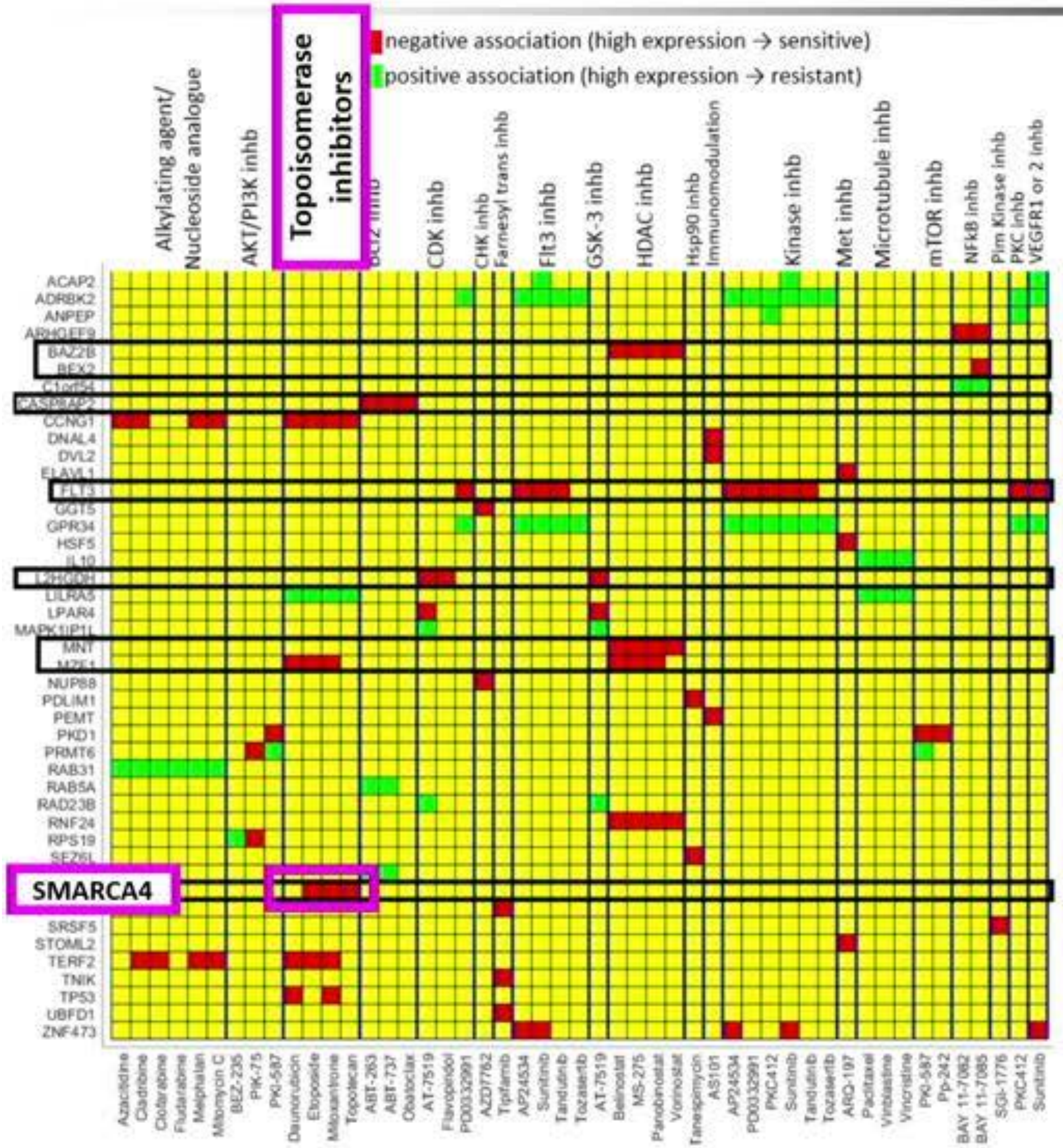

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- **Clinical importance:**
  - Mitoxantrone – included in nearly all first line AML treatment
  - Etiposide, mitoxantrone – 2 of the 3 drugs used in the MEC regimen, a common therapy for relapsed AML
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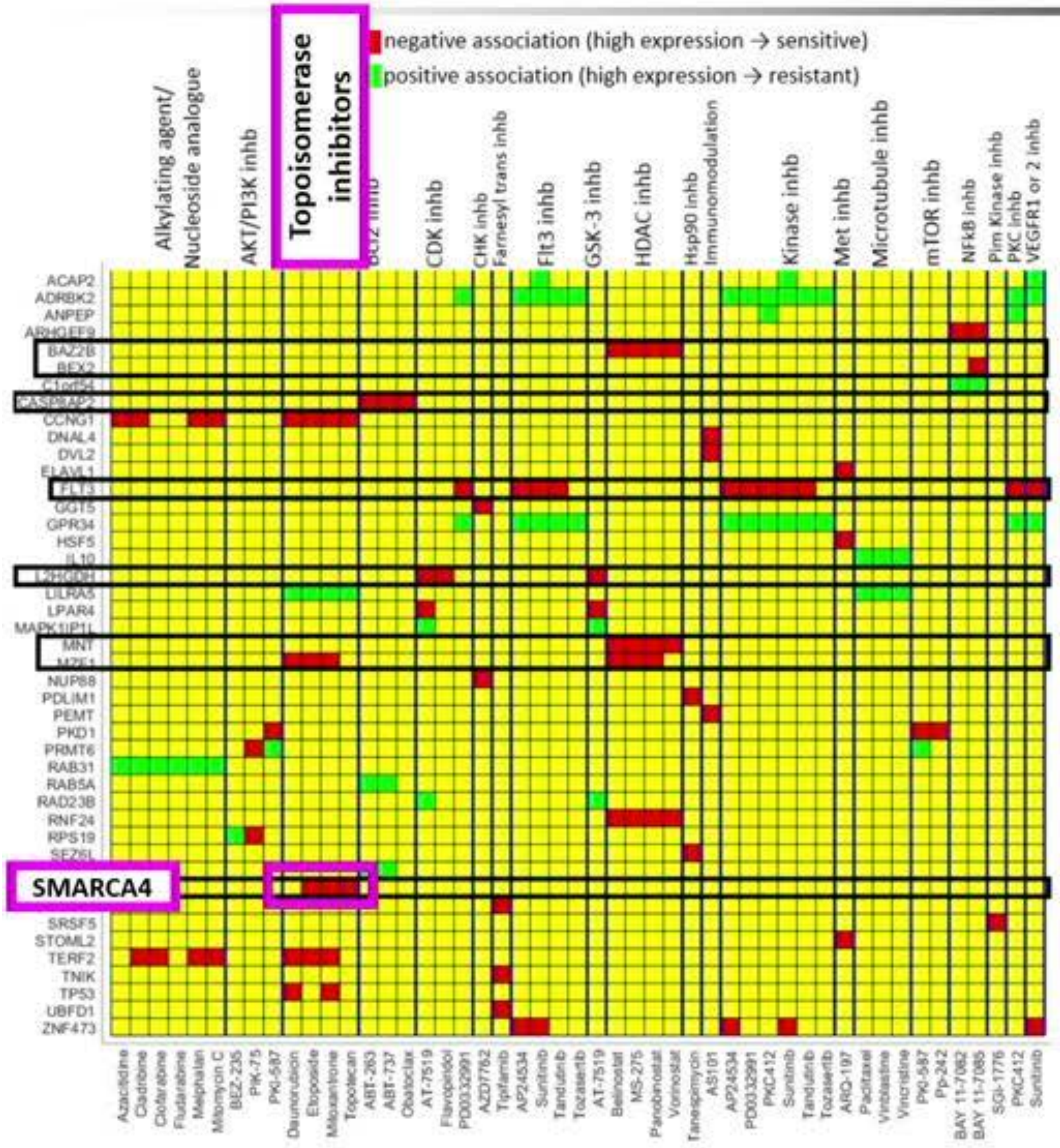

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- ***SMARCA4 would not have been captured purely based on the degrees of associations***
  - SMARCA4 is a significant expression hub.

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Experimental validation – SMARCA4 over-expression drives sensitivity to etoposide & mitoxantrone

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Etoposide

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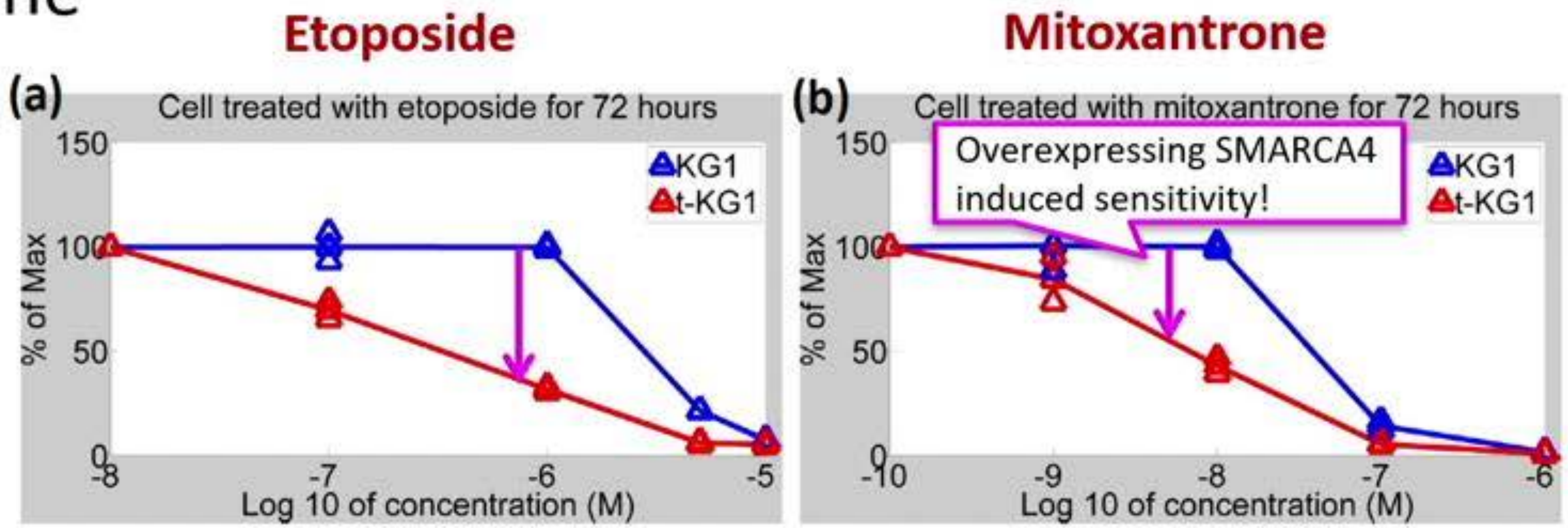

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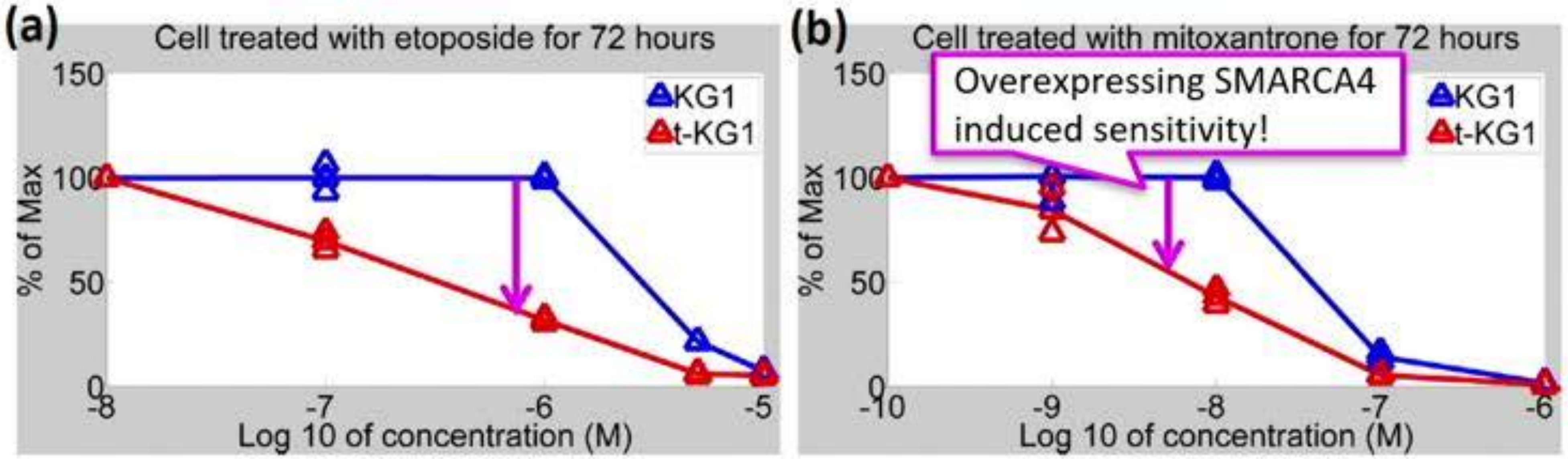

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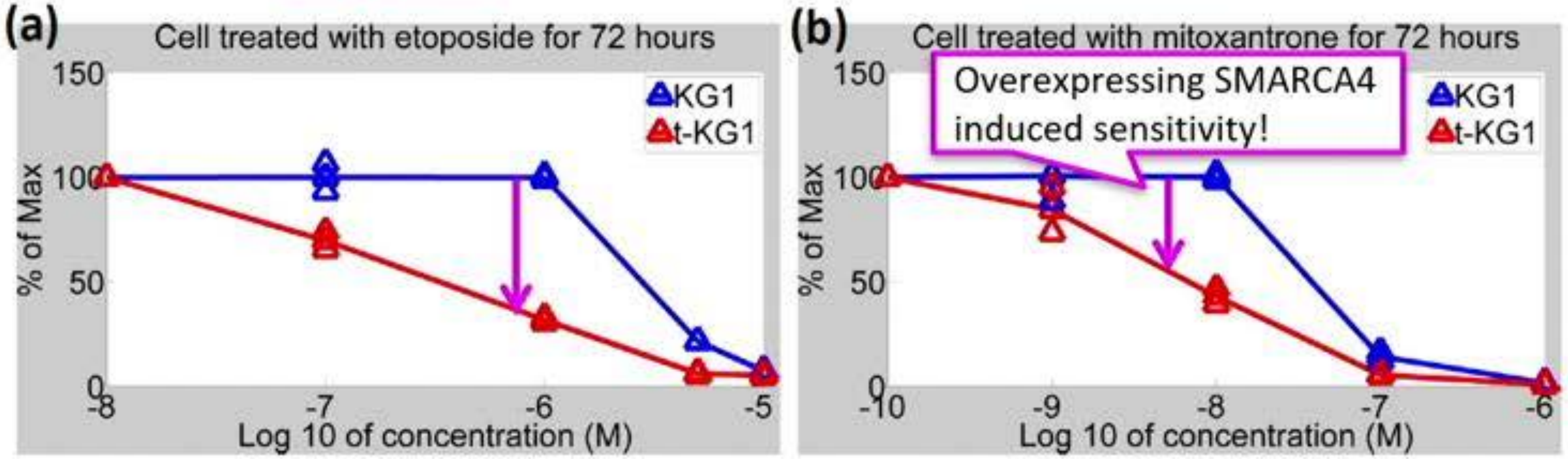

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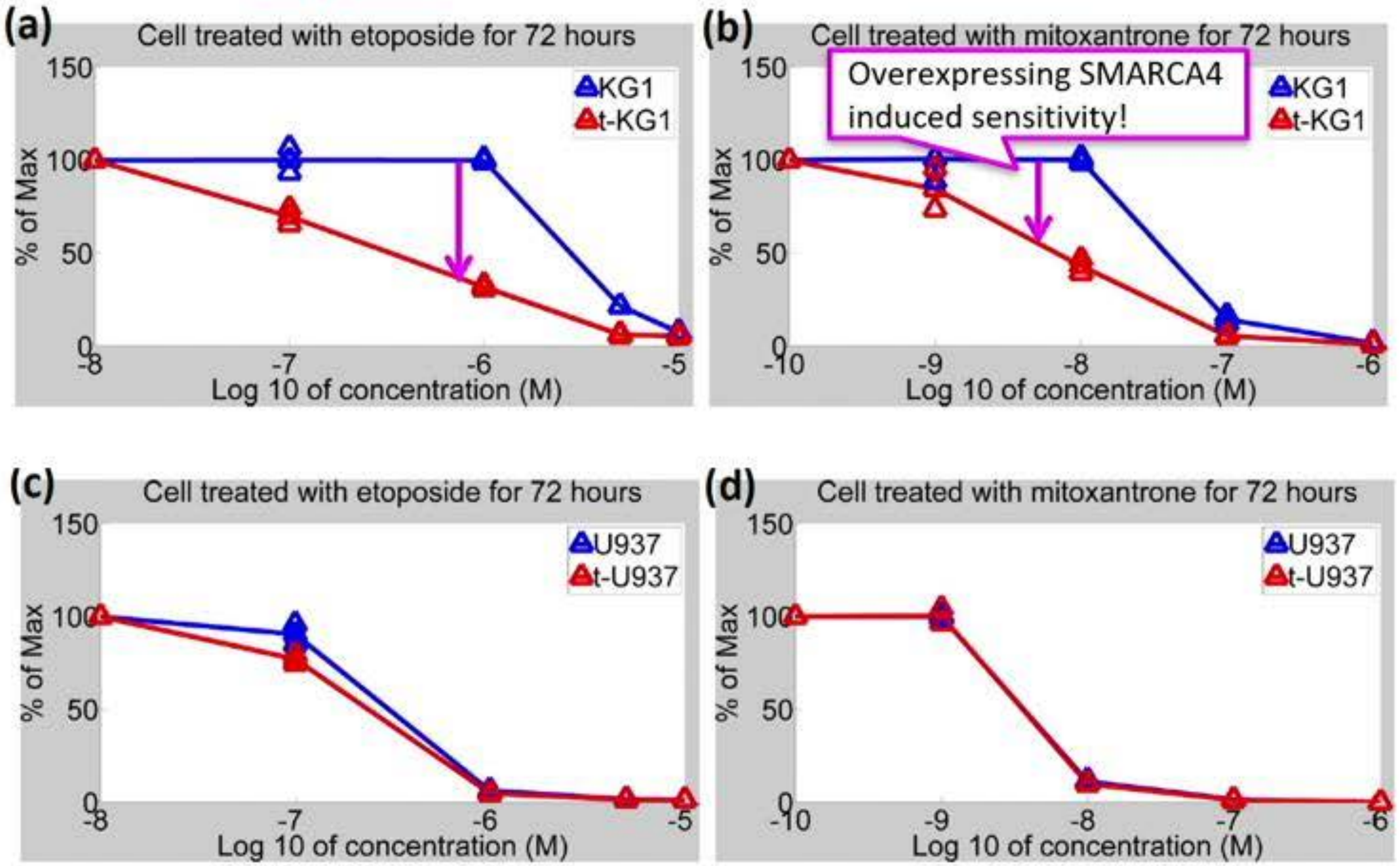


Interpretable ML can transform important areas of medicine

Prediction & decision support systems in hospitals

- Make interpretable predictions from complex models.

Cancer precision medicine

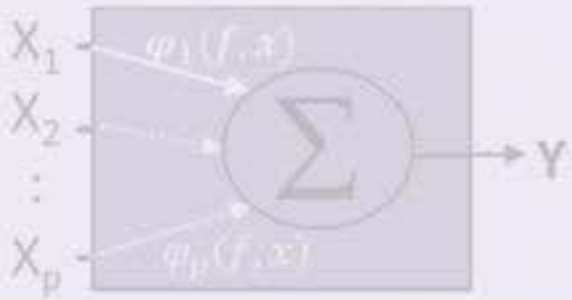
- Learn interpretable feature representations.

Alzheimer's disease therapeutic target discovery

- Integrate data sets for statistical power and interpretability.

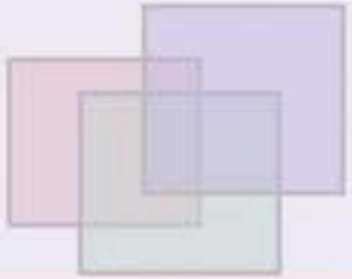
General ML techniques

Black Box



ML model

Data integration



Bedside applications

Basic science

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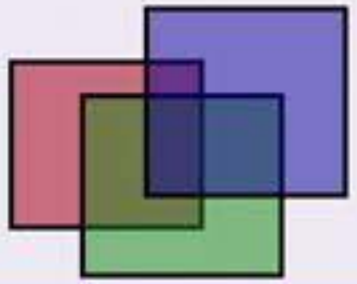

Bedside applications

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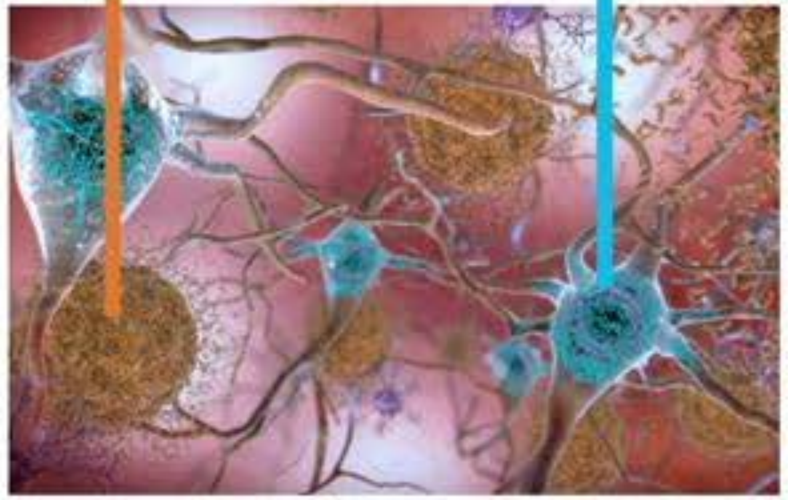

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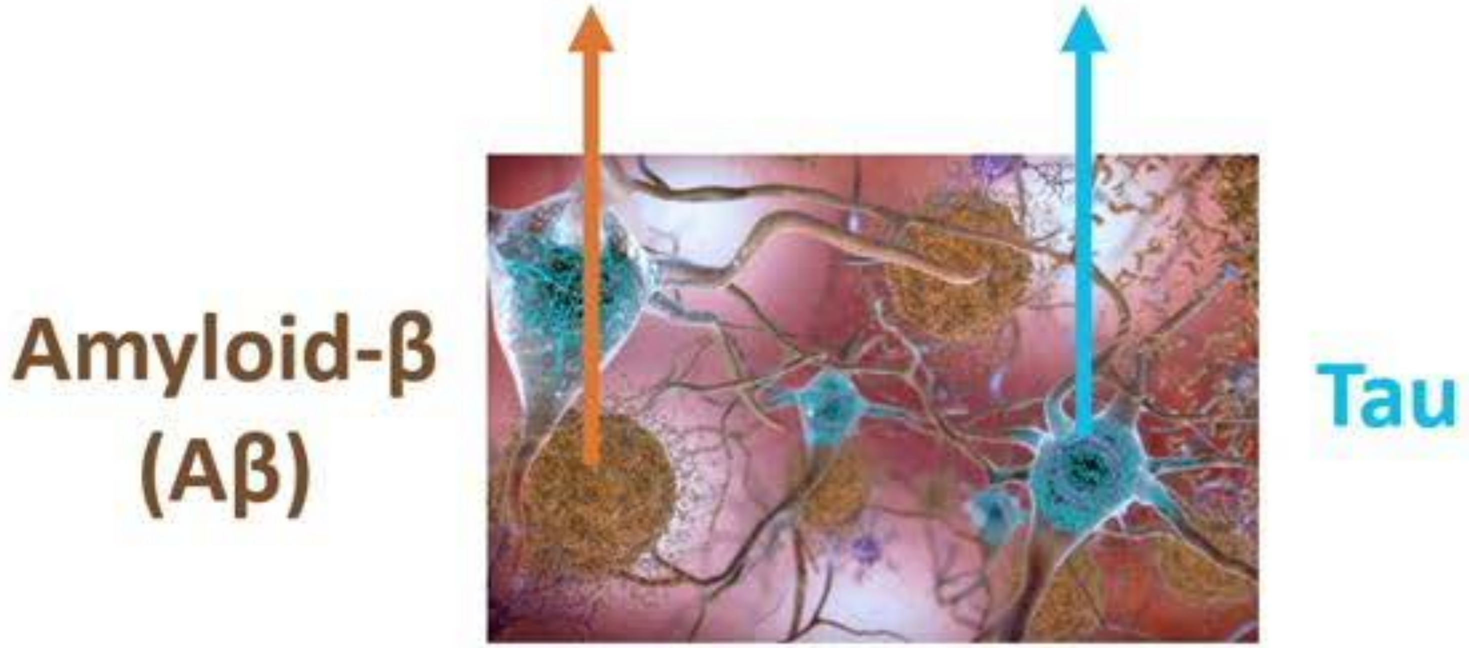

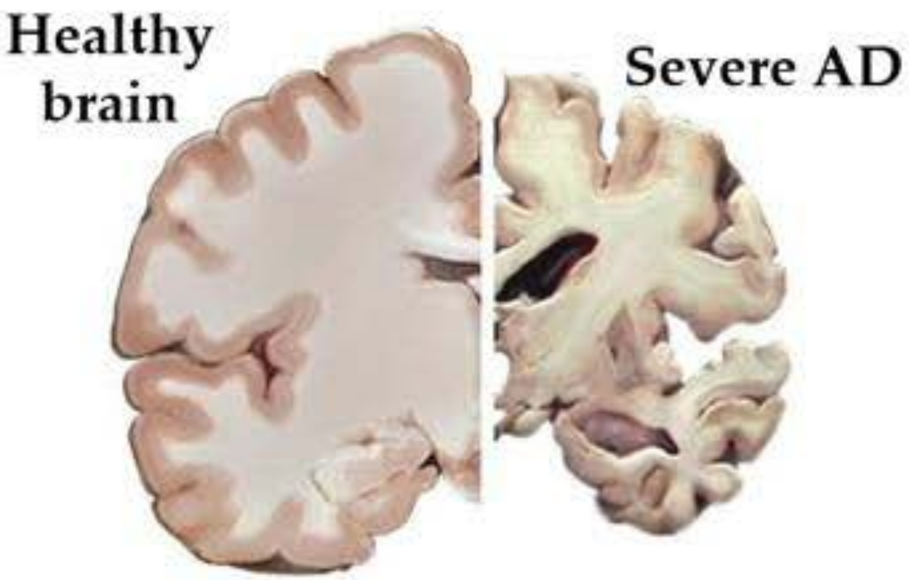

What do we need to identify the molecular basis of Aβ or tau level?

INPUT

- We need expression and phenotype data.

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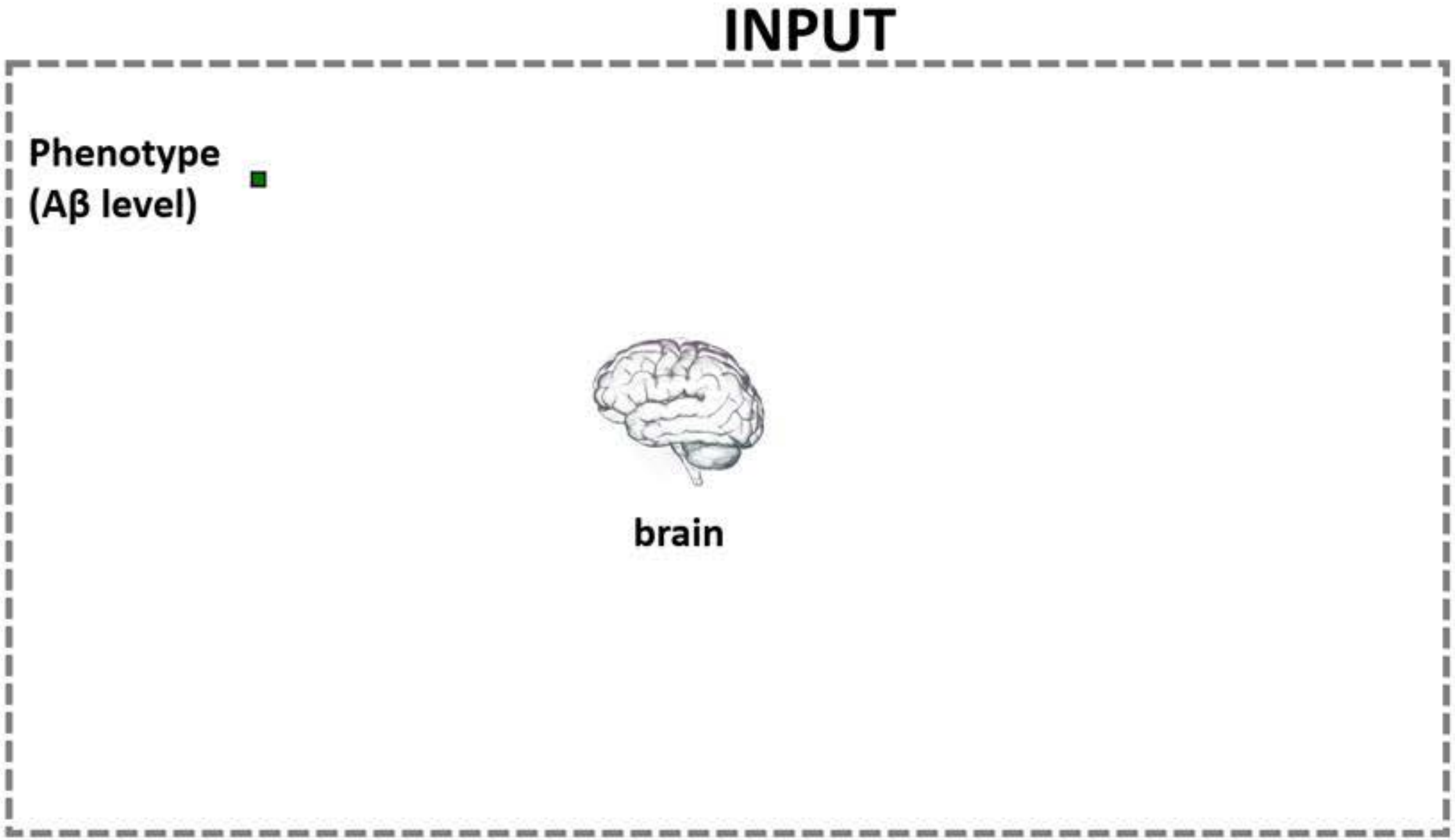

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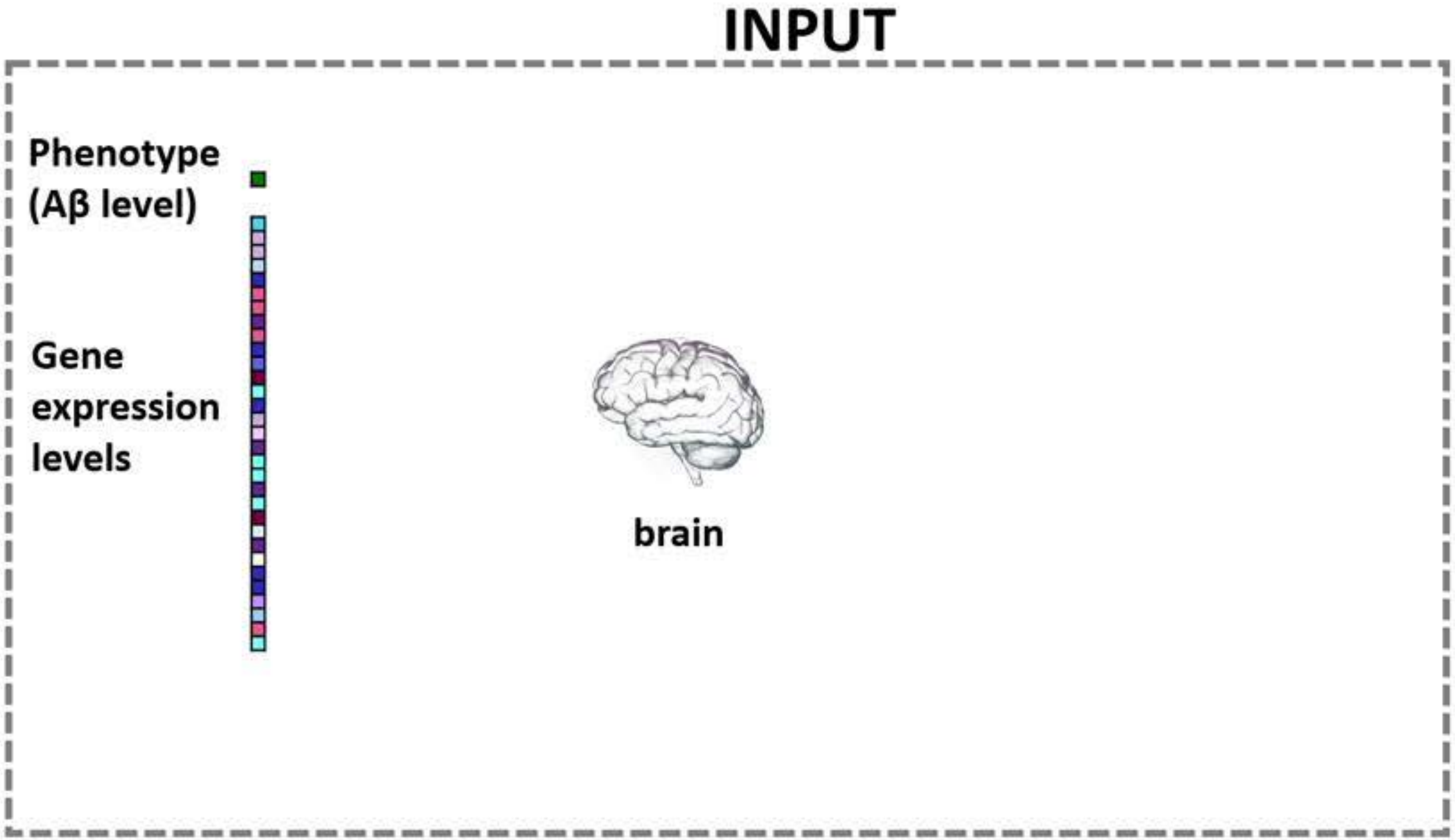

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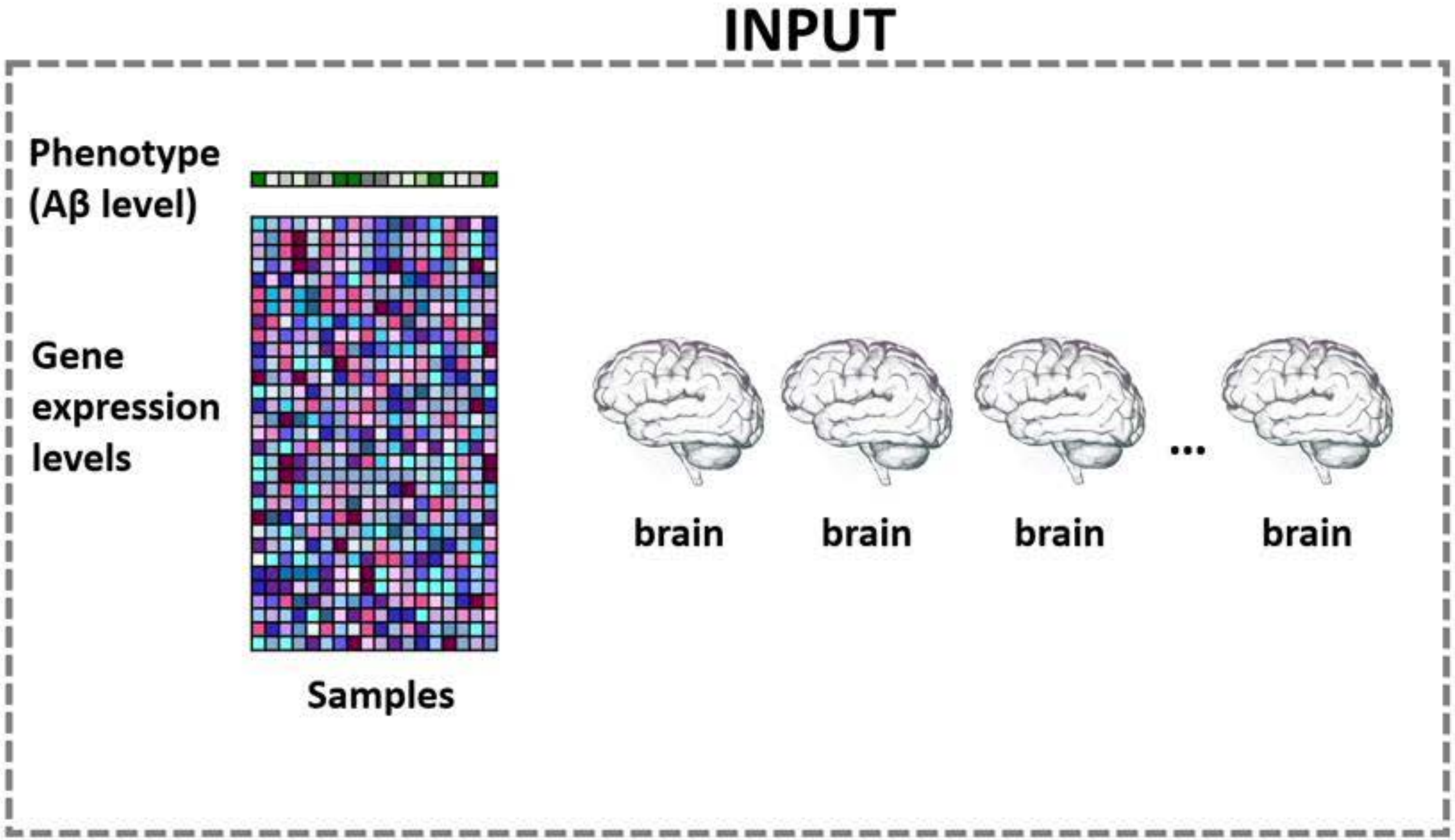

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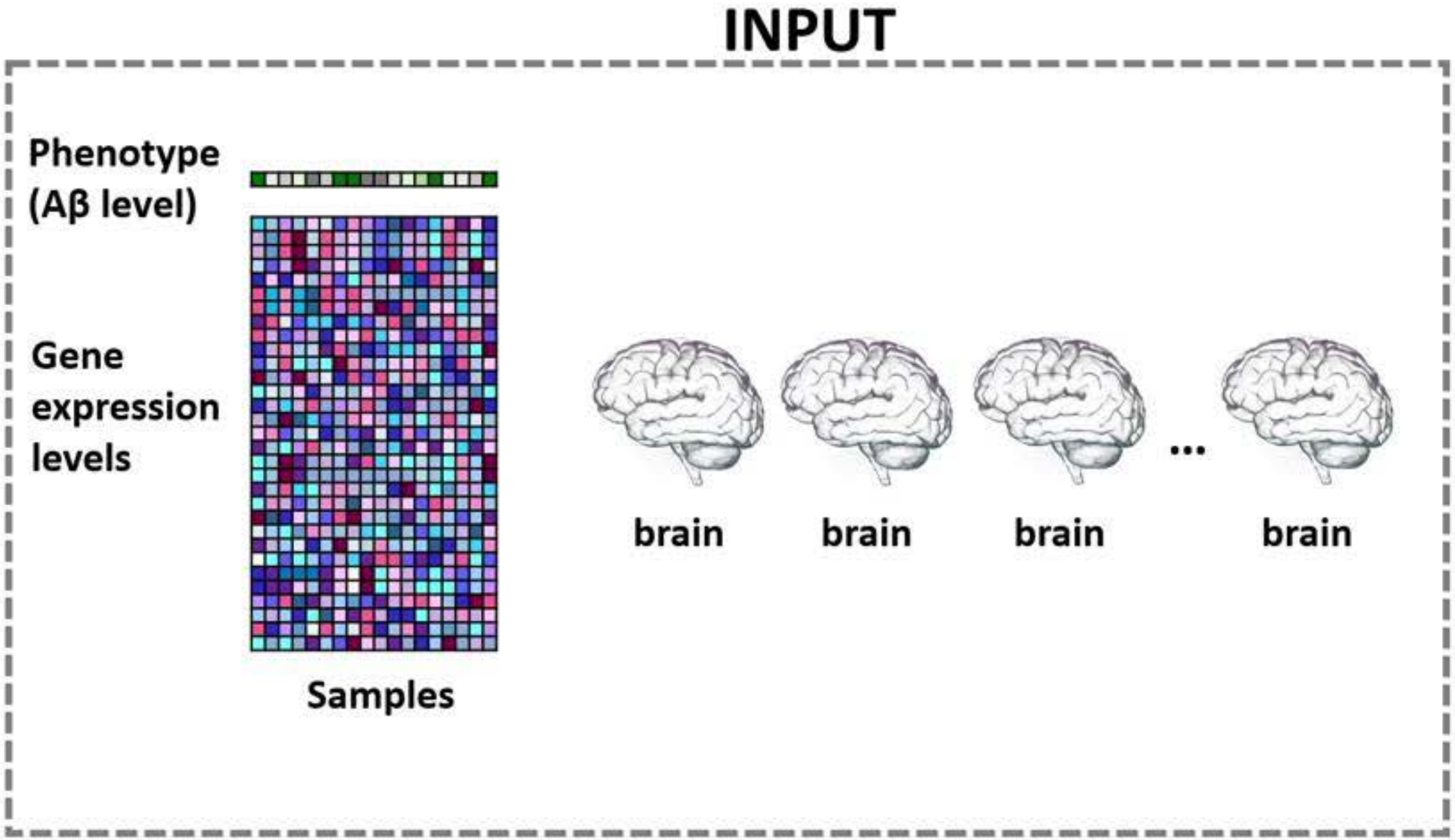

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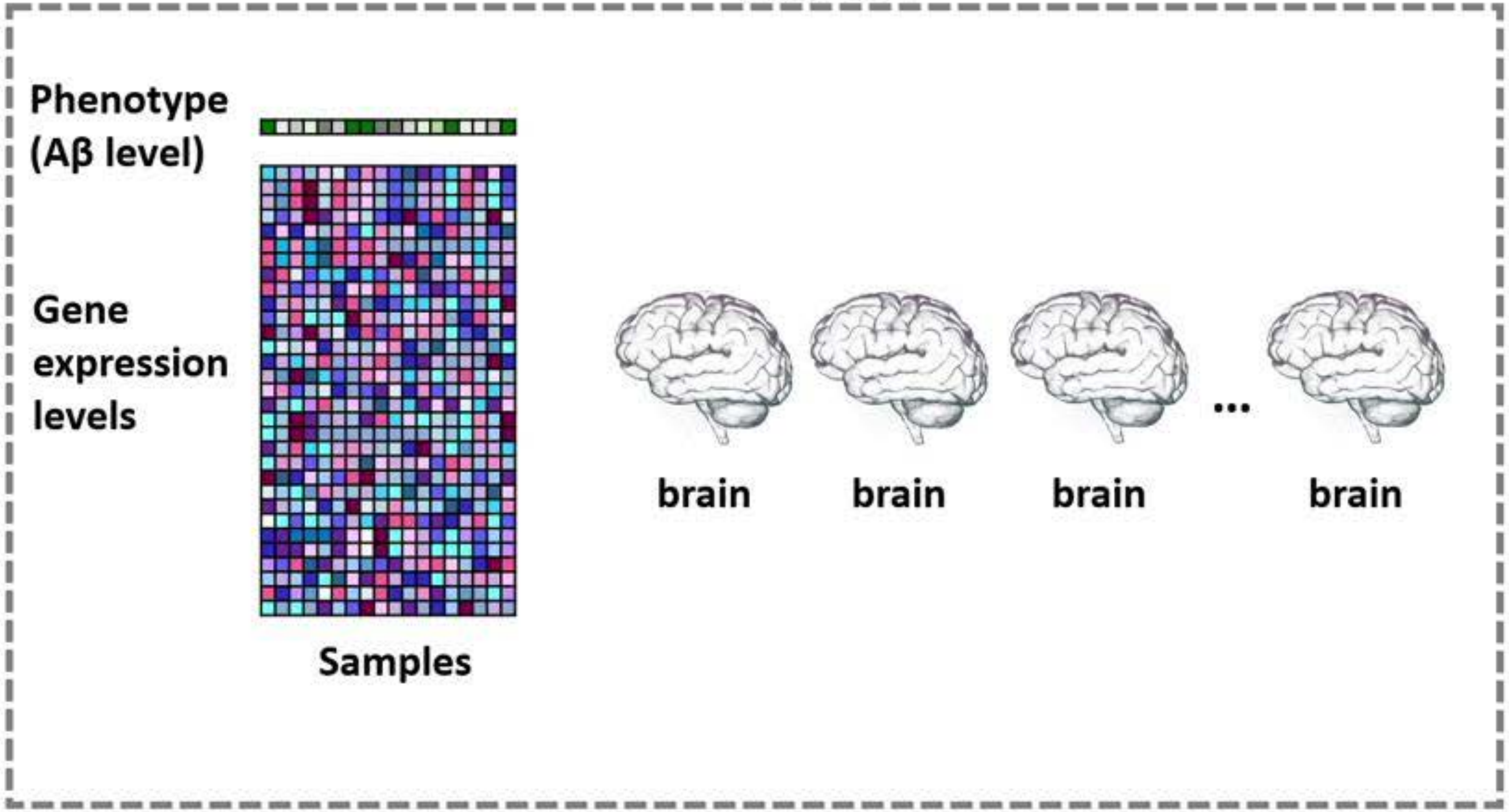

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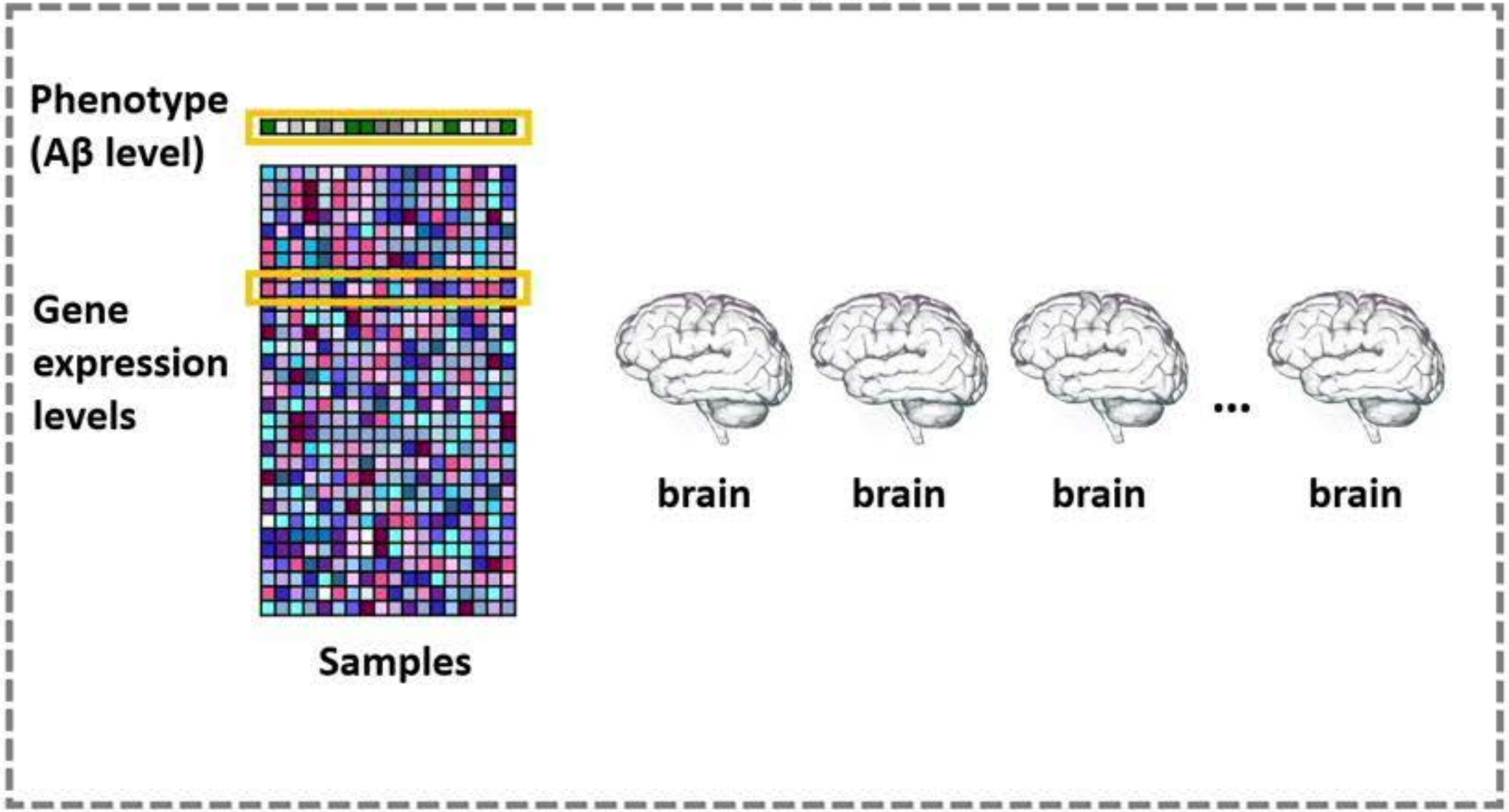

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AD expression data is limited and discrepancies across studies post challenges

Safiye

Neuropathology
Internal Medicine
AD Research Center

Dirk Keene

Paul Crane

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AD expression data is limited and discrepancies across studies post challenges

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- Expression and neuropathology measured in **1,742 samples from 9 brain regions.**

Region acronym	Brain region	Sample size
ACT-TCx	Temporal cortex	85
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ACT-HIP	Hippocampus	80
ACT-FWM	Forebrain white matter	81
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MSBB-BM10	Brodmann area 10 (frontopolar cortex)	244
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- Different tools and methods are used to quantify neuropathology

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AD expression data is limited and discrepancies across studies post challenges

Safiye

- Expression and neuropathology measured in **1,742 samples from 9 brain regions.**

Region acronym	Brain region	Sample size
ACT-TCx	Temporal cortex	85
ACT-PCx	Parietal cortex	79
ACT-HIP	Hippocampus	80
ACT-FWM	Forebrain white matter	81
ROSMAP-DPFCx	Dorsolateral prefrontal cortex	538
MSBB-BM10	Brodmann area 10 (frontopolar cortex)	244
MSBB-BM36	Brodmann area 36 (ectorhinal cortex)	200
MSBB-BM44	Brodmann area 44 (opercular part of the inferior frontal gyrus)	208
MSBB-BM22	Brodmann area 22 (posterior part of the first temporal gyrus)	227

- Different brain regions have different cell type compositions, functions, and relevance to AD.
- Different tools and methods are used to quantify neuropathology
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Neuropathology
Internal Medicine
AD Research Center

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- Different tools and methods are used to quantify neuropathology
- Different subject compositions or experimental procedures (batch effects, and confounders)
- **We need a powerful ML algorithm that can incorporate reliable prior knowledge to help us focus on true signals.**

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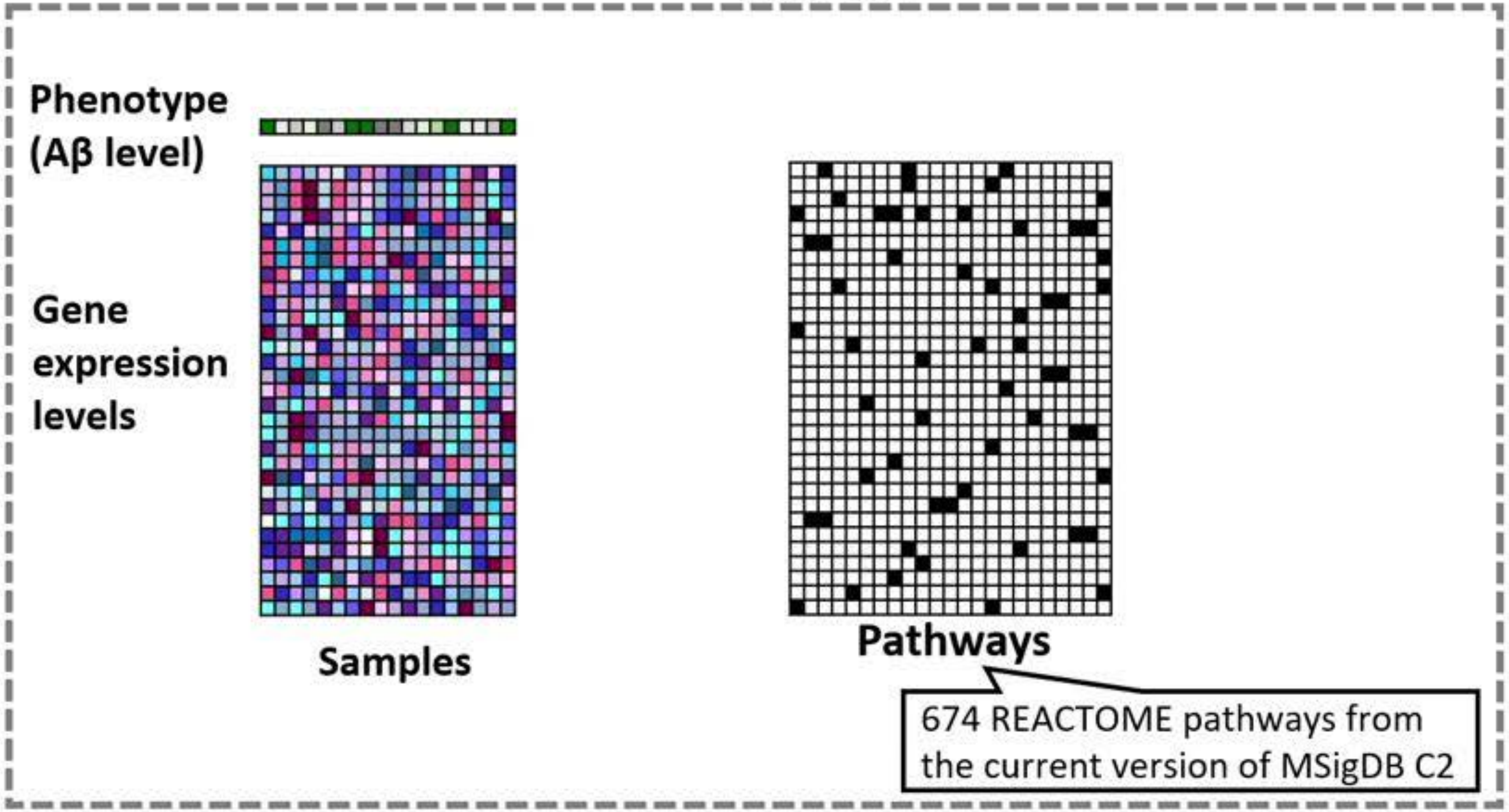
EMBARKER (EMpowering Big datA with prioR Knowledge for Expression markeR discovery)

Safiye

INPUT



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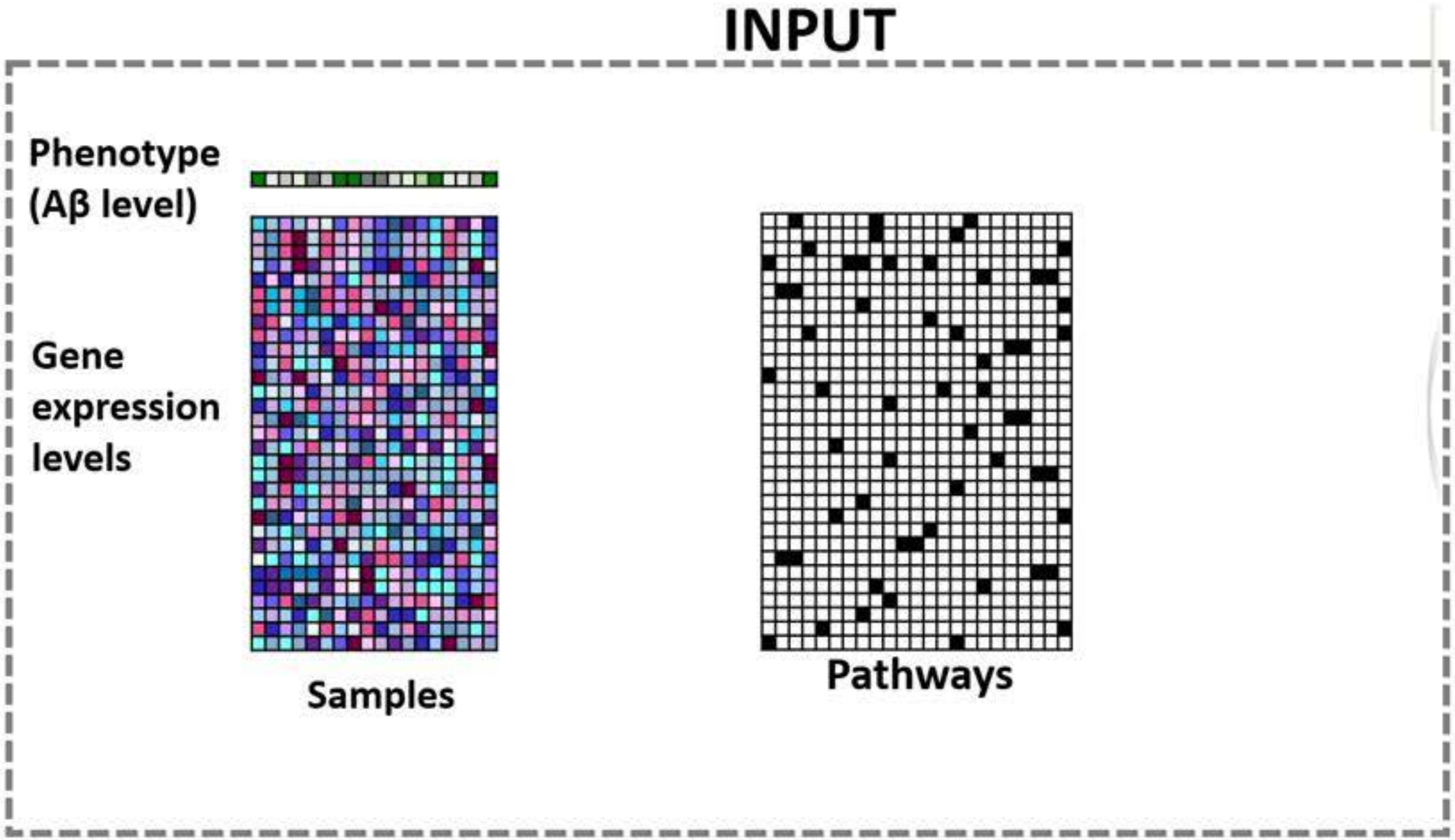

Safiye Celik, Josh C. Russell, Cezar R. Pestana, Ting-I Lee, Shubhabrata Mukherjee, Paul K. Crane, C. Dirk Keene, Jennifer F. Bobb, Matt Kaeberlein*, and Su-In Lee*. **EMBARKER: A hierarchical Bayesian approach empowering big data with prior knowledge for expression marker discovery and its application to AD.** *Under Review*

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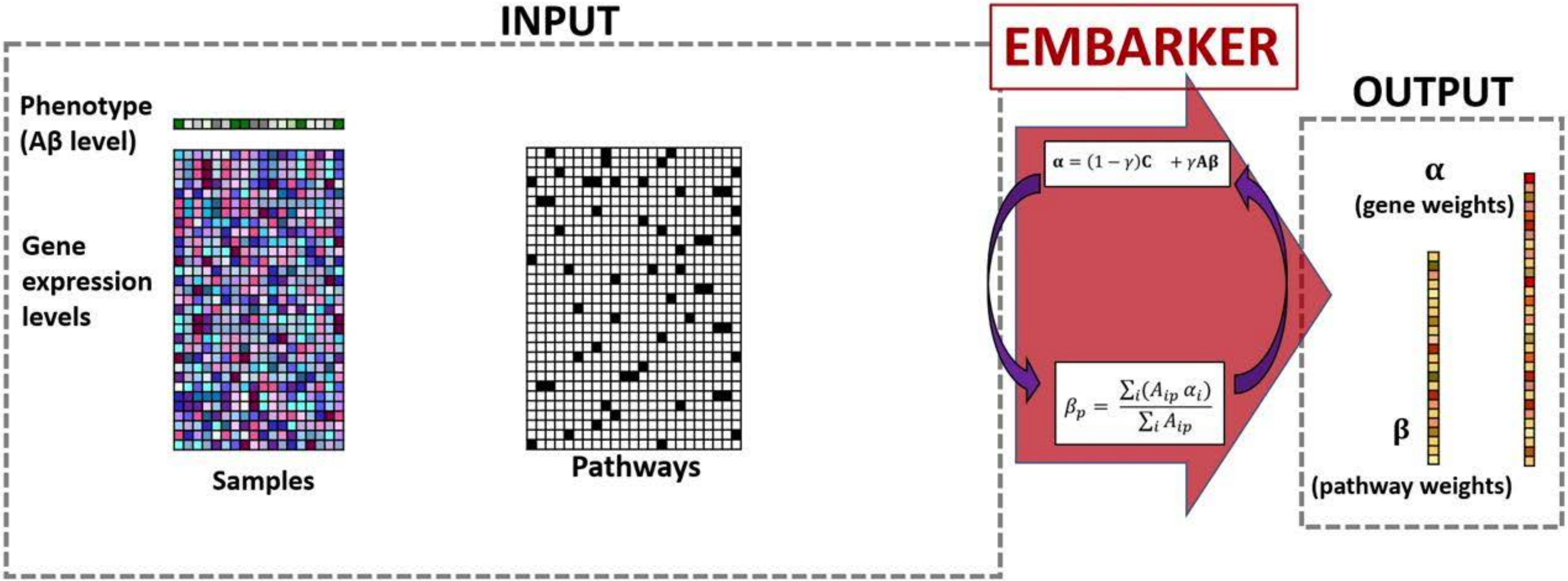

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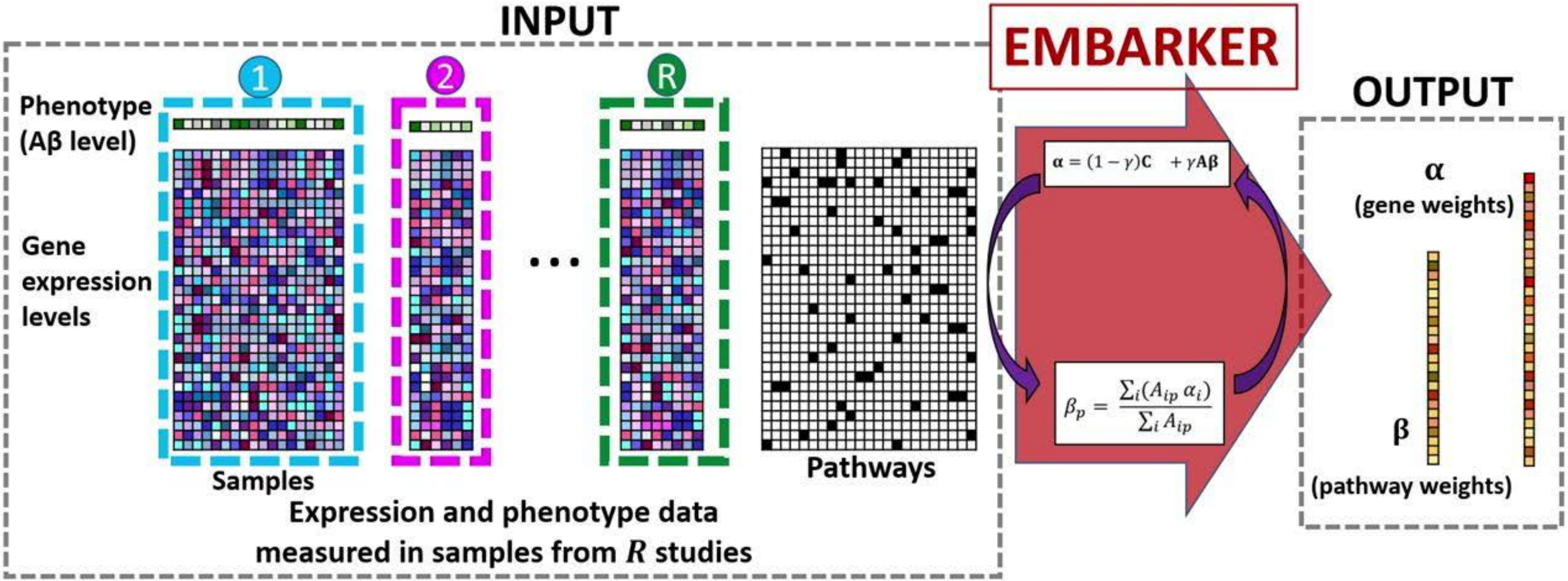

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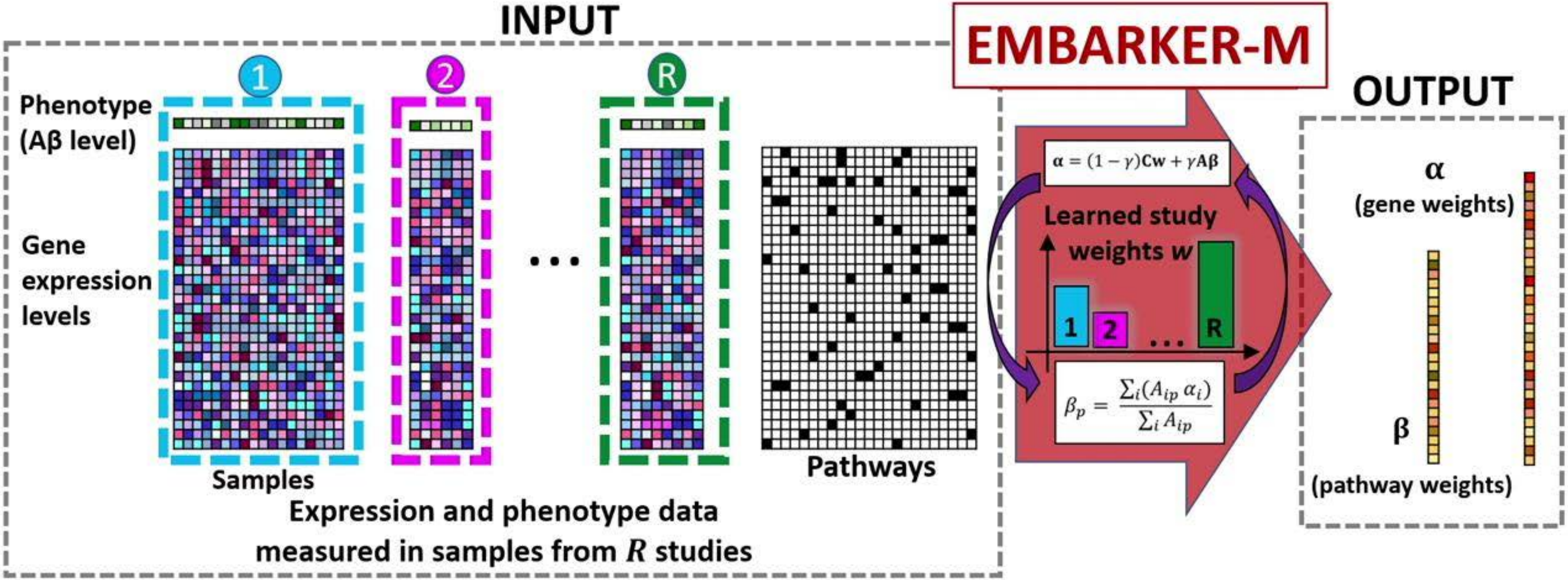

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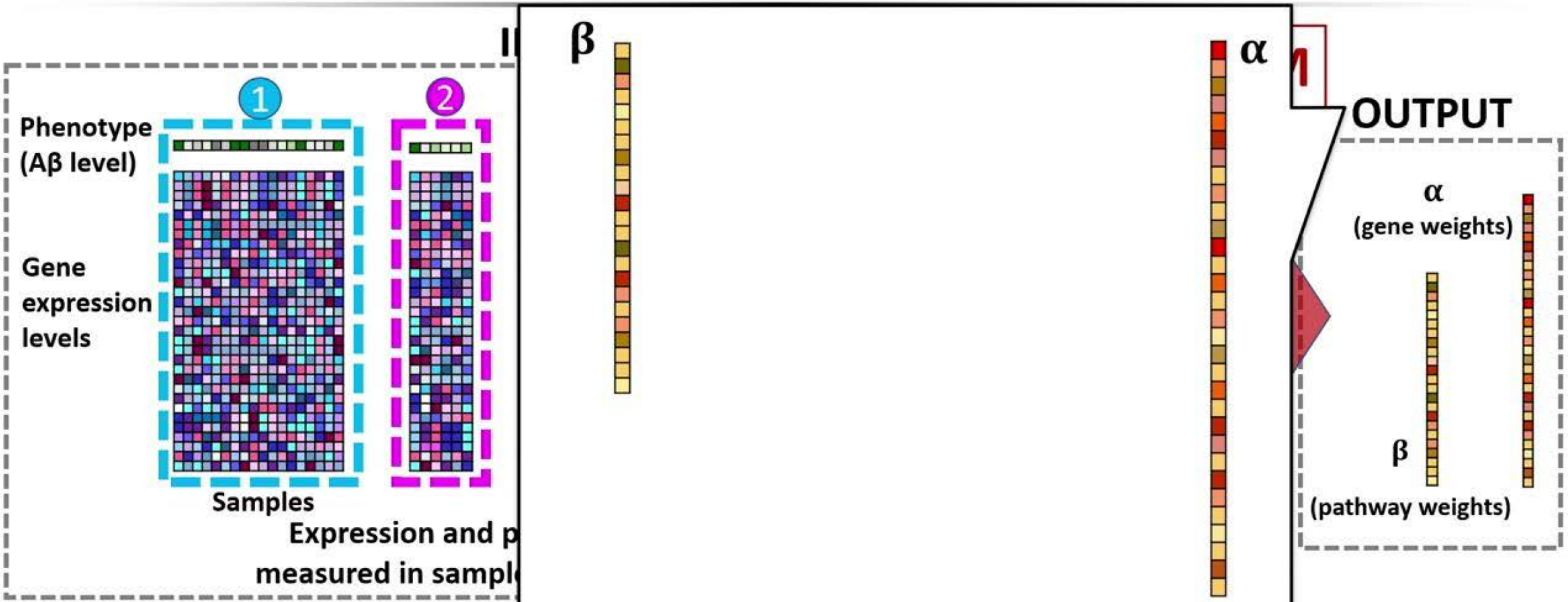

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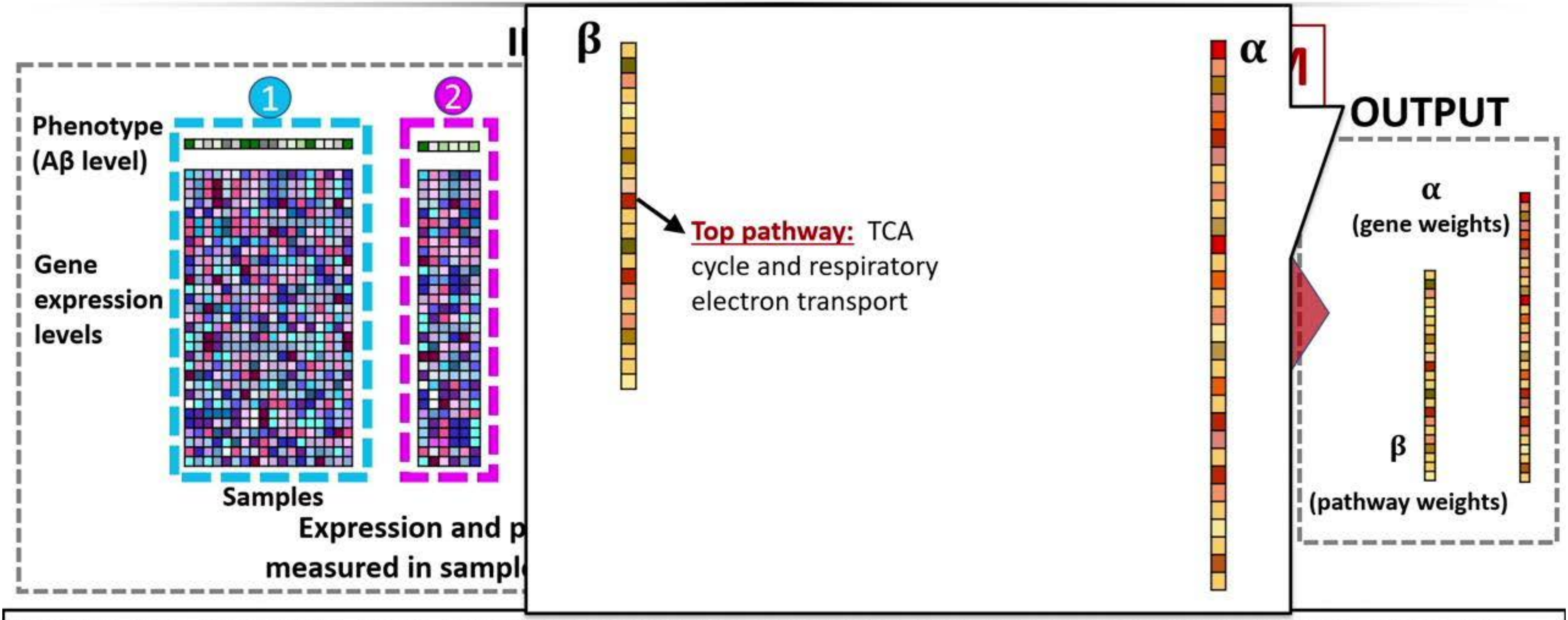

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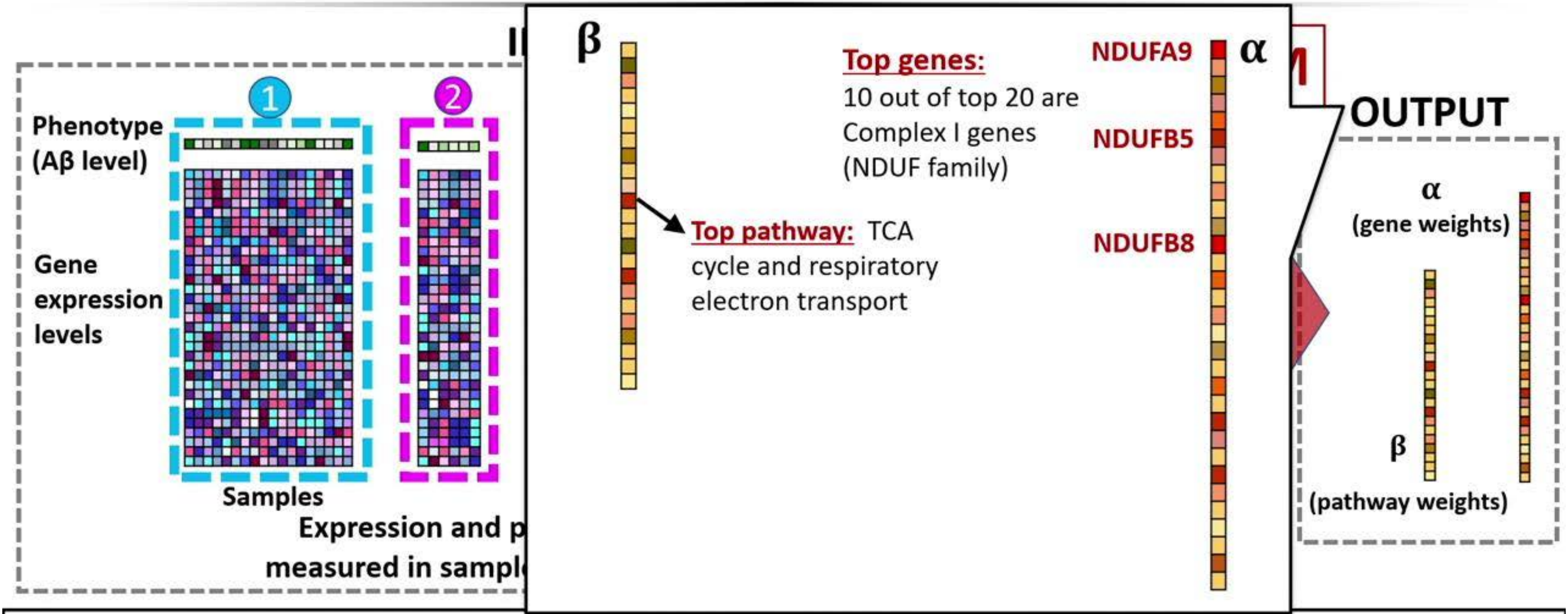

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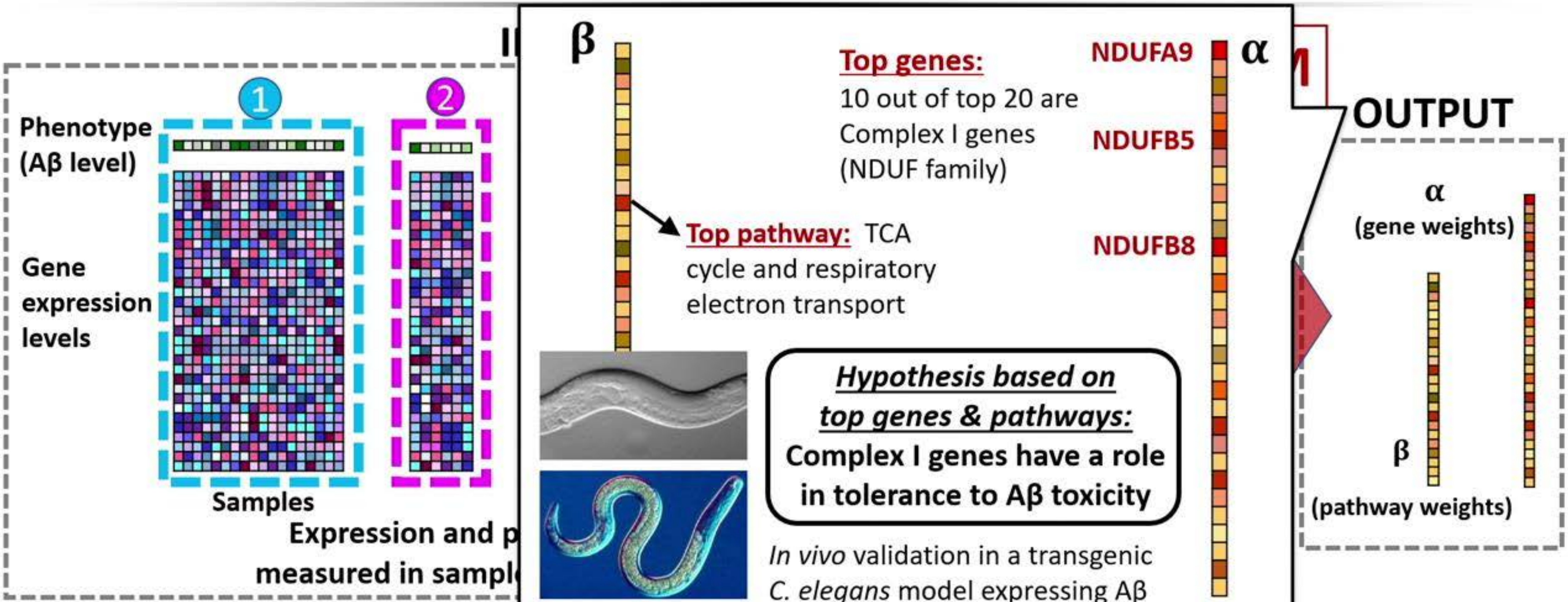

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In vivo validation – Inhibition of mitochondrial complex I subunit NDUFA9 leads to tolerance to Aβ toxicity

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- If we knock down the worm homolog of NDUFA9, would we see delay in paralysis?

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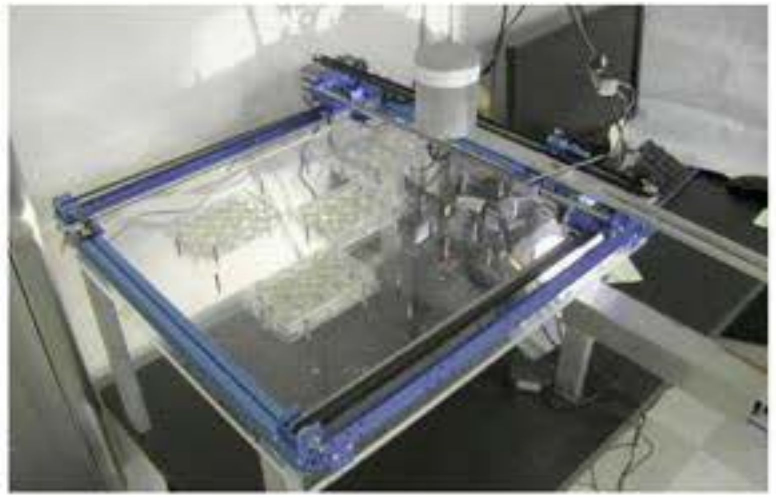
- Paralysis assay using the WormBot in Kaeberlein lab



- 144 experiments per run
- Automated software
- Time-lapse movies
- Efficiency (2 min vs. 3.5 hr)

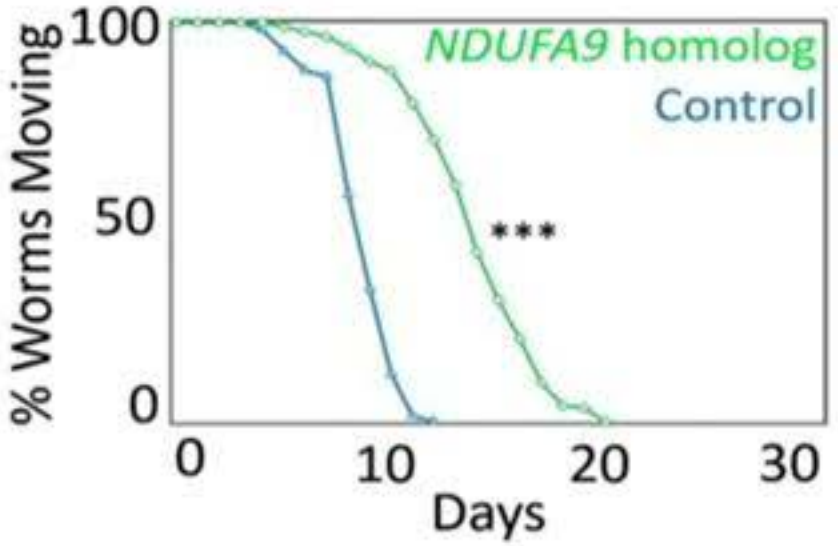
Control

Treatment


Ben Blue


Jason Pitt

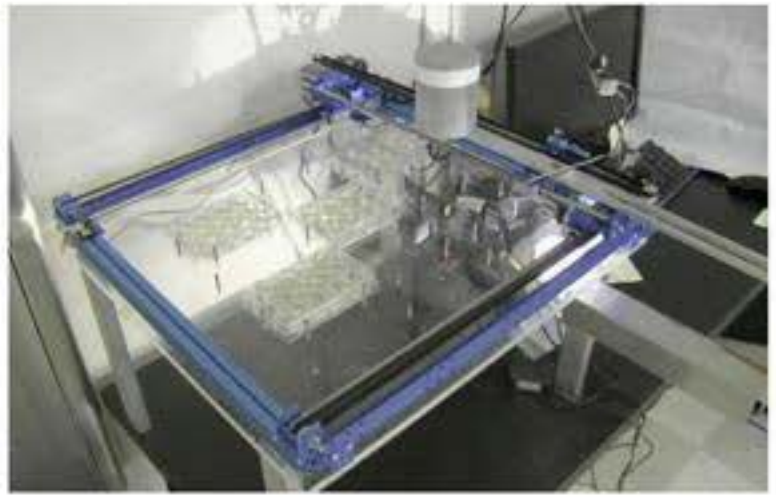
Pitt et al., unpublished



ndrial complex I
toxicity


Josh Russell


Matt Kaeberlein



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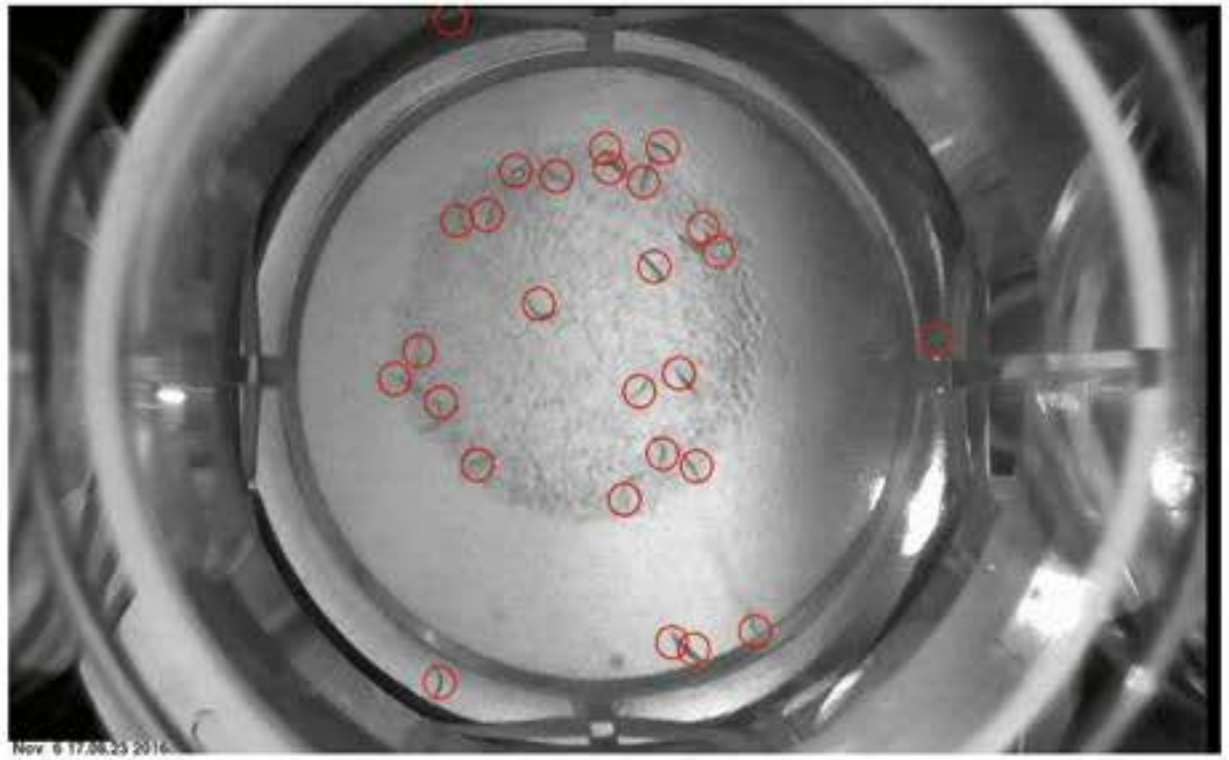

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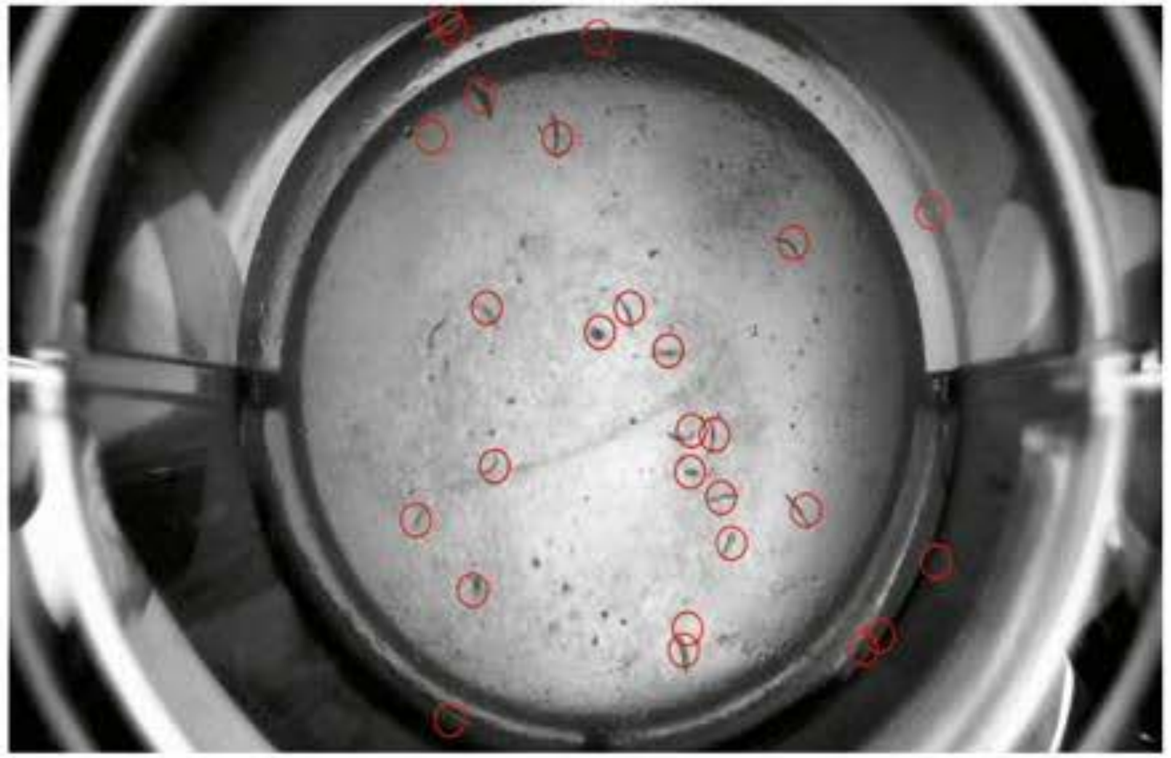

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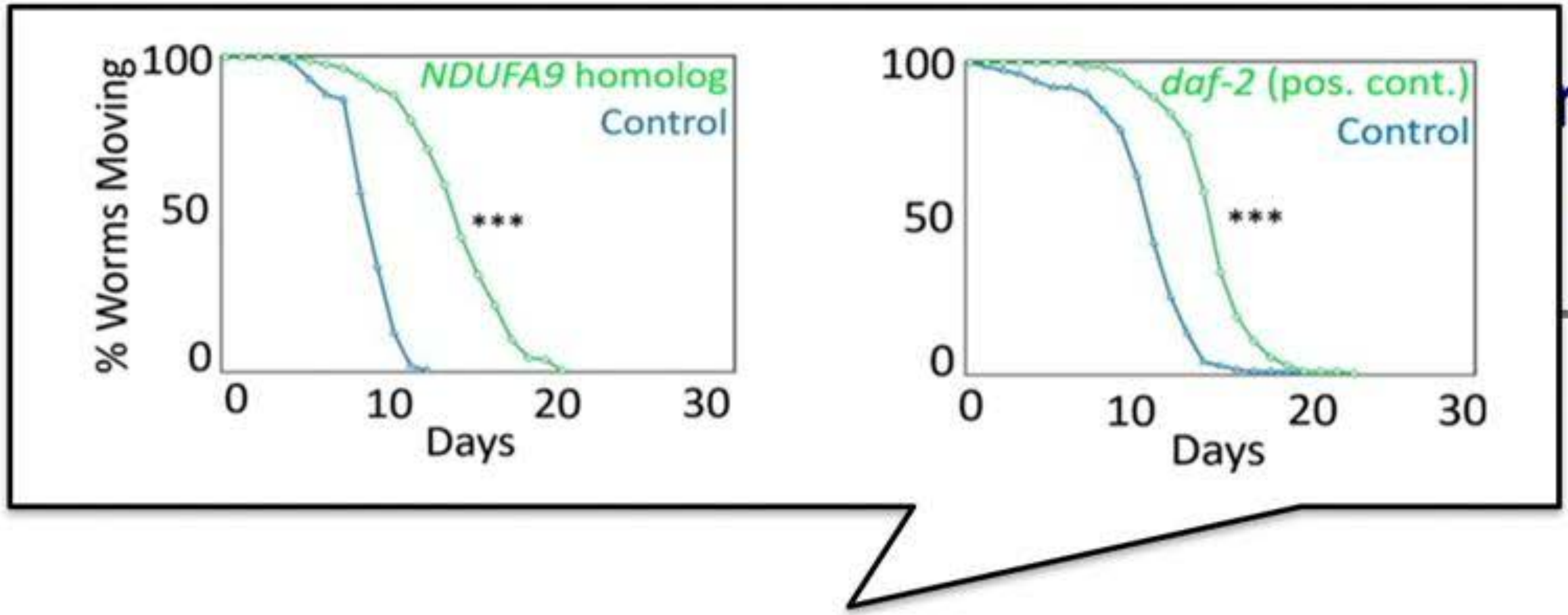

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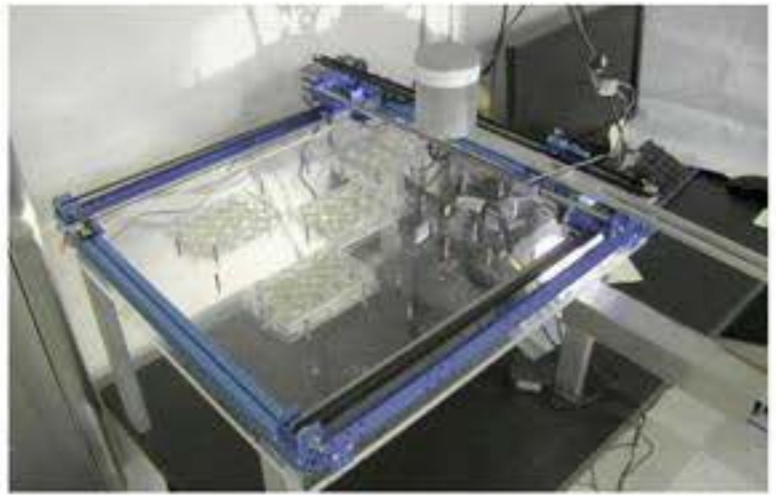

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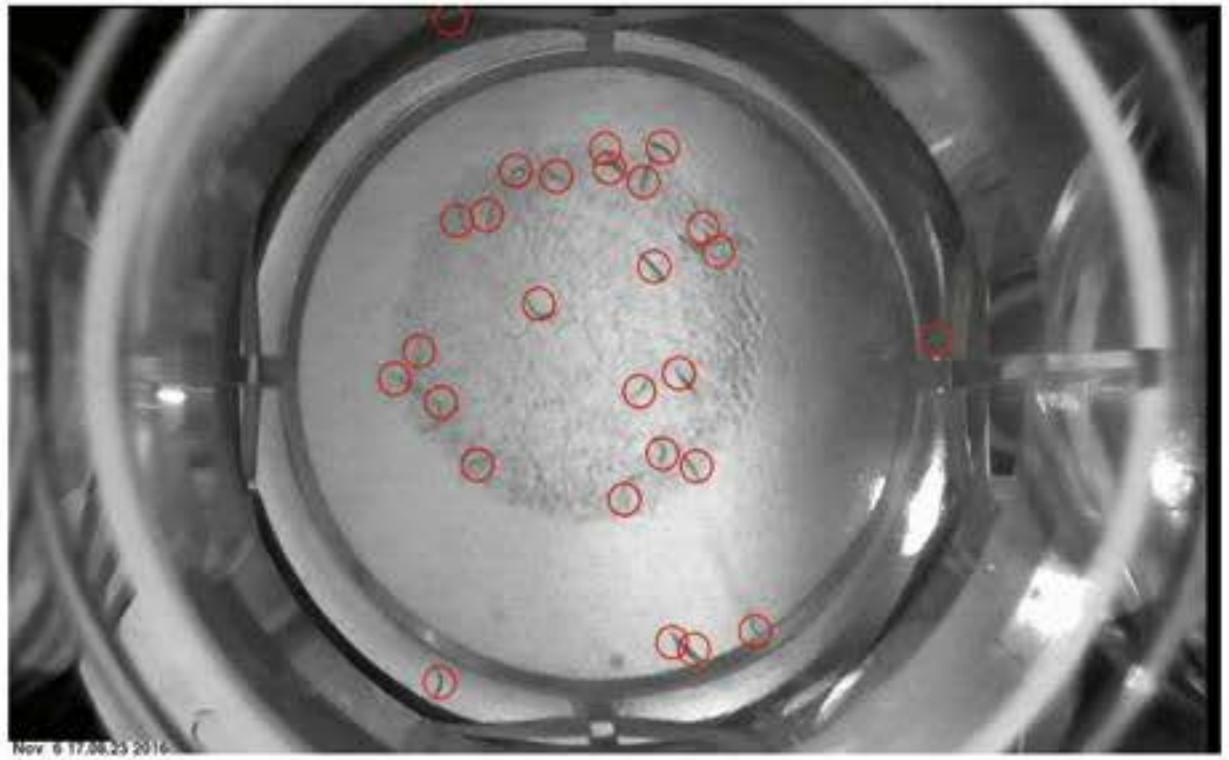

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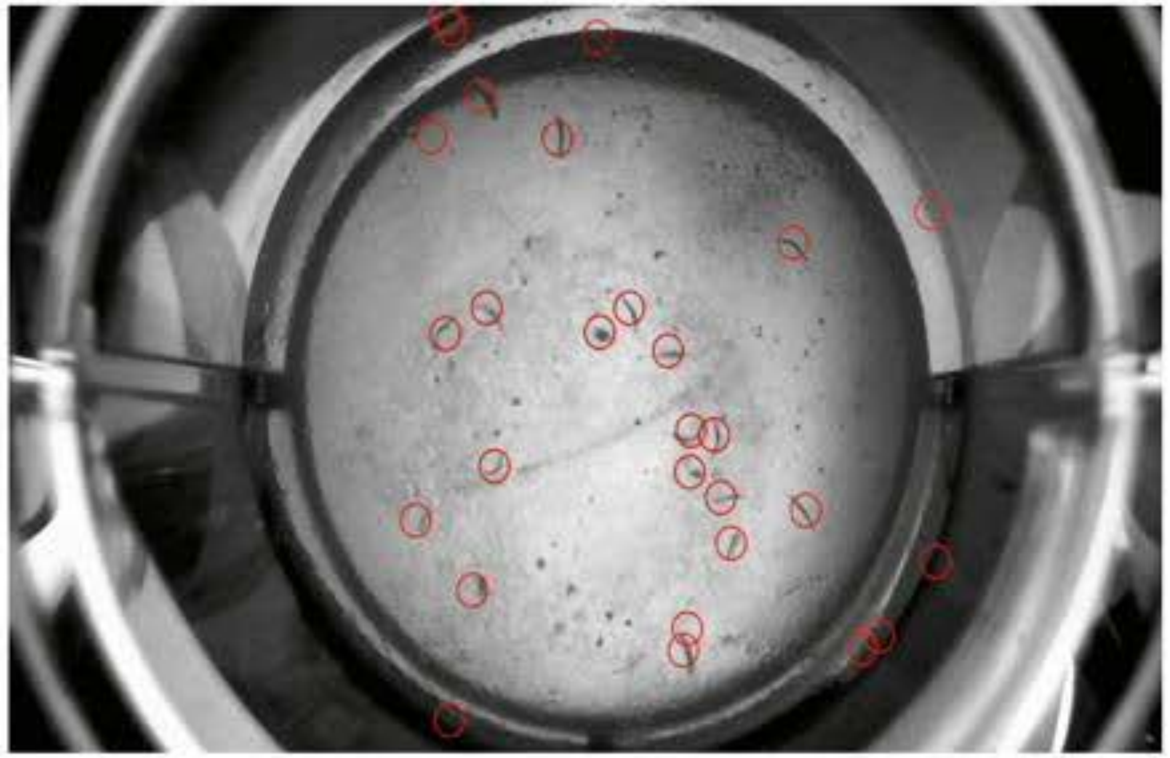

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Knockdown of 12 other Complex I genes also robustly protected against Aβ toxicity

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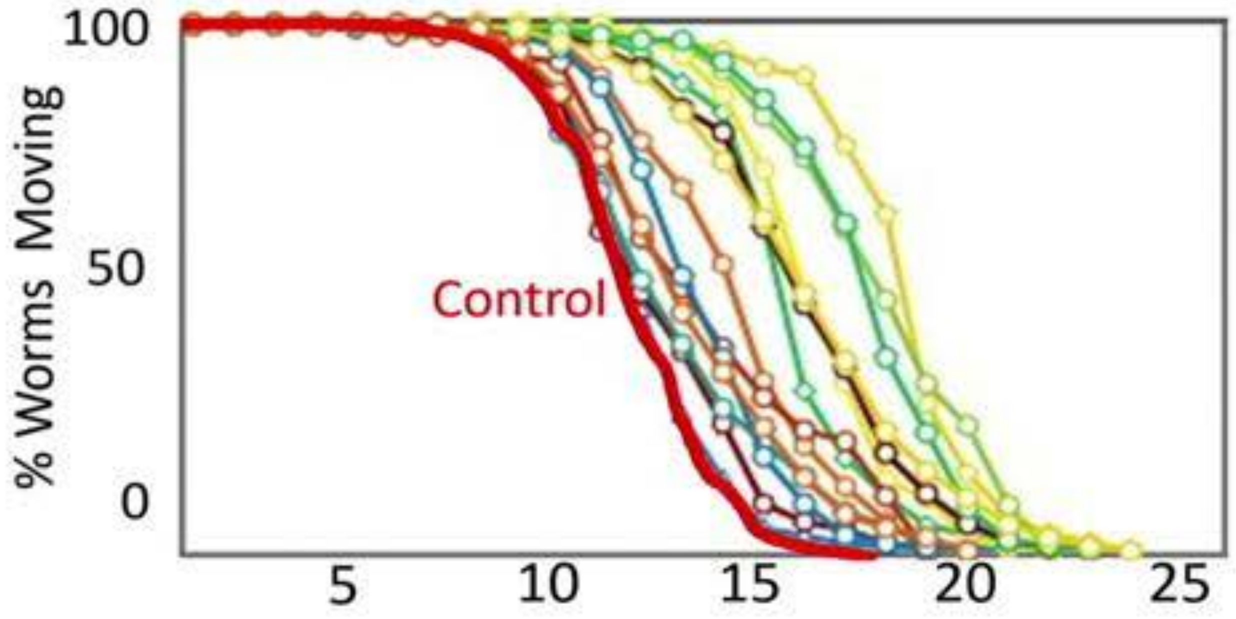

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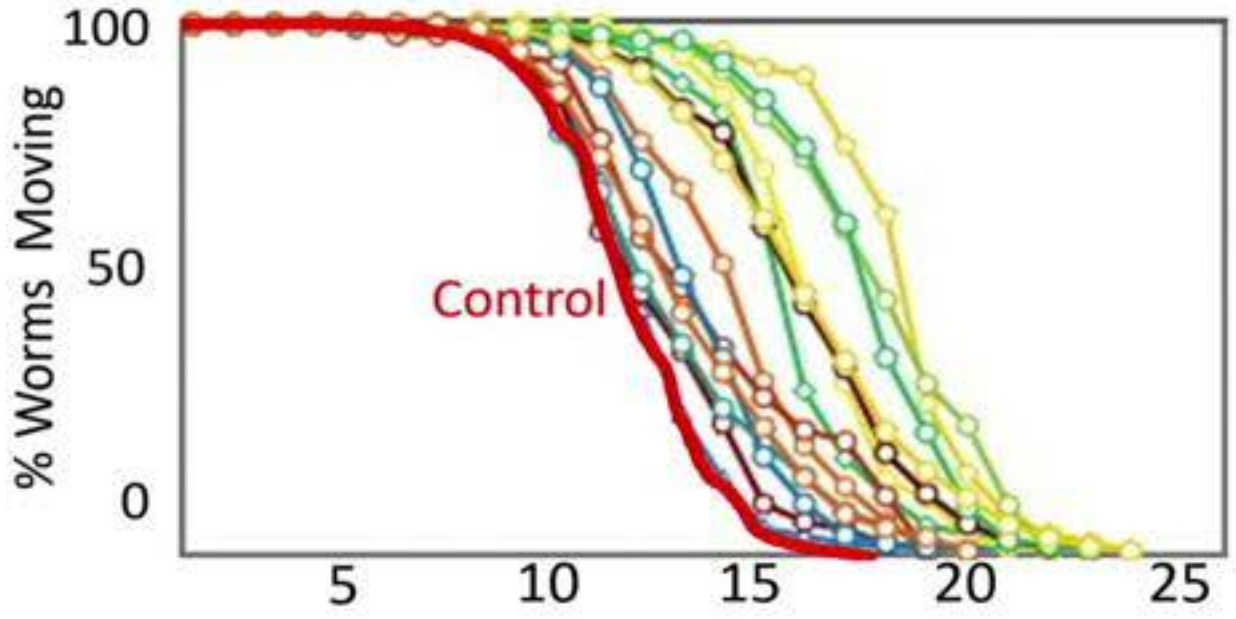

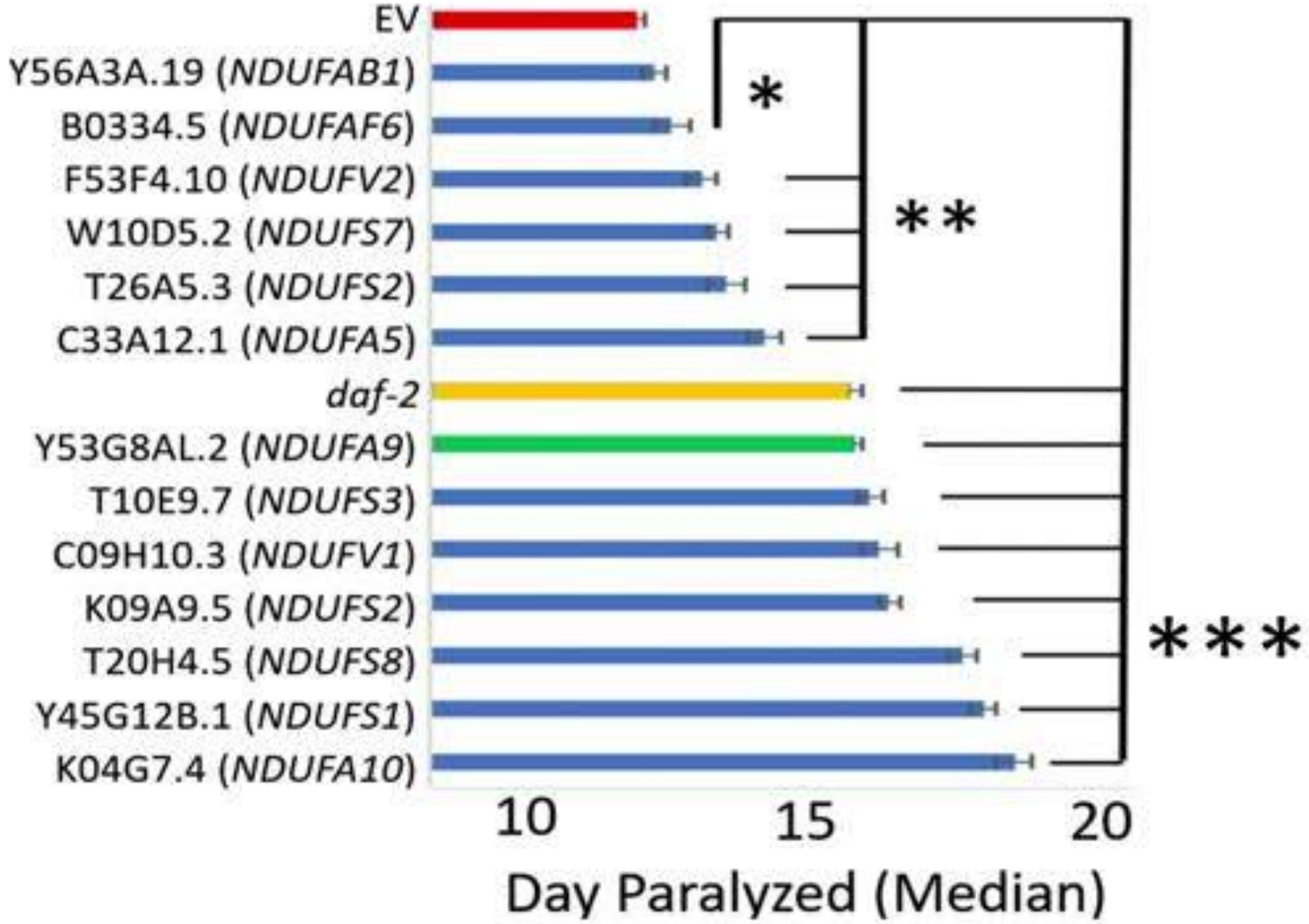

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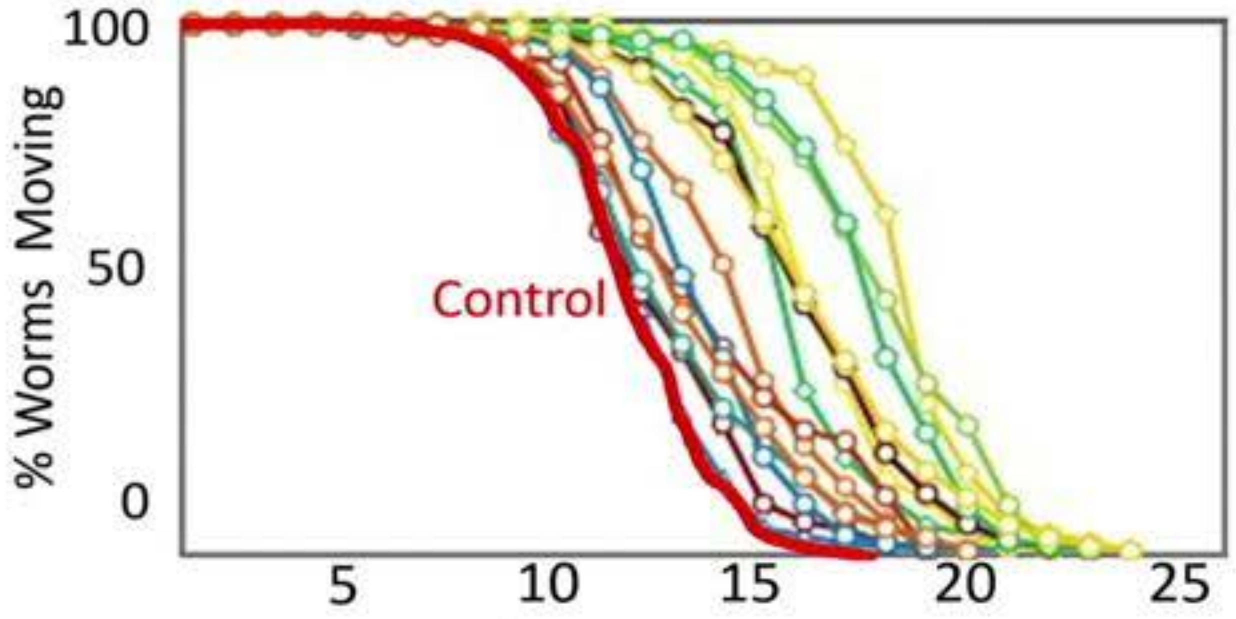

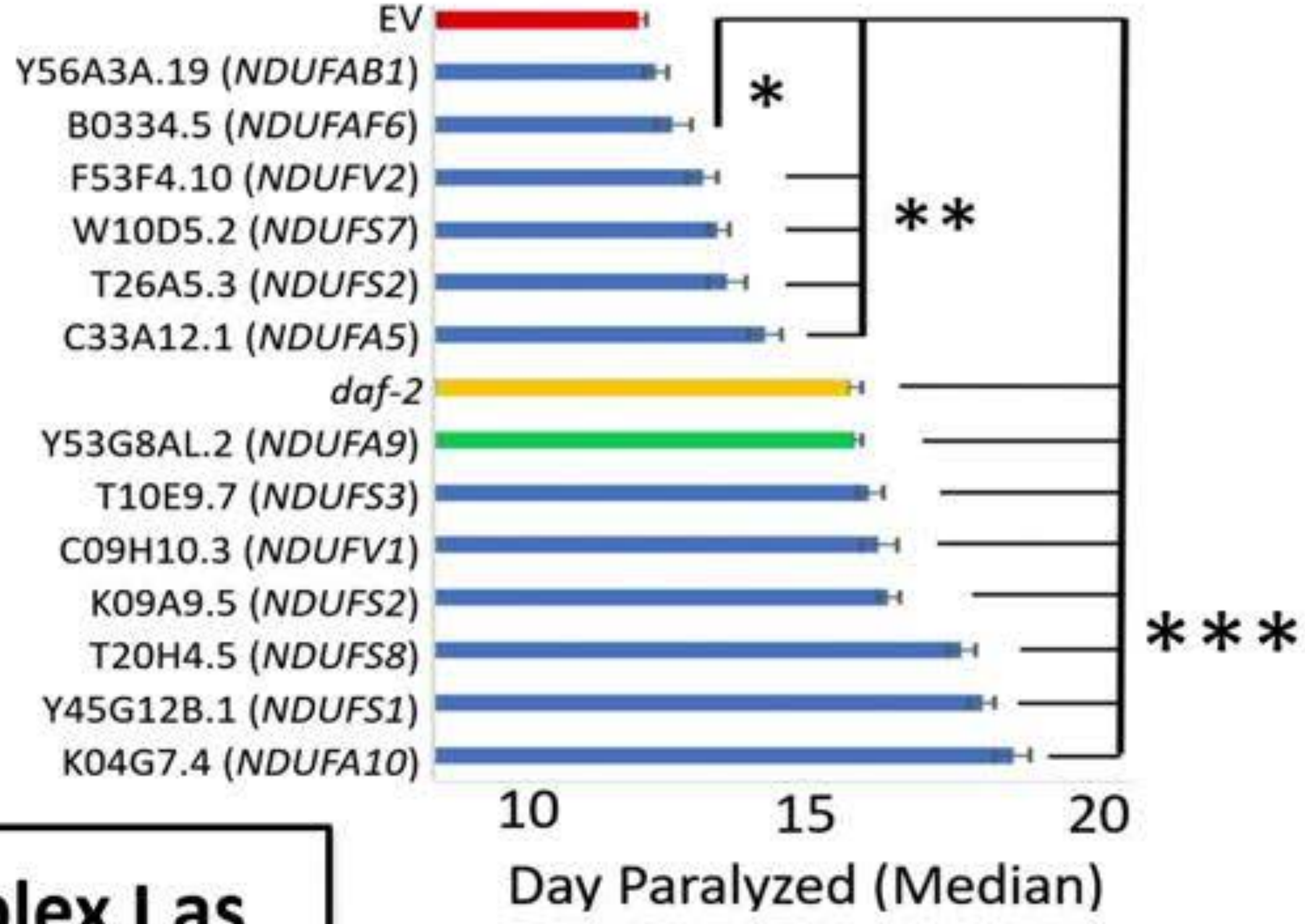

EMBARKER-M pinpoints mitochondrial Complex I as a critical mediator of proteostasis and a promising pharmacological avenue toward treating AD

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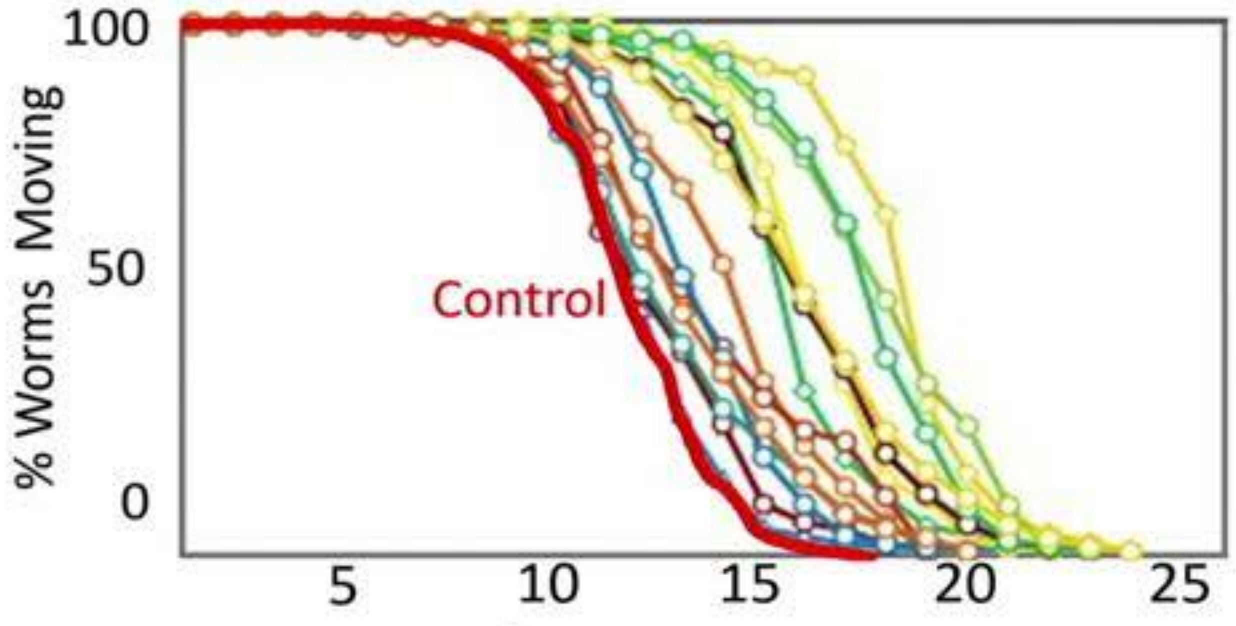
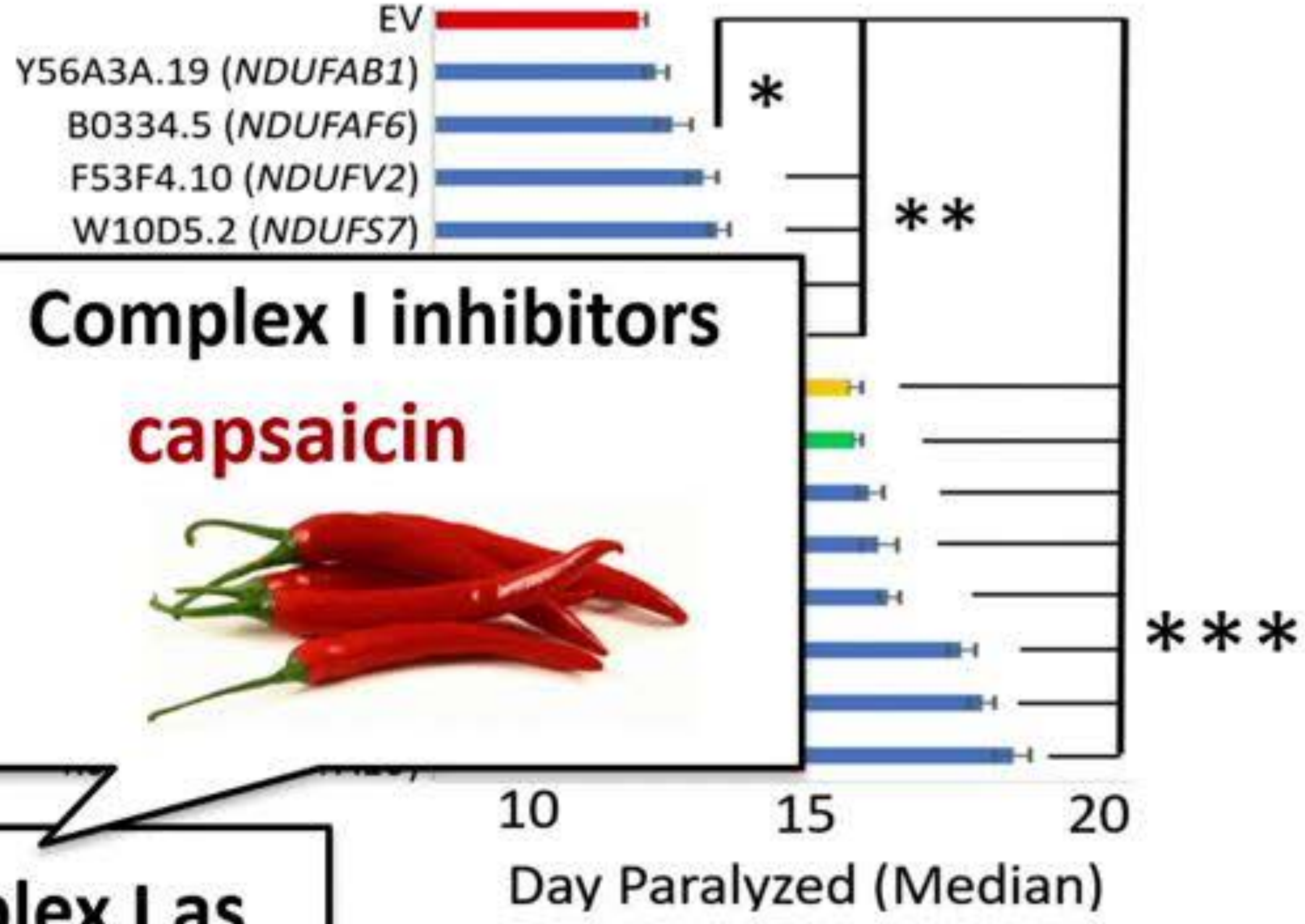




Complex I inhibitors

capsaicin

EMBARKER-M pinpoints mitochondrial Complex I as a critical mediator of proteostasis and a promising pharmacological avenue toward treating AD

New AI/ML techniques can enable new ways to treat patients and to make biological discoveries from data

Prediction & decision support systems in hospitals

- Make interpretable predictions from complex models.

Cancer precision medicine

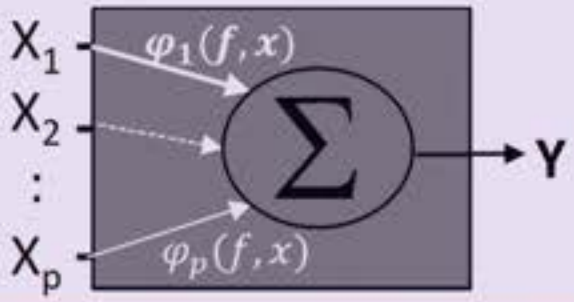
- Learn interpretable feature representations.

Alzheimer's disease therapeutic target discovery

- Integrate data sets for statistical power and interpretability.

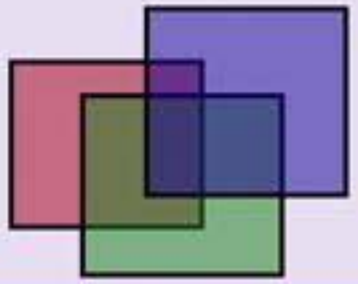
General ML techniques

Black Box



ML model

Data integration



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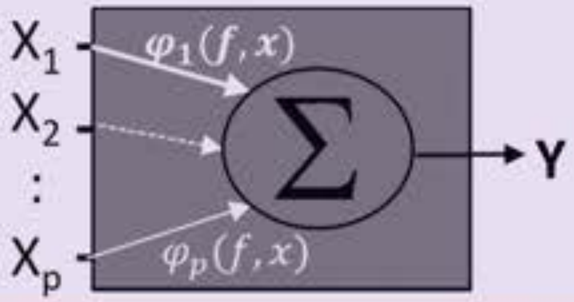

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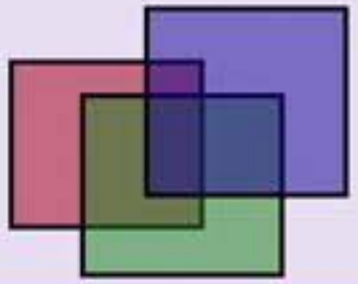

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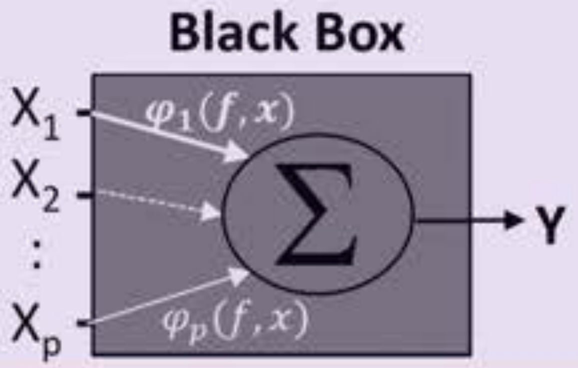

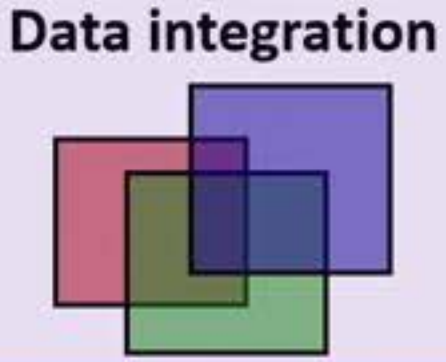

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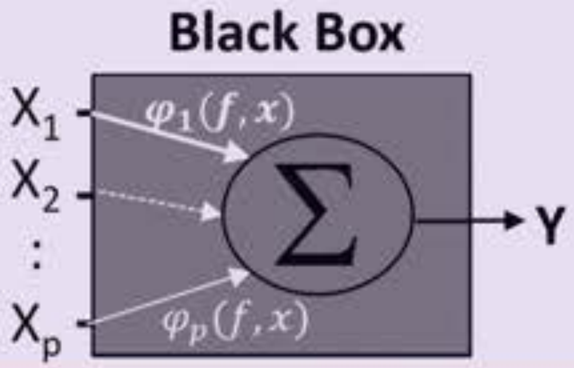

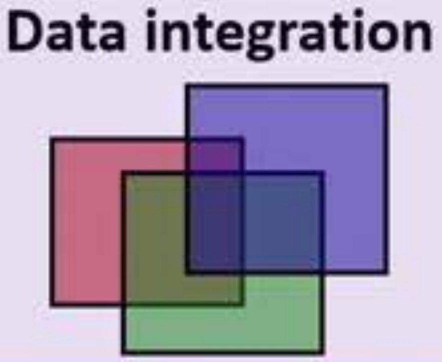

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EMBARKER

Lee Lab

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OF COMPUTER SCIENCE & ENGINEERING

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Scott Lundberg

Nao Hiranuma

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Nicasia Beebe-Wang

Ian Covert

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Pascal Sturmfels

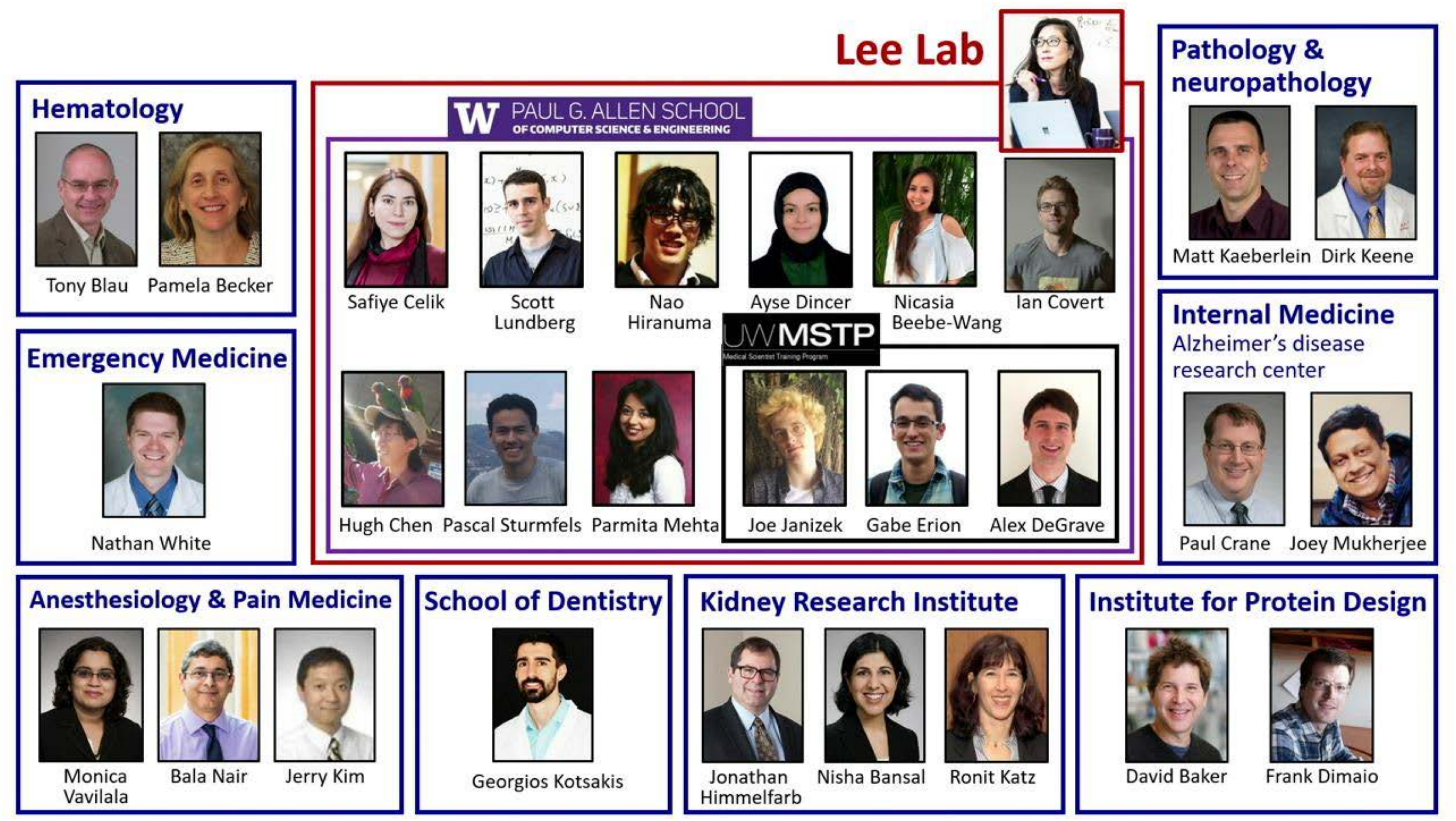
Parmita Mehta

UWMSTP
Medical Scientist Training Program

Joe Janizek

Gabe Erion

Alex DeGrave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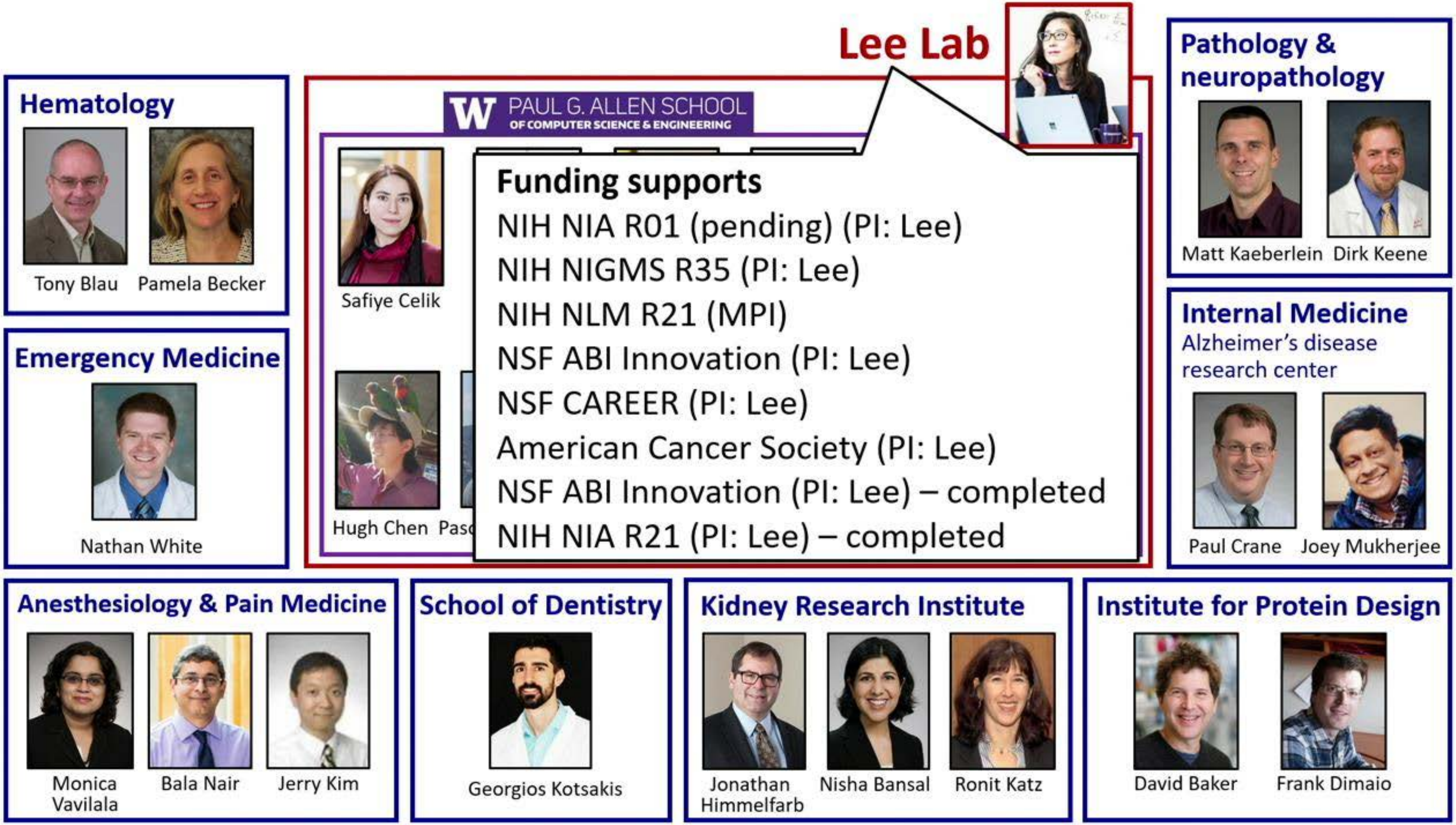

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Pasc
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NIH NIA R01 (pending) (PI: Lee)
NIH NIGMS R35 (PI: Lee)
NIH NLM R21 (MPI)
NSF ABI Innovation (PI: Lee)
NSF CAREER (PI: Lee)
American Cancer Society (PI: Lee)
NSF ABI Innovation (PI: Lee) – completed
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