



# Inference with Predicted Data

**What do we do after we have machine learned  
(or AI'd?) everything?**

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October 15, 2025

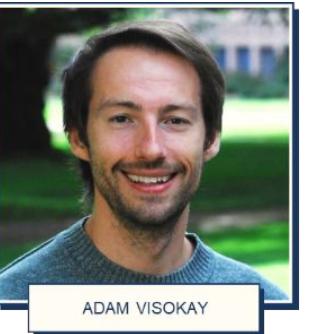
# First, Some Acknowledgements



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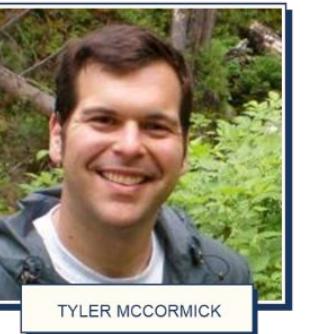
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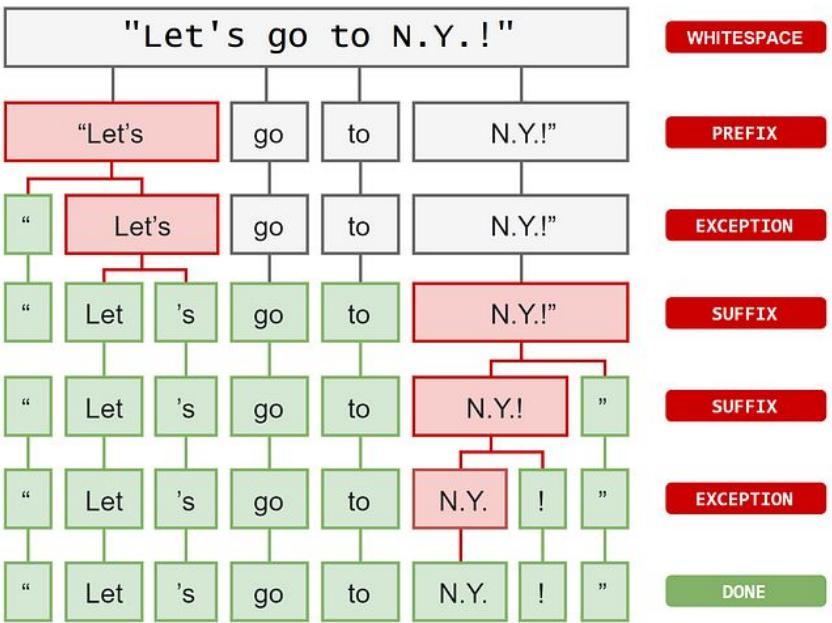
JEFF LEEK

*This slide is by no means exhaustive, but it represents individuals who have contributed most recently to the papers I will be highlighting in this talk.*

# What is AI?

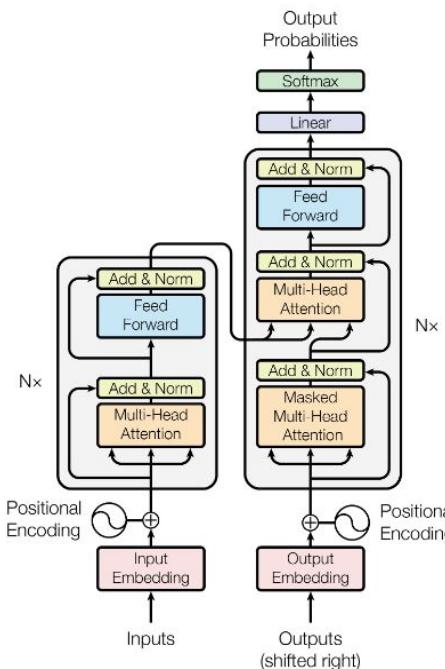
# What is AI? A three part definition

## Data



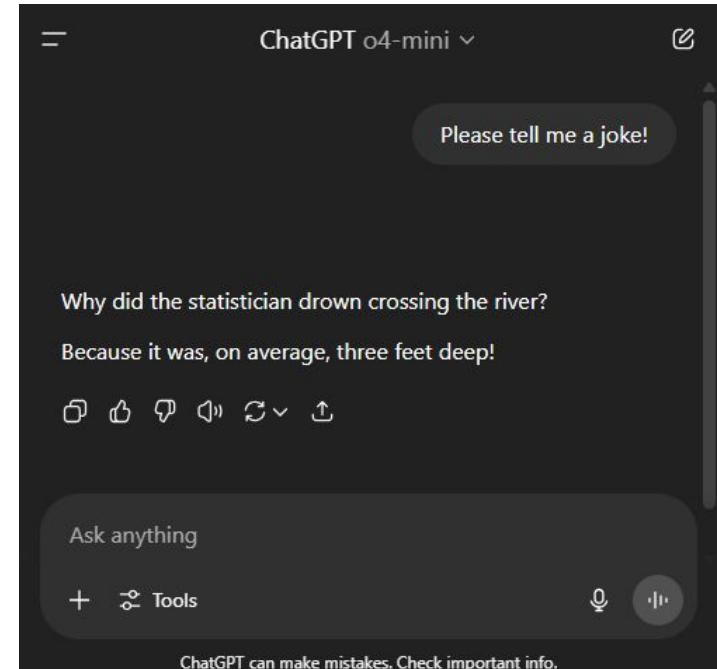
<https://www.innerdoc.com/periodic-table-of-nlp-tasks/14-tokenization/>

## Algorithm



<https://arxiv.org/abs/1706.03762>

## Interface



<https://chatgpt.com/>

# Why is AI all over the news?

# How attention changed the game in AI (2017)

## Attention Is All You Need

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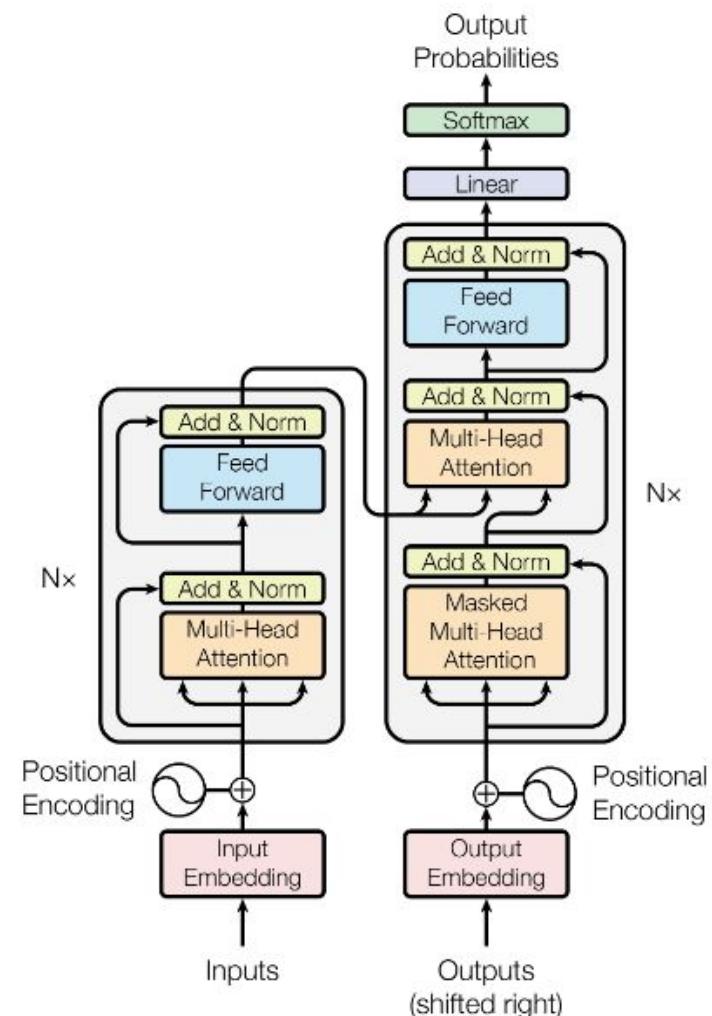
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### Abstract

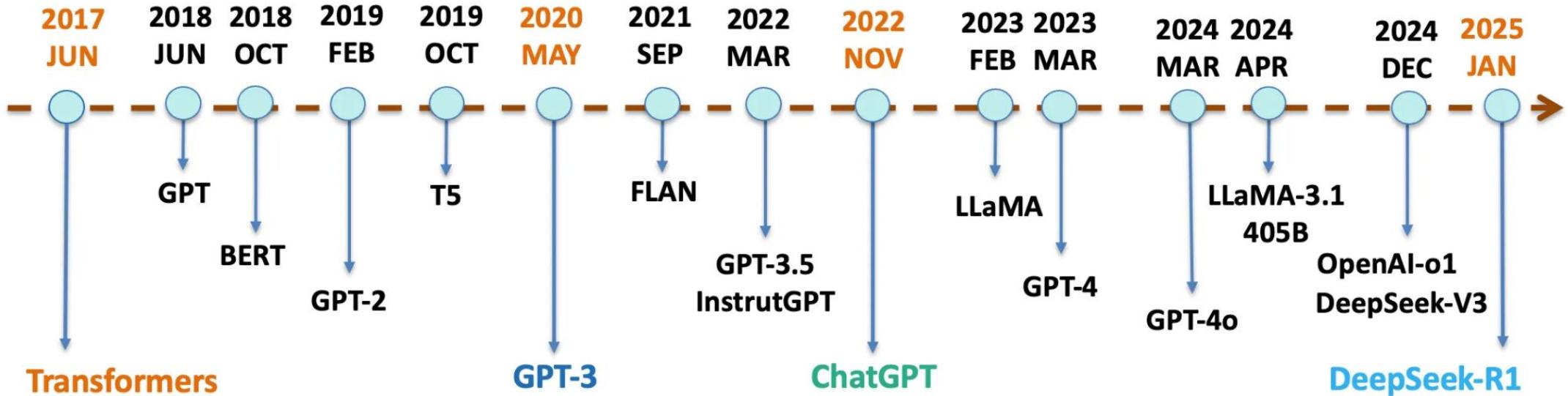
The dominant sequence transduction models are based on complex recurrent or convolutional neural networks that include an encoder and a decoder. The best performing models also connect the encoder and decoder through an attention mechanism. We propose a new simple network architecture, the Transformer, based solely on attention mechanisms, dispensing with recurrence and convolutions entirely. Experiments on two machine translation tasks show these models to be superior in quality while being more parallelizable and requiring significantly less time to train. Our model achieves 28.4 BLEU on the WMT 2014 English-to-German translation task, improving over the existing best results, including ensembles, by over 2 BLEU. On the WMT 2014 English-to-French translation task, our model establishes a new single-model state-of-the-art BLEU score of 41.0 after training for 3.5 days on eight GPUs, a small fraction of the training costs of the best models from the literature.

[https://proceedings.neurips.cc/paper\\_files/paper/2017/file/3f5ee243547dee91fdb053c1c4a845aa-Paper.pdf](https://proceedings.neurips.cc/paper_files/paper/2017/file/3f5ee243547dee91fdb053c1c4a845aa-Paper.pdf)



# LLM breakthroughs have driven AI's current momentum

## A Brief History of LLMs

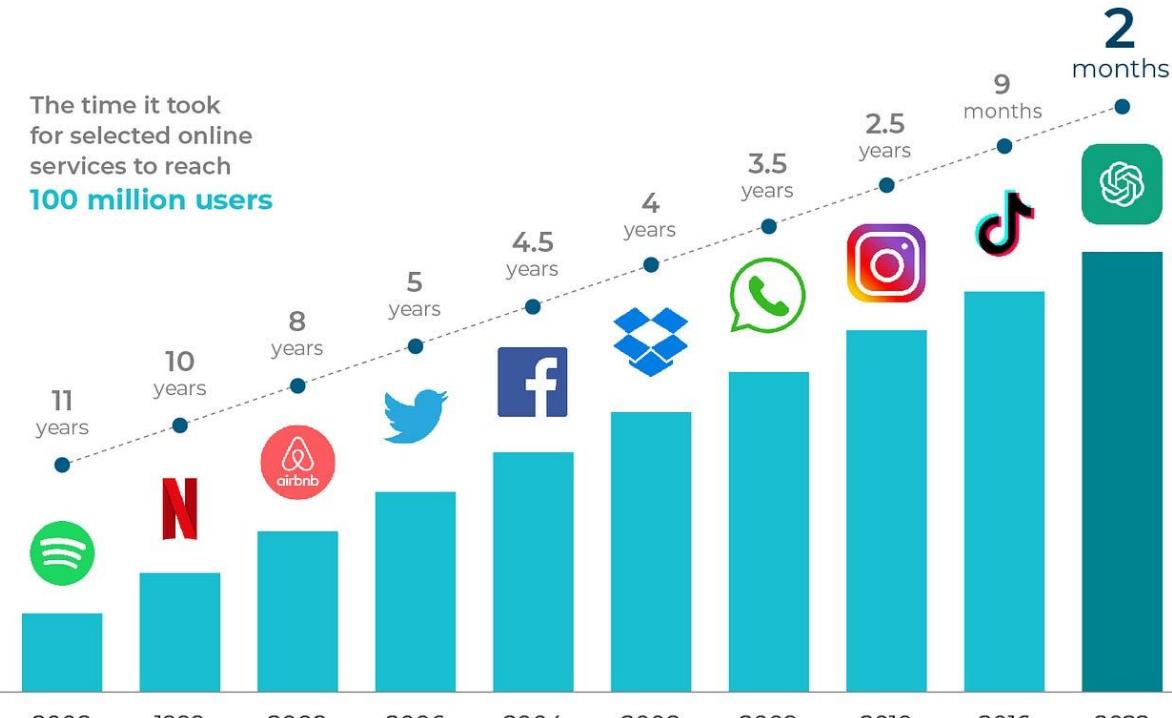


<https://medium.com/@lmpo/a-brief-history-of-lmms-from-transformers-2017-to-deepseek-r1-2025-dae75dd3f59a>

# AI is everywhere, and it is spreading faster than ever



## Chat-GPT sprints to 100 million users



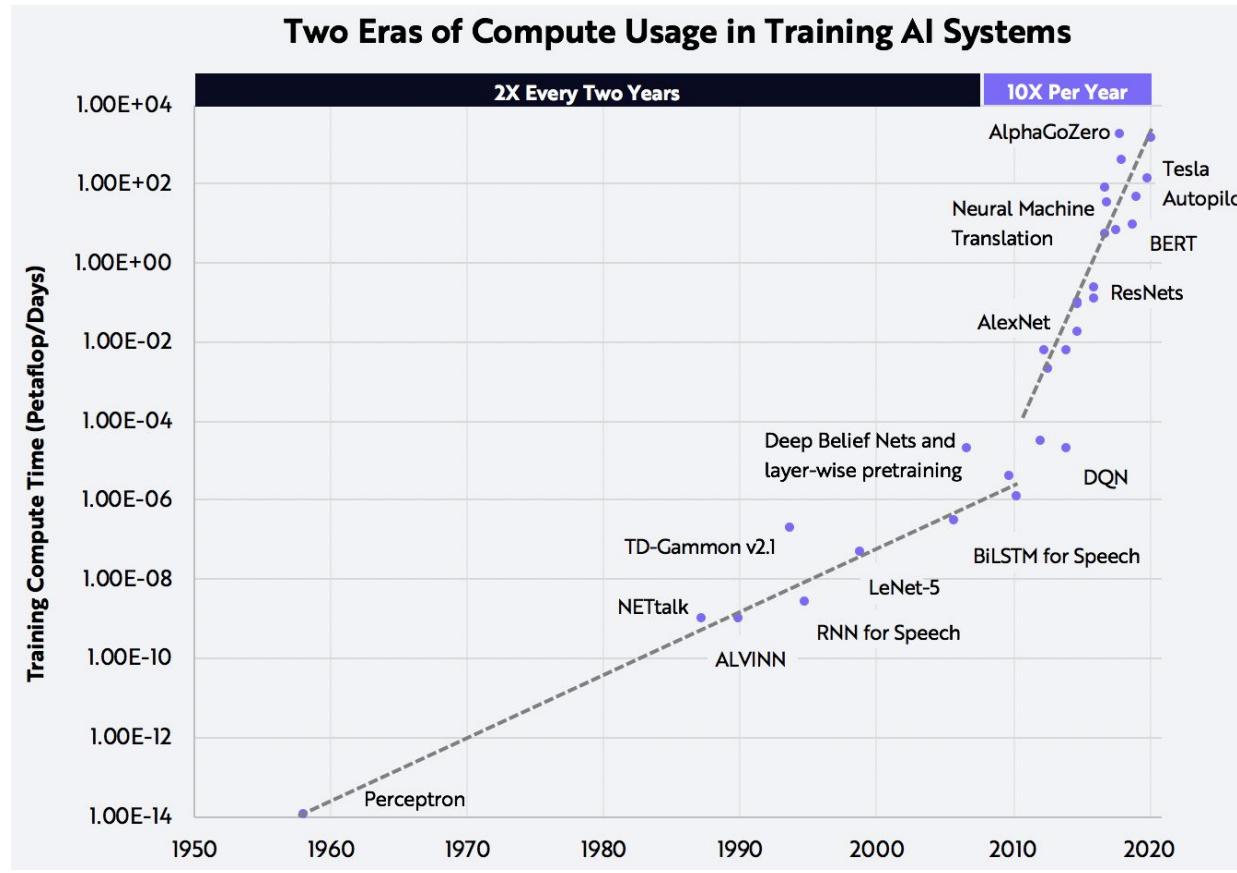
<https://www.nebulys.com/blog/2024-the-year-of-llm-user-intelligence>

Source: World of Statistics

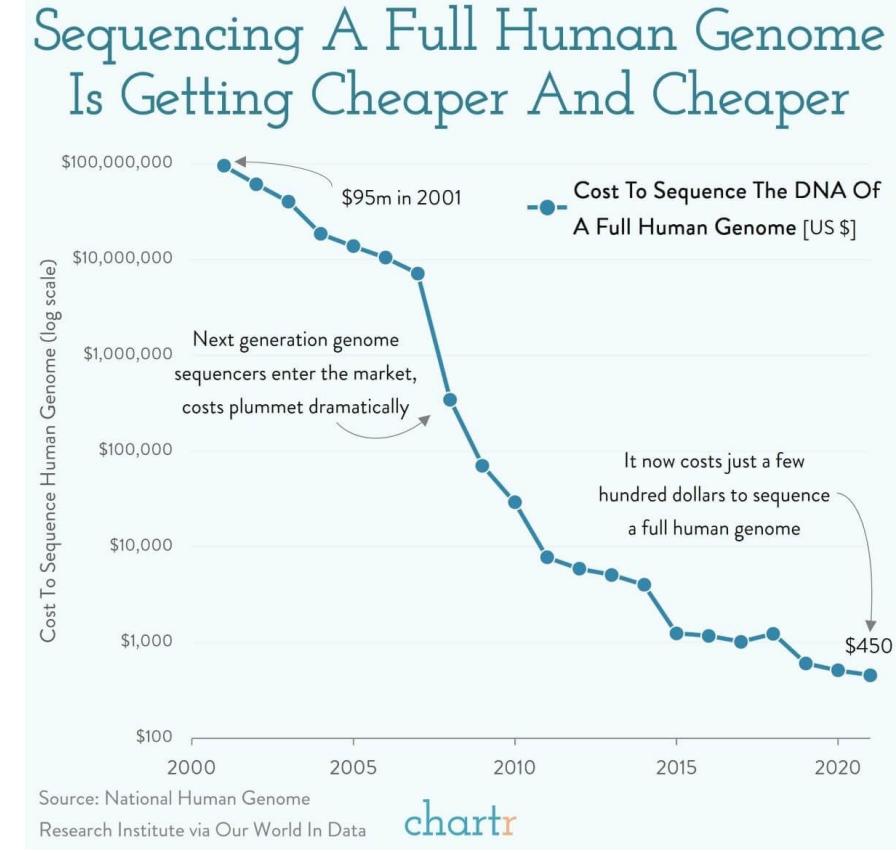


Why is now different, and what  
does that mean for us?

# Simultaneous Revolutions in Computing and Biology



<https://www.ark-invest.com/articles/analyst-research/ai-training>



<https://digitalfoolab.com/graph-week-genome-sequencing-price-going/>

# We can now predict complex genetic traits with AI/ML

PRS for disease susceptibility, imputed expression from genotype arrays, TWAS, ...

The image displays three academic journal articles from *nature genetics*, *eLife*, and *elife sciences* illustrating the use of AI/ML in genetics.

- nature genetics* Article:** Published on June 18, 2018, titled "A transcriptome-wide association study in women identifies new candidates for breast cancer". The lead author is Lang Wu, and the article is published in *Nature Genetics* 50, 968–978 (2018). It has 13k accesses and 219 citations.
- eLife* Article:** Published on Mar 5, 2019, titled "An atlas of polygenic risk scores to highlight putative causal regions across the human genome". The lead author is Tom G Richardson, and it is published in *eLife*. It has 102 Altmetric mentions.
- elife sciences* Article:** Published on Jul 8, 2019, titled "Identifying gene expression programs of cell-type identity and cellular activity with single-cell RNA-Seq". The lead author is Dylan Kotliar, and it is published in *elife sciences*.

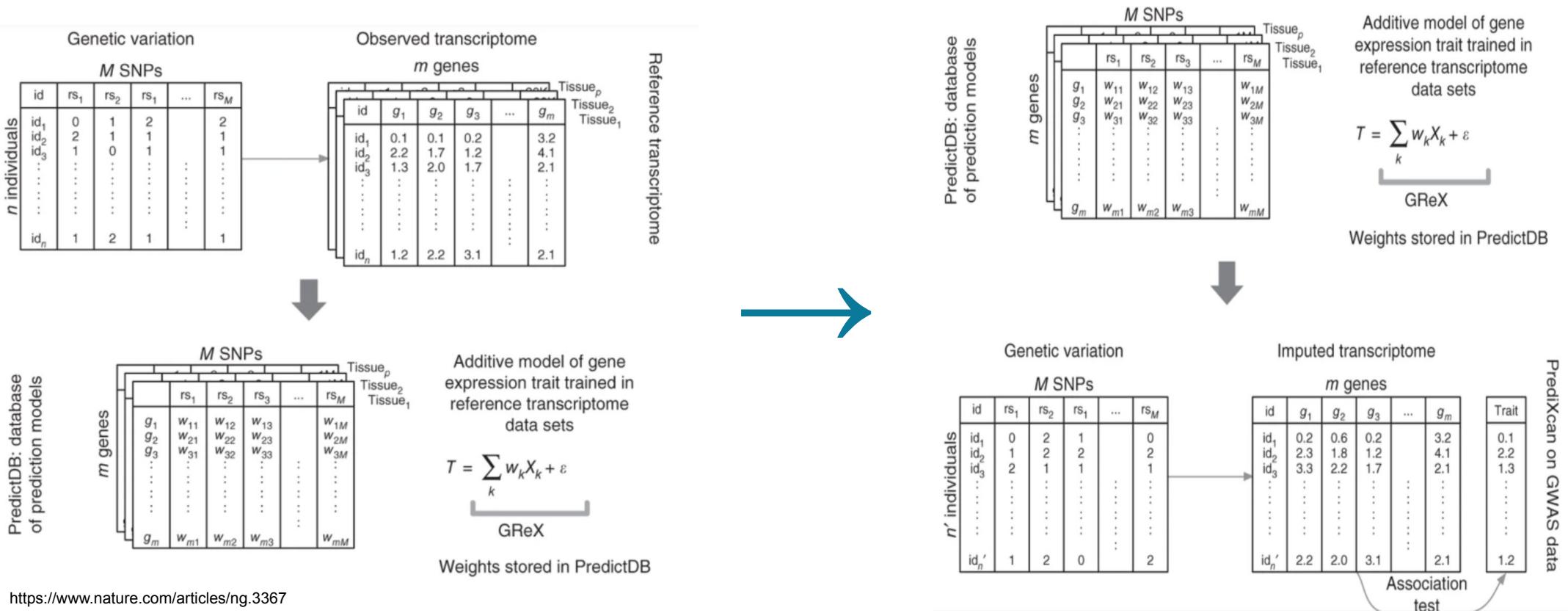
<https://www.nature.com/articles/s41588-018-0132-x>

<https://elifesciences.org/articles/43657>

<https://elifesciences.org/articles/43803>

# Example: Common two-stage workflow of a TWAS

1) Model training in a reference panel → 2) Expression imputation and association testing in data



<https://www.nature.com/articles/ng.3367>

# How does this relate to statistical inference?

A simple sample size calculation

N = Sample Size

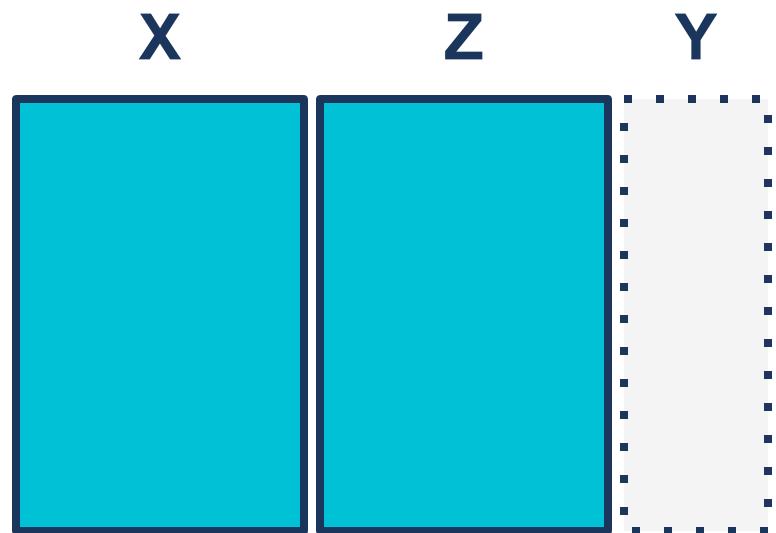
# How does this relate to statistical inference?

A simple sample size calculation

$$N = \frac{\$ \text{ You Have}}{\$ \text{ Per Sample}}$$

# In many cases, unlabeled features are cheap and easy to collect

Certain outcomes of interest, however, can be time-consuming or costly to obtain



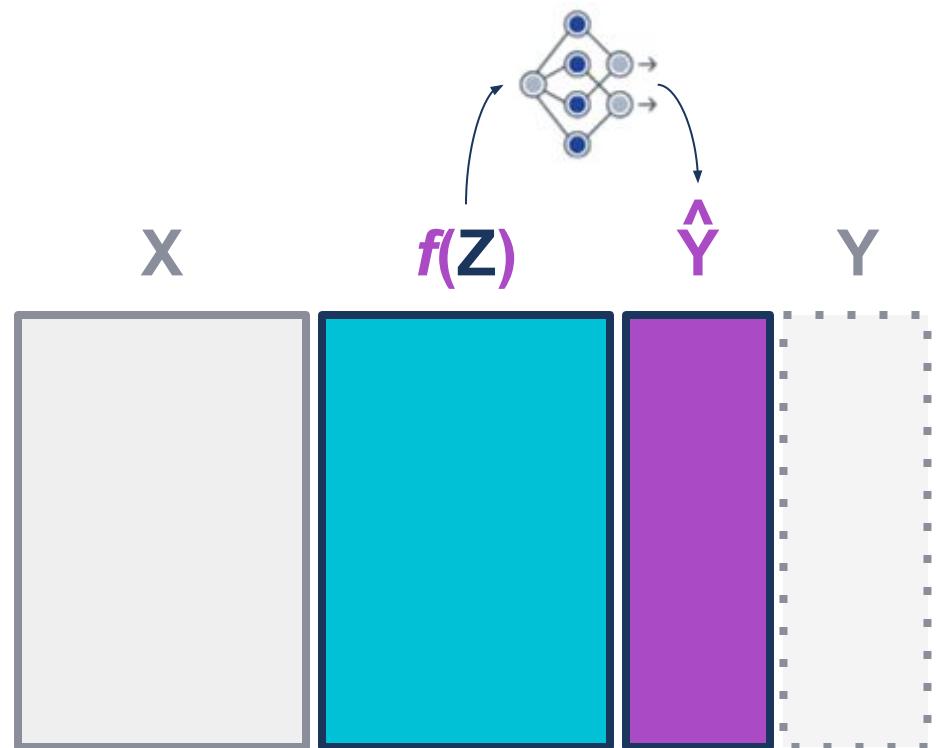
**X:** Covariates of Interest

**Z:** Predictive Features

**Y:** (Missing) Outcome of Interest

$f(\text{Data you can get}) = (\text{Data you want})\text{-}ish$

Modern studies use accessible data and AI/ML to predict hard-to-measure outcomes



$X$ : Covariates of Interest

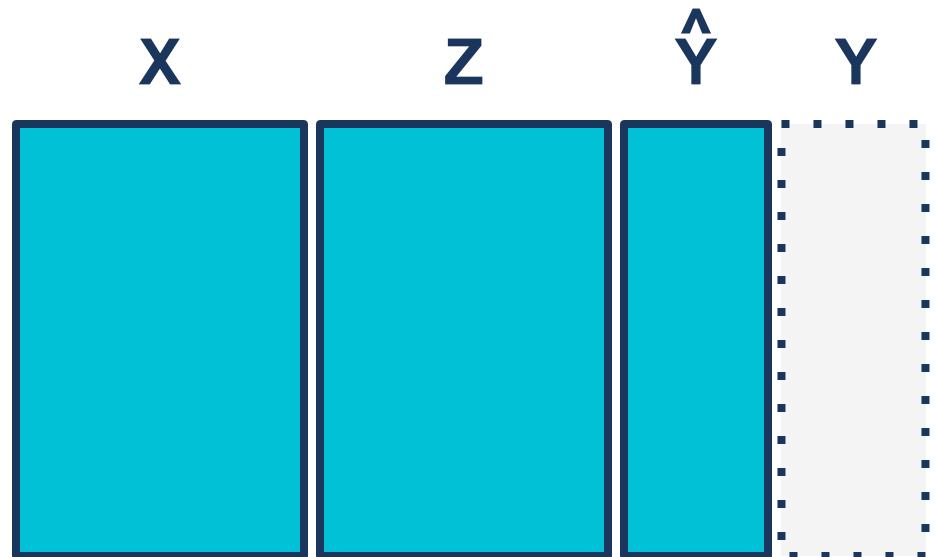
$Z$ : Predictive Features

$Y$ : (Missing) Outcome of Interest

$\hat{Y}$ : Predicted Outcome

# AI/ML-generated predictions are then treated as measured data

These predicted outcomes are used in downstream analyses or in policy decision-making



**X:** Covariates of Interest

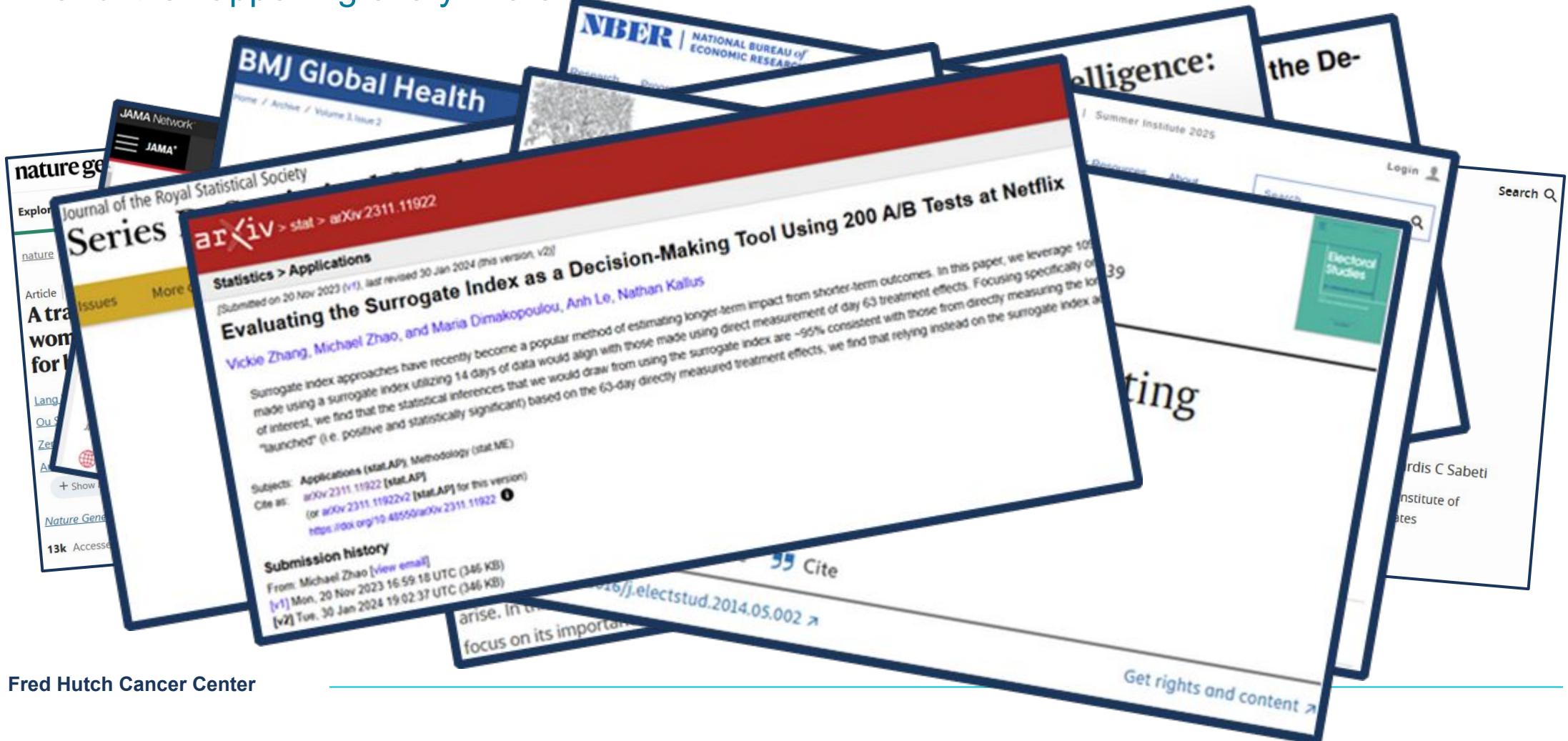
**Z:** Predictive Features

**Y:** (Missing) Outcome of Interest

**$\hat{Y}$ :** Predicted Outcome

# Using predictions as surrogates is appealing...

... and it is happening everywhere



But when our goal is downstream inference/hypothesis testing

# This can cause problems

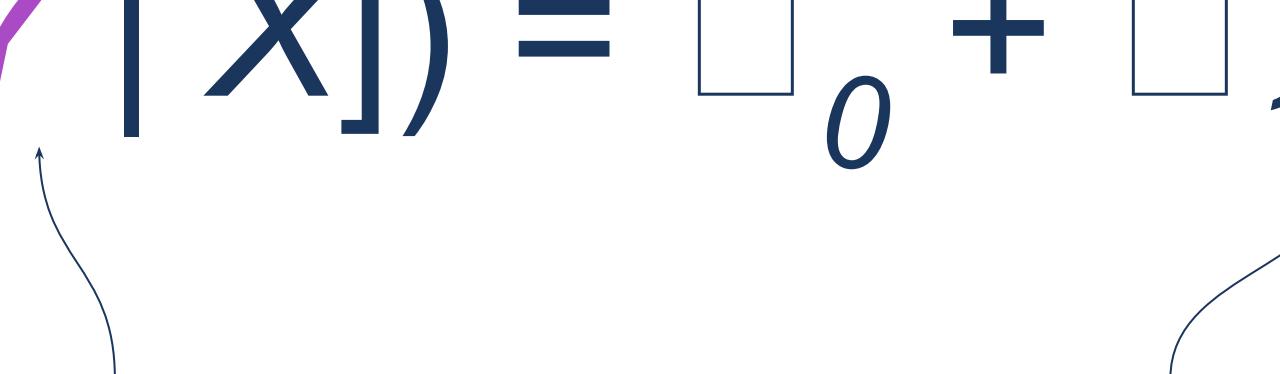
$$g(E[Y | X]) = \boxed{\phantom{0}}_0 + \boxed{\phantom{0}}_1 X$$

The diagram illustrates the inputs to the function  $g$ . On the left, a wavy arrow points from the text "gene expression" up towards the term  $E[Y]$ . On the right, another wavy arrow points from the text "drug dose" up towards the variable  $X$ .

But when our goal is downstream inference/hypothesis testing

This can cause problems

$$g(E[\hat{Y} | X]) = \square_0 + \square_1 X$$



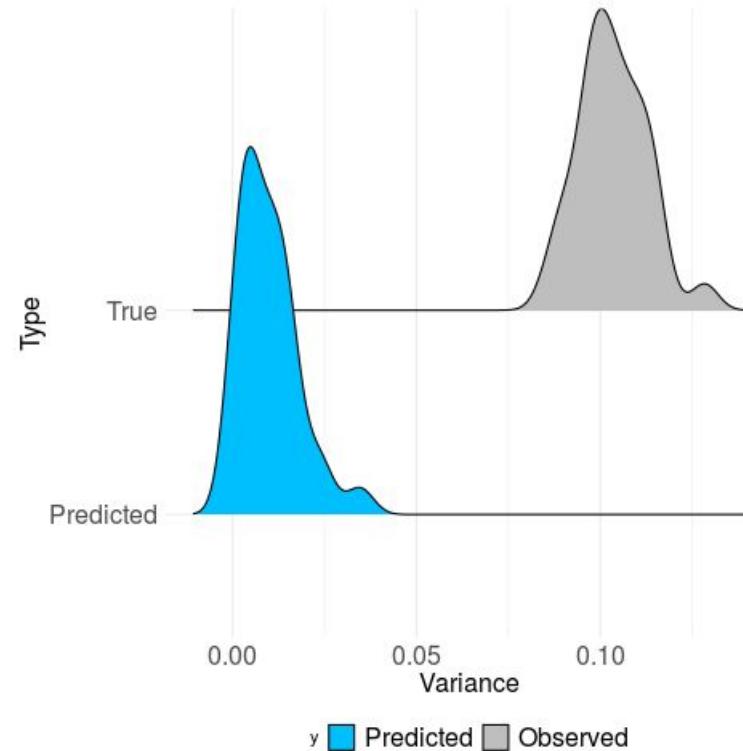
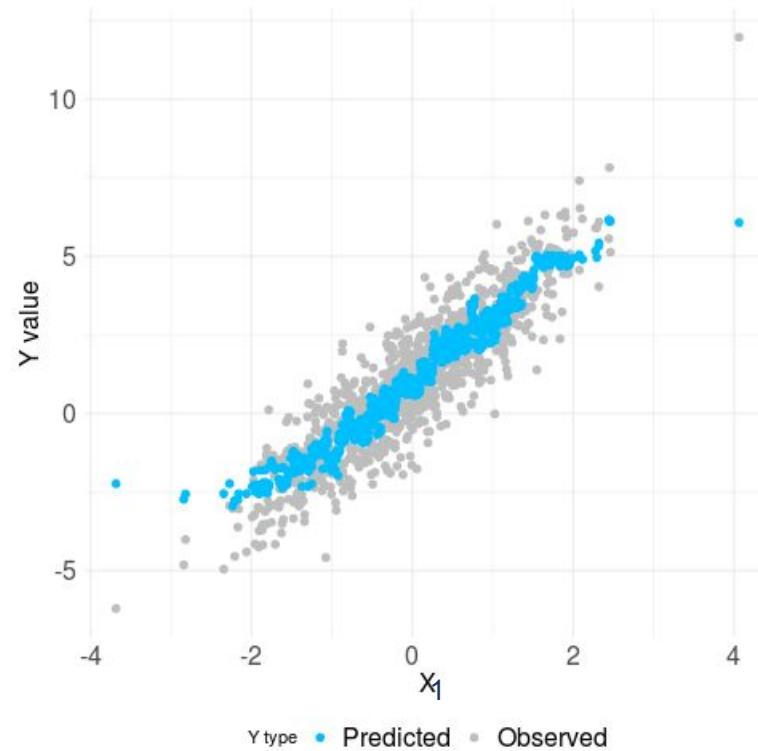
predicted gene expression      drug dose



# Where can this go wrong?

# High predictive accuracy $\neq$ good information for inference

Bias & inability to propagate uncertainty from the predictions to the downstream model



## Simulation Setup:

$$X_1 \sim N(0, 1)$$

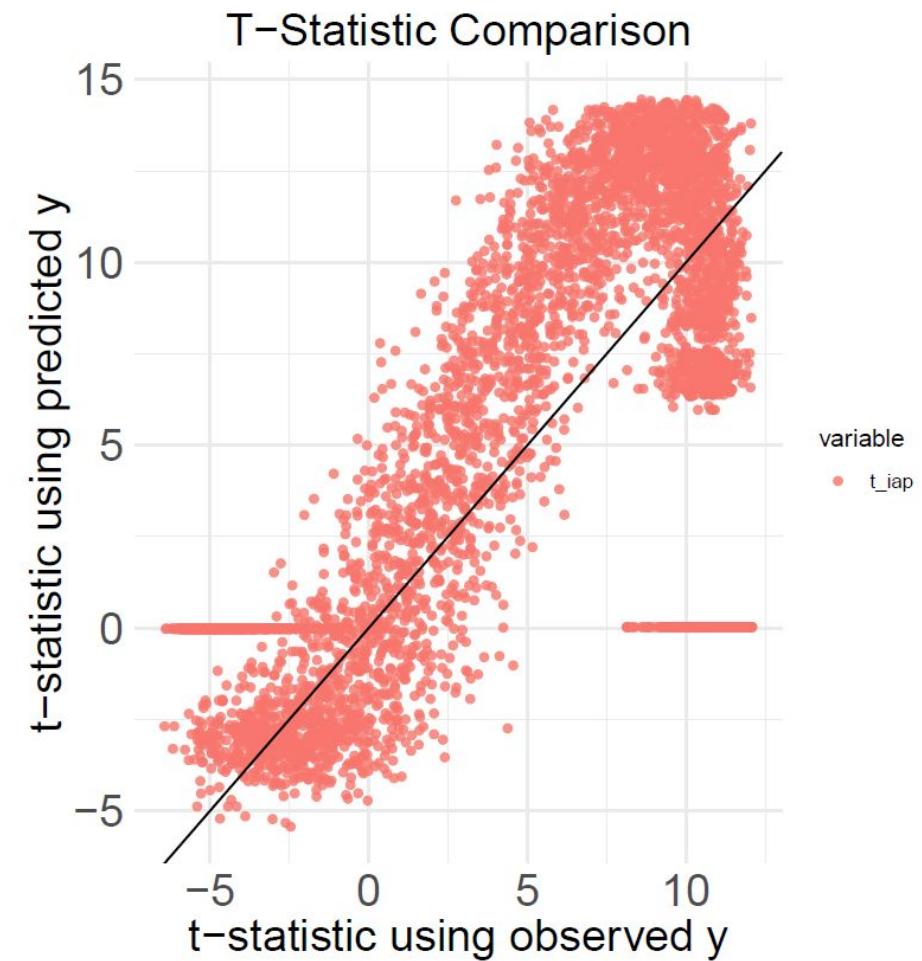
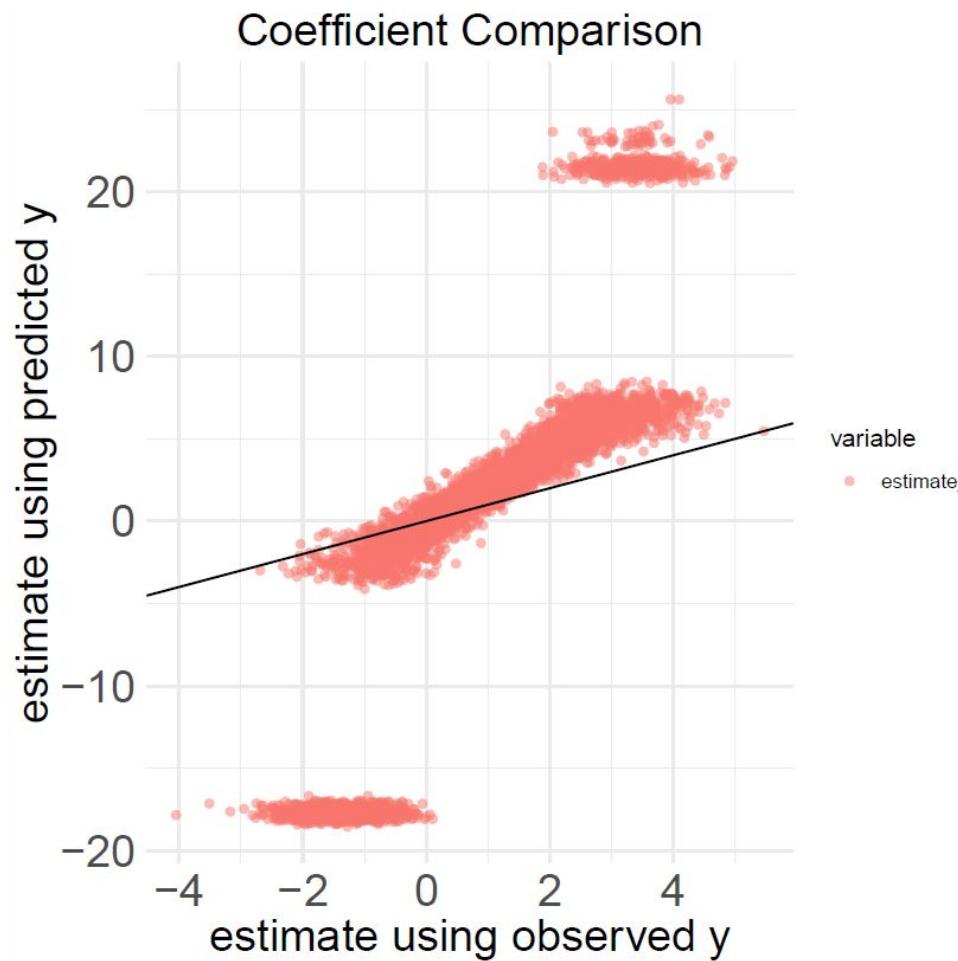
$$X_2 \sim N(0, 1)$$

$$\mu = 1 + \gamma X_1$$

$$Y \sim N(\mu, 1)$$

$$\hat{Y} = \hat{\beta}_0 + \hat{\beta}_1 X_1 + \hat{\beta}_2 X_2$$

# It gets worse when we compare coefficients/test statistics





# Where does this leave us?

# Many AI/ML models are often “black boxes”

We don't have access to their operating characteristics or training data

## Matters arising

### Transparency and reproducibility in artificial intelligence

<https://doi.org/10.1038/s41586-020-2766-y>

Received: 1 February 2020

Accepted: 10 August 2020

 Check for updates

<https://www.nature.com/articles/s41586-020-2766-y>

Benjamin Haibe-Kains<sup>1,2,3,4,5</sup>, George A Farnoosh Khodakarami<sup>1,2</sup>, Massive Anal Directors\*, Levi Waldron<sup>9</sup>, Bo Wang<sup>2,3,5,6</sup>, Anshul Kundaje<sup>13,14</sup>, Casey S. Greene<sup>15,16</sup>, Jeffrey T. Leek<sup>18</sup>, Keegan Korthauer<sup>19,20</sup>, Robert Tibshirani<sup>25,26</sup>, Trevor Hastie<sup>25,26</sup>, & Hugo J. W. L. Aerts<sup>6,7,33,34</sup>

ARISING FROM S. M. McKinney et al. *Nature*

**Table 1 | Essential hyperparameters for reproducing the study for each of the three models**

	Lesion	Breast	Case
Learning rate	Missing	0.0001	Missing
Learning rate schedule	Missing	Stated	Missing
Optimizer	Stochastic gradient descent with momentum	Adam	Missing
Momentum	Missing	Not applicable	Not applicable
Batch size	4	Unclear	2
Epochs	Missing	120,000	Missing

This is hard to model correctly

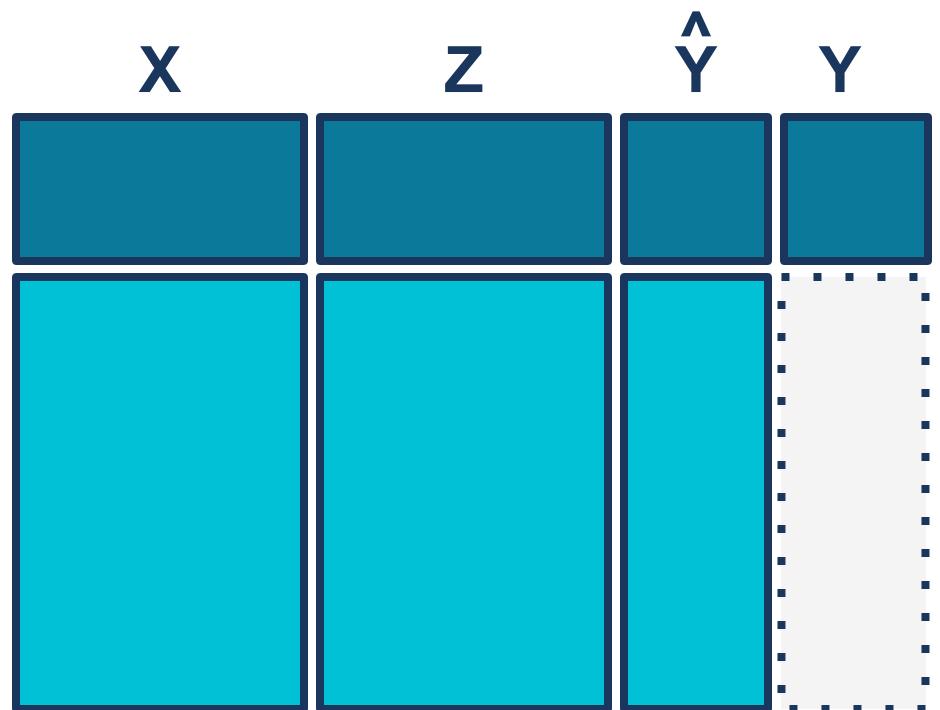
And it depends on our upstream (black box) prediction algorithm

$$g(E[\hat{Y} | X]) = \square_0 + \square_1 X$$

predicted gene expression      drug dose

# We need methods for “inference with predicted data” (IPD)

Leverage a subset of data with gold-standard outcomes to calibrate inference in the larger study



: Labeled    : Unlabeled

**X:** Covariates of Interest

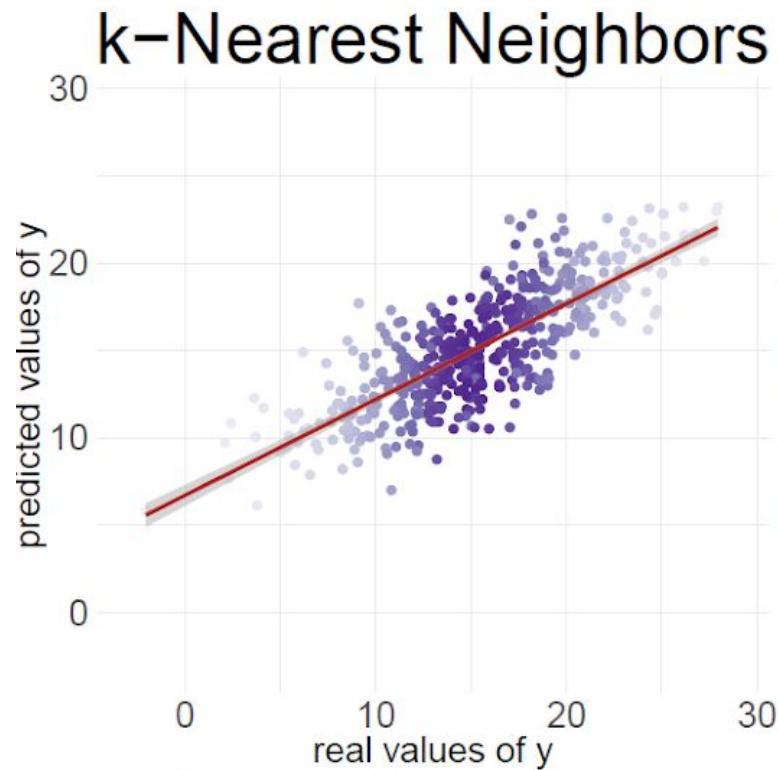
**Z:** Predictive Features

**Y:** (Missing) Outcome of Interest

**$\hat{Y}$ :** Predicted Outcome

# Post-Prediction Inference (Wang et al., 2020)

A key observation that the predicted and true outcomes often have a simple relationship



**PNAS**

RESEARCH ARTICLE | STATISTICS | [a](#)

f X in e

Methods for correcting inference based on outcomes predicted by machine learning

Siruo Wang, Tyler H. McCormick, and Jeffrey T. Leek [Authors Info & Affiliations](#)

Edited by Robert Tibshirani, Stanford University, Stanford, CA, and approved October 6, 2020 (received for review January 24, 2020)

November 18, 2020 | 117 (48) 30266-30275 | <https://doi.org/10.1073/pnas.2001238117>

22,004 | 37

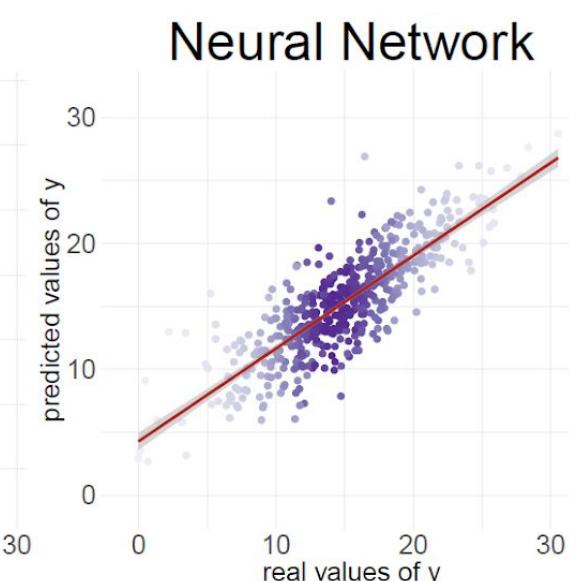
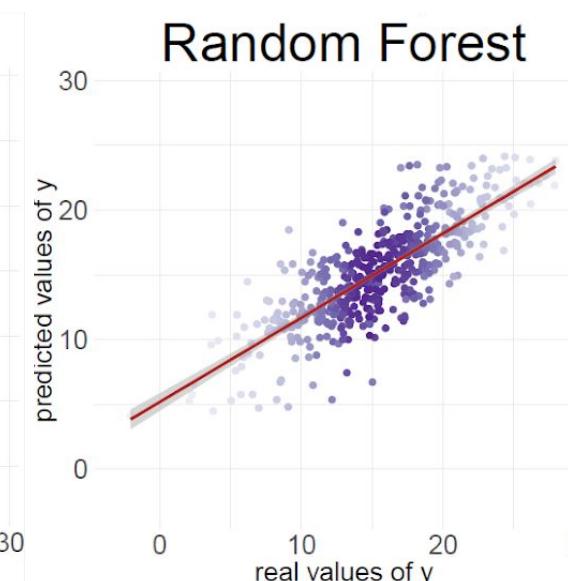
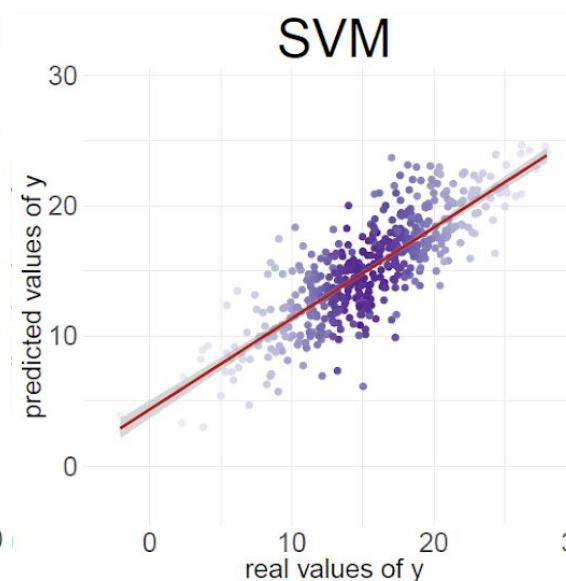
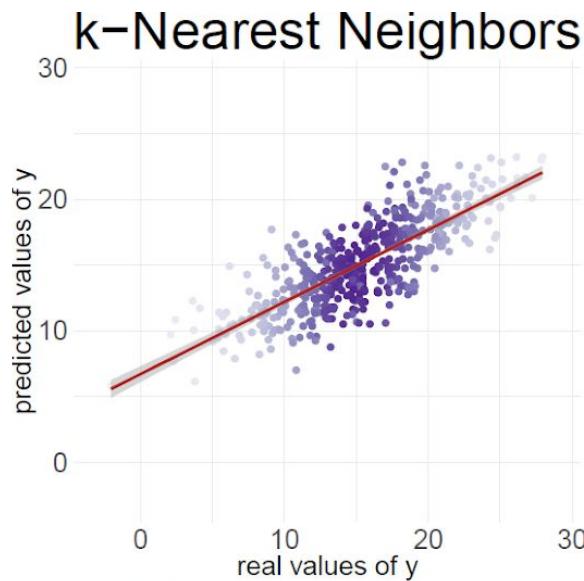
Significance

Machine learning is now being used across the entire scientific enterprise. Researchers commonly use the predictions from random forests or deep neural networks in downstream statistical analysis as if they were observed data. We show that this approach can lead to extreme bias and uncontrolled variance in downstream statistical models. We propose a statistical adjustment to correct biased inference in regression models using predicted outcomes—regardless of the machine-learning model used to make those predictions.

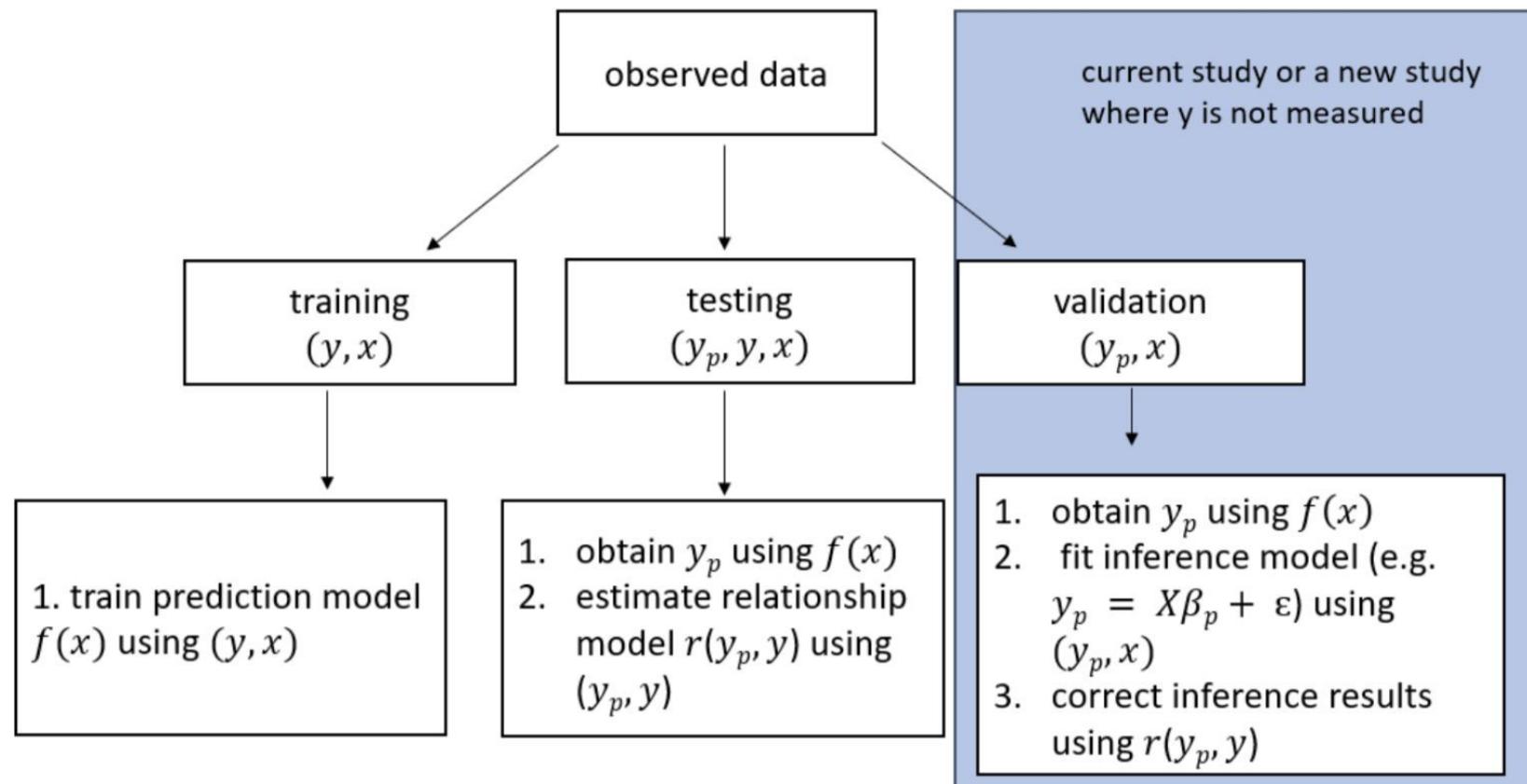
<https://www.pnas.org/doi/abs/10.1073/pnas.2001238117>

# Predicted and true outcomes often have a simple relationship

Regardless of the predictive model used



# Post-Prediction Inference models this relationship in the labeled data



$y$ : observed outcome     $x$ : observed covariate     $y_p$ : predicted outcome  
 $f(x)$ : prediction model     $r(y_p, y)$ : relationship model

PostPI uses the testing set to correct inference in the validation set

Consider a downstream linear regression

$$Y = \mathbf{X}^\top \beta + \varepsilon, \quad \mathbb{E}[\varepsilon | \mathbf{X}] = 0.$$

Fit a linear relationship model in the labeled set:

$$Y_{\mathcal{L}} = \gamma_0 + \gamma_1 f(Z_{\mathcal{L}}) + \eta, \quad \mathbb{E}[\eta | f(Z_{\mathcal{L}})] = 0.$$

then form pseudo-outcomes in the unlabeled set:

$$Y_{\mathcal{U}}^* = \hat{\gamma}_0 + \hat{\gamma}_1 f(Z_{\mathcal{U}})$$

Their final estimator is:

$$\hat{\beta}_{\text{PostPI}} = (\mathbf{X}_{\mathcal{U}}^{\textcolor{brown}{\top}} \mathbf{X}_{\mathcal{U}})^{-1} \mathbf{X}_{\mathcal{U}}^{\top} Y_{\mathcal{U}}^* \quad (3)$$

For inference, PostPI approximates the conditional variance

$$\text{Var}(Y_{\mathcal{U}} \mid \mathbf{X}_{\mathcal{U}}) \approx \sigma_r^2 + \gamma_1^2 \sigma_p^2,$$

their standard error estimator is

$$SE(\hat{\beta} \mid \mathbf{X}_{\mathcal{U}}) = \sqrt{(\mathbf{X}_{\mathcal{U}}^\top \mathbf{X}_{\mathcal{U}})^{-1} (\hat{\sigma}_r^2 + \hat{\gamma}_1^2 \hat{\sigma}_p^2)}. \quad (5)$$

This mirrors linear regression, with a scalar residual variance and inverse Gram matrix

# We propose a moment-based generalization to PostPI

This relaxes several assumptions from the original method

PostPI assumes the prediction error,  $\eta$ , is uncorrelated with the covariates,  $X$ . In many realistic settings,  $\eta$  will share structure with  $X$ , so the bias is nonzero.

$$\begin{aligned}\beta &= \left[ \mathbb{E}(XX^\top) \right]^{-1} \{ \gamma_1 \mathbb{E}[Xf(Z)] + \mathbb{E}(X\eta) \} \\ &\neq \gamma_1 \left[ \mathbb{E}(XX^\top) \right]^{-1} \mathbb{E}[Xf(Z)] = \beta_{\text{PostPI}},\end{aligned}$$

PostPI's residual variance has two components, one from the relationship model and one from the 'naive' model

$$SE(\hat{\beta} | X_u) = \sqrt{\left( X_u^\top X_u \right)^{-1} (\hat{\sigma}_r^2 + \hat{\gamma}_1^2 \hat{\sigma}_p^2)}.$$

As the precision matrix scales as  $O(1/N)$ , this term vanishes as the size of the unlabeled set ( $N$ ) goes to infinity

# Our proposal reduces to PostPI if its assumptions hold

but extends to more general settings if it does not, with more theoretical guarantees

Assuming independent  $\mathcal{L}$  and  $\mathcal{U}$ , we estimate  $\hat{\gamma}_0$ ,  $\hat{\gamma}_1$ , and  $\hat{\eta}_i = Y_i - \hat{\gamma}_0 - \hat{\gamma}_1 f(Z_i)$ , from the *labeled* set, and covariances from both the *labeled* ( $\mathcal{L}$ ) and *unlabeled* ( $\mathcal{U}$ ) sets, where we define the following empirical moments:

$$\hat{C}_{\mathbf{X}f}^{\mathcal{U}} = \frac{1}{N} \sum_{i=n+1}^{n+N} \mathbf{X}_i f_i, \quad \hat{C}_{\mathbf{X}\eta}^{\mathcal{L}} = \frac{1}{n} \sum_{i=1}^n \mathbf{X}_i \hat{\eta}_i, \quad \hat{M}_{\mathbf{XX}}^{\mathcal{U}} = \frac{1}{N} \sum_{i=n+1}^{n+N} \mathbf{X}_i \mathbf{X}_i^\top.$$

Then, our extended estimator is given by

$$\hat{\beta} = \left( \hat{M}_{\mathbf{XX}}^{\mathcal{U}} \right)^{-1} \left( \hat{\gamma}_1 \hat{C}_{\mathbf{X}f}^{\mathcal{U}} + \hat{C}_{\mathbf{X}\eta}^{\mathcal{L}} \right). \quad (4)$$

If  $\mathbb{E}[\mathbf{X}\eta] = 0$ , then (4) reduces to the original PostPI estimator. Otherwise, (4) extends PostPI to settings where the prediction error is correlated with  $\mathbf{X}$ .

# We also generalize the variance estimation

Consider the following covariance matrices:

$$M = \mathbb{E}(XX^\top), \quad S_1 = \text{Var}[Xf(\mathbf{Z})], \quad S_2 = \text{Var}(X\eta).$$

We can show that the estimated standard error is

$$\hat{\text{SE}}(\hat{\beta}) = \sqrt{\frac{1}{N} \left( \hat{M}_{\mathbf{X}\mathbf{X}}^U \right)^{-1} \left( \hat{\gamma}_1^2 \hat{S}_1^U + \frac{N}{n} \hat{S}_2^L \right) \left( \hat{M}_{\mathbf{X}\mathbf{X}}^U \right)^{-1}}, \quad (6)$$

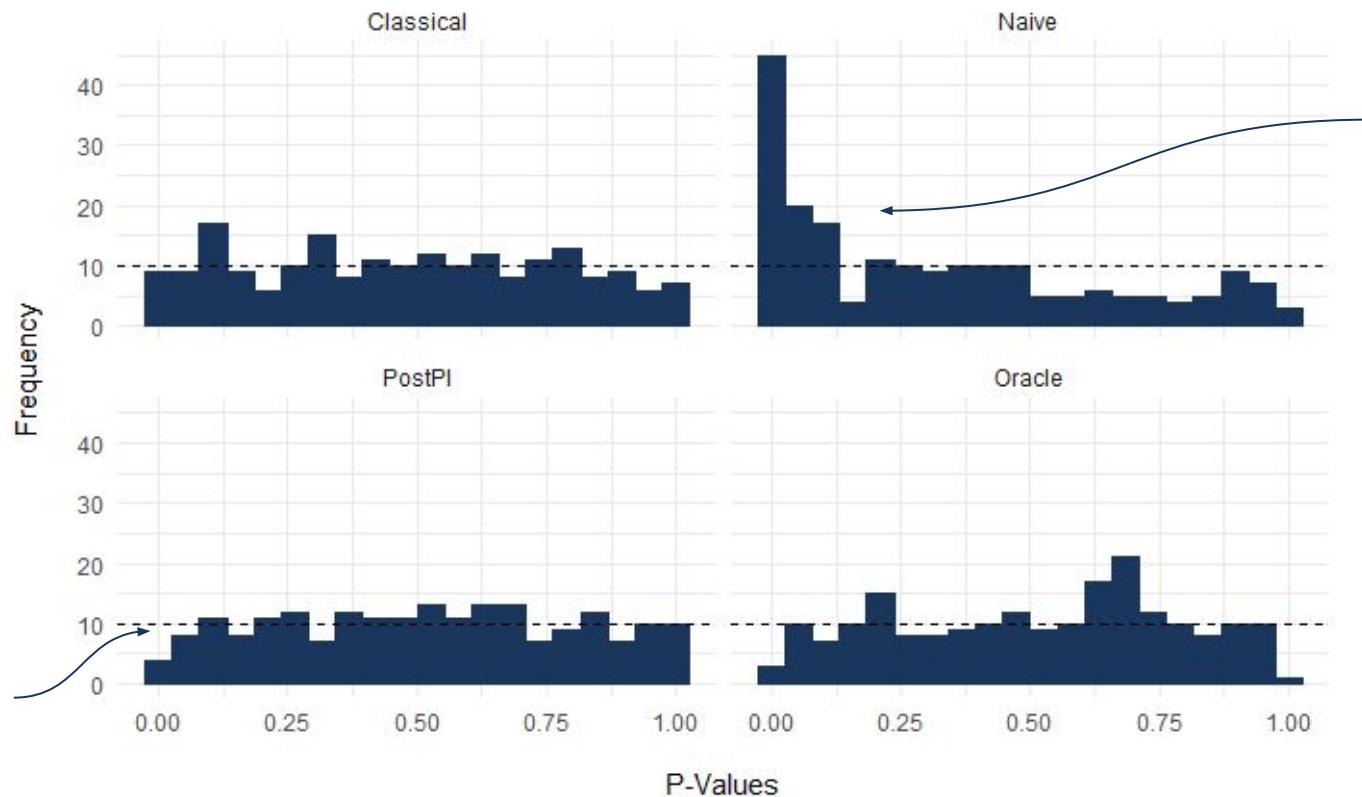
with  $S_1$  and  $S_2$  estimated by their sample analogs in the *unlabeled* and *labeled* sets, respectively. For scalar  $S_1$ ,  $S_2$ , and for  $n = N$ , (6) reduces to (5). We form Wald-type confidence intervals as  $c^\top \hat{\beta} \pm z_{1-\alpha/2} \sqrt{c^\top \text{Var}(\hat{\beta}) c}$ .

# IPD methods calibrate inference for proper Type 1 error control

P-values should be uniform (flat) under the null hypothesis

**True Effect = 0**

**Controls Type 1  
error appropriately**

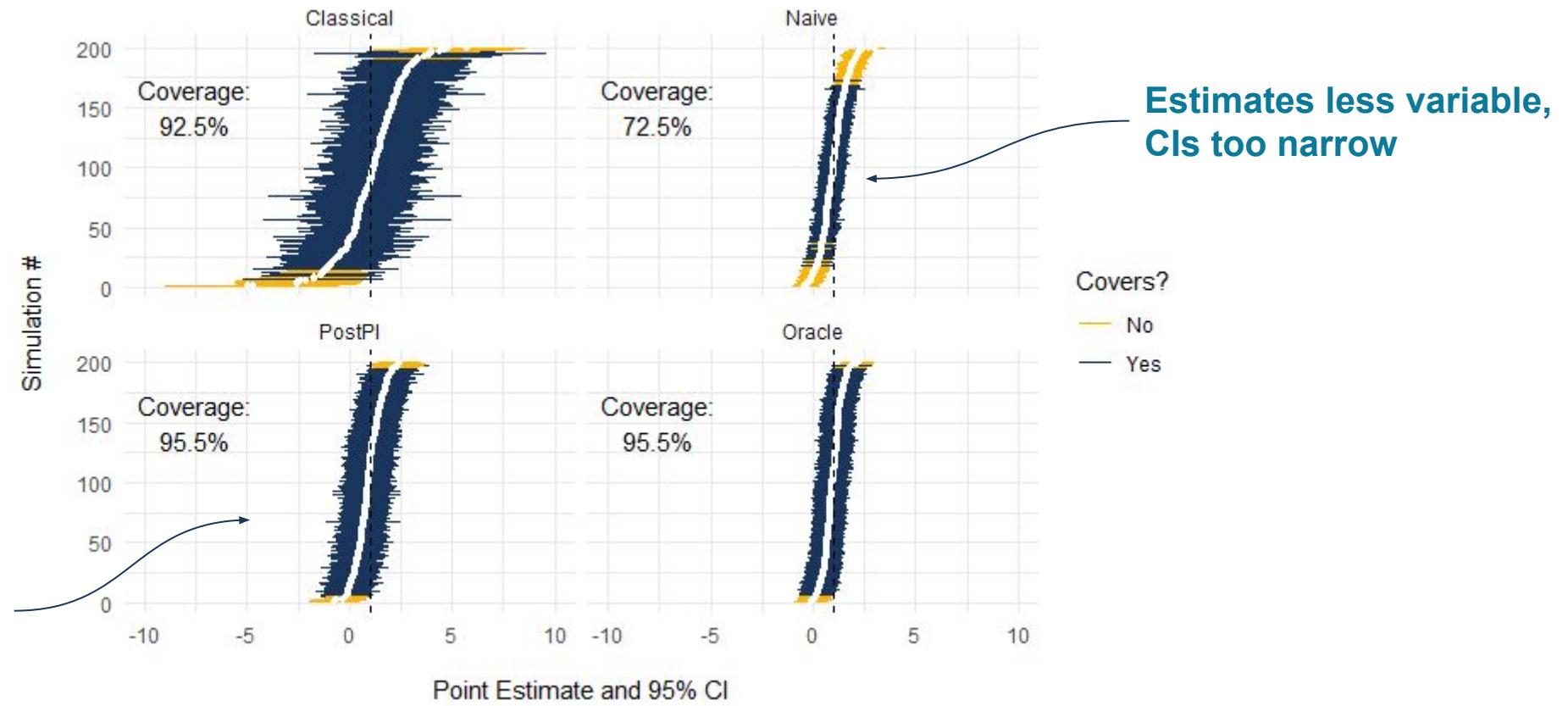


**Does not control  
Type 1 error**

# And nominal coverage (% of CIs that contain the true parameter)

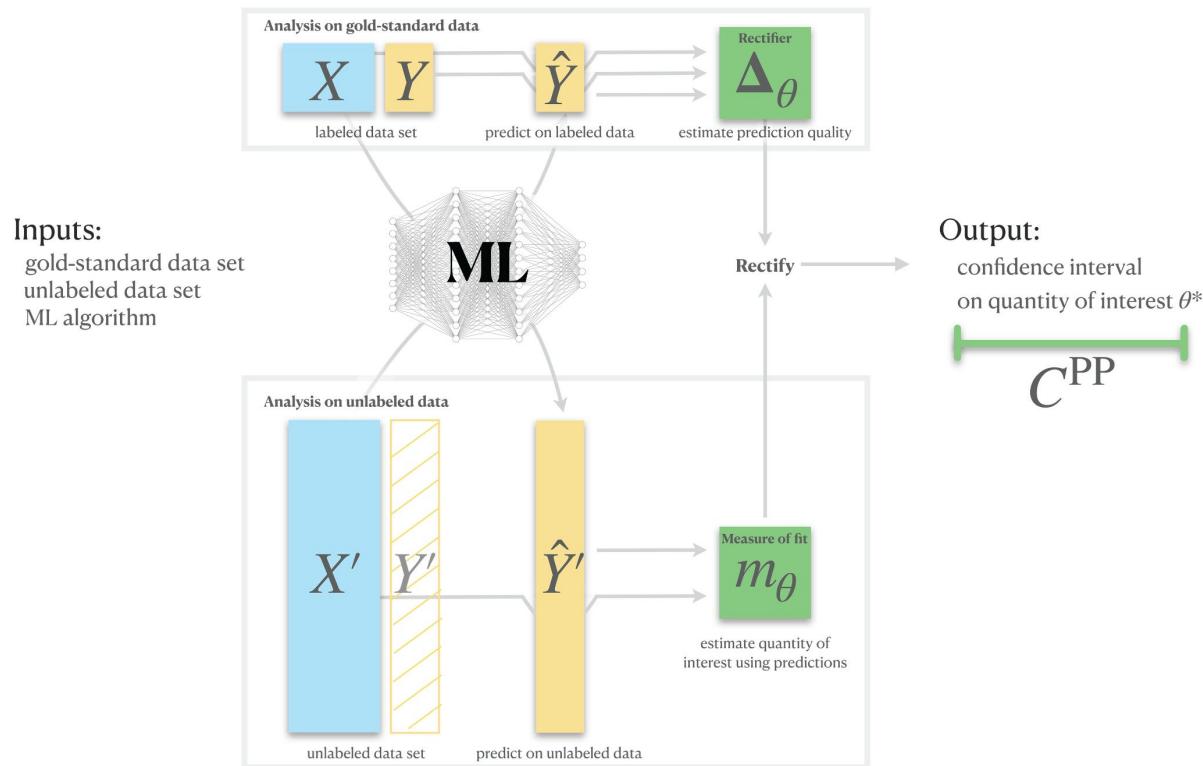
CIs are narrower than complete data analysis, but wider than the ideal, i.e., there is “no free lunch”

**True Effect = 1**



# Prediction-Powered Inference (Angelopoulos et al., 2023)

'Rectify' the estimates and inference by modeling  $\hat{Y} - \hat{Y}' = X_1 + X_2 + \dots$



**Science**

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HOME > SCIENCE > VOL. 382, NO. 6671 > PREDICTION-POWERED INFERENCE

f X in t m e

**Prediction-powered inference**

ANASTASIOS N. ANGELOPOULOS, STEPHEN BATES, CLARA FANNJIANG, MICHAEL I. JORDAN, AND TIJANA ZRNIC Authors Info & Affiliations

SCIENCE • 9 Nov 2023 • Vol 382, Issue 6671 • pp. 669-674 • DOI: 10.1126/science.adf6000

23,498 30

**Editor's summary**

Over the past decade, there has been rapid progress in the development of large-scale machine learning (ML) systems that provide predictions related to various scientific phenomena. Unfortunately, the standard statistical approaches used to calculate confidence intervals and *P* values from gold standard data lose their statistical validity for ML-derived data. Angelopoulos *et al.* introduced "prediction-powered inference," a standardized protocol for constructing valid confidence intervals and *P* values that enables the power and scale of ML systems to be used as predictors while ensuring responsible and reliable scientific inferences. The method has been demonstrated on a broad range of real datasets and offers a promising statistical approach for using ML to derive scientific conclusions responsibly. —Yury Suleymanov

<https://www.science.org/doi/10.1126/science.adf6000>

# Methods for inference with predicted data are rapidly evolving

Driven by the pace of AI/ML method development and the need for domain-specific solutions



# The {ipd} R Package



Implements recent IPD methods in a consistent manner and with ‘tidy’ helper functions



Software Note



R Package

```
library(ipd)

df <- simdat(model="ols") |>

  filter(set_label != "training")

fit <- ipd(Y ~ f ~ X1,
            method = "chen",
            model = "ols",
            data = df,
            label = "set_label")

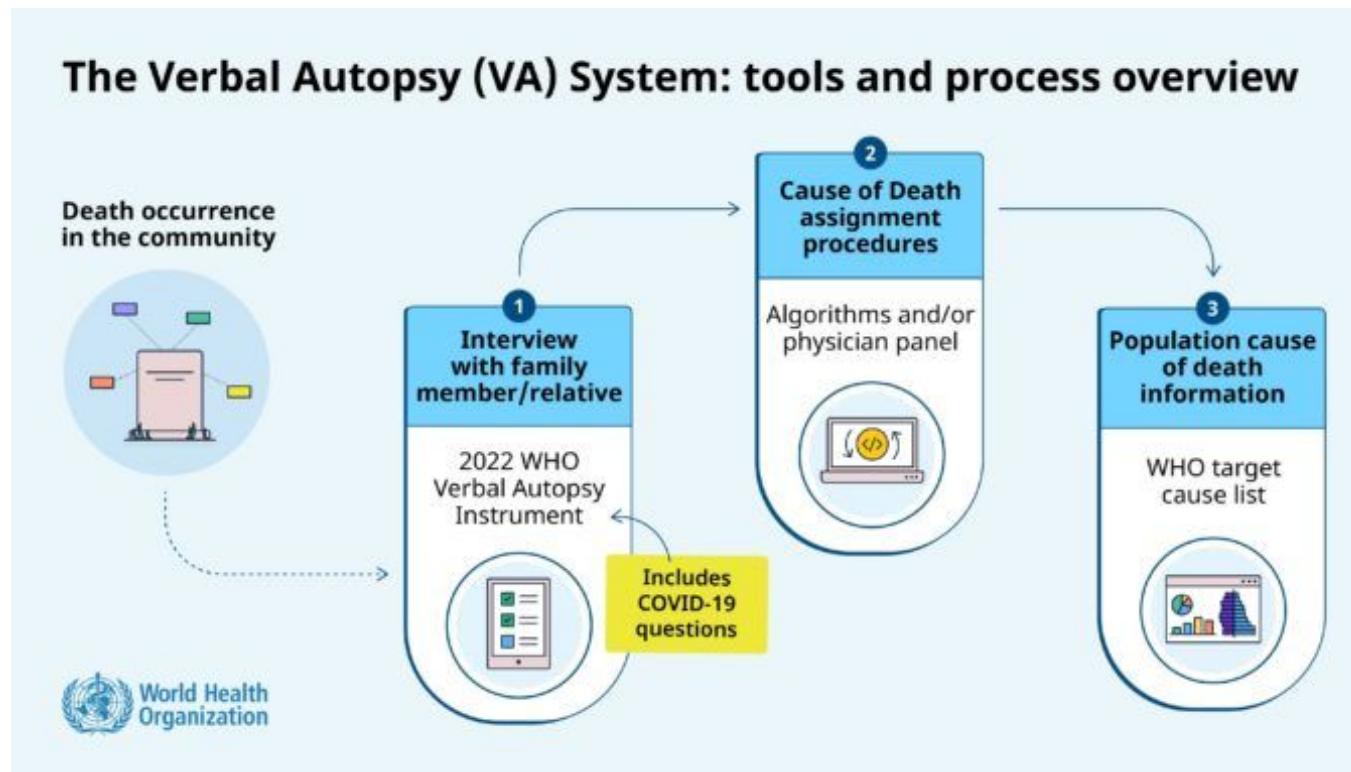
summary(fit)

results <- tidy(fit)
```

# Case Study: Verbal Autopsy

< 1/3 of global deaths are assigned a medically-certified cause

Verbal autopsy (VA) is a time-consuming, resource-intensive process



<https://publichealthnotes.com/verbal-autopsy-and-mpdsr/>

# Recent work leverages unstructured interviews for automated VA

Narrative summaries + AI/ML predictions would be less resource intensive than current standard

UNPROCESSED VA TEXT NARRATIVE
Deceased started to ill while at working place, He came home while experiencing cough with chest pain, difficult in breathing, tiredness and blood vision. The after visited Belfast clinic to get treatment but no improvement. Afterwards deceased complained of stomach pain. Then after experienced diarrhea. He was given traditional medicine but did not change. Afterwards he vomiting worms and diarrhea continued. He continued using traditional medicine and the condition remains the same. Three days before death deceased sneezed a thing like a worm. He died at home and he also experienced hot body. It was examined that his chest and throat developed wounds. Treatment given but no change. His lower lip also had rash that at time chapping and a lot of blood will comes out. After treatment that lip became healed He was taken to traditional healer, but condition unchanged. He was taken Tintswalo hospital, where he was admitted Oxygen supplier was given but he finally passed away on the third day at hospital. A week before death he complained about body pain. At the beginning deceased also had cough and complained of headache during the night only throughout the illness. A month before death he experienced hiccup which continued until death but recurrent, he skips days not defecating When defecate the stool were hard then after yellowish and black few days before death. Deceased also developed ring worms on both checks but healed before death
PROCESSED VA TEXT NARRATIVE
['cough', 'cough', 'chest', 'pain', 'tiredness', 'blood', 'vision', 'stomach', 'pain', 'vomit', 'worms', 'diarrhea', 'sneezed', 'worm', 'hot', 'chest', 'throat', 'lip', 'rash', 'chapping', 'blood', 'lip', 'pain', 'cough', 'headache', 'hiccup', 'defecating', 'defecate', 'stool', 'yellowish', 'ring', 'worms']

<https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0308452>

RecID: Symptoms from questionnaire	Extracted symptoms from textual data
A1: fever, cough, breath, chest pain, whooping	cough, whooping, cough, screaming, vomited, hot, swollen
A2: cancer, fever, sweating, breath low, yellow, abdomen pain, urine, hair, weight loss	stomach, vaginal bleeding, womb, cancer treatment, painful,stomach bleeding, urinating, swollen breast
A3: hypertension, asthma, low breath, weight loss, swollen legs, alcohol intake	passing stools, swollen
A4: hypertension, skin, urine, weight loss, swollen legs, excessive drinking	develop, sore toe, toes infection, wounds, grow infection, smell, worms, swollen
A5: fever, breath, chest pain, weight loss, excessive drinking, sweating	carrying, heavy box, twisted, pains, toes, affected, toes, swell, pain, blood, clot, removed, swell, huge, lump bursts, holes lump, chest, armpits, groin, throat, lumps, busted, puss coming
A6: TB, epilepsy, fever, cough, breath low, chest pain, diarrhoea, convulsion, vomiting, stiff neck	swollen, diarrhoea, stools, cough, go, toilet
A7: nil	pain, treated, looking better, weak, admitted, drips injection, worse
A8: hiv, fever, cough, low breath, yellow, alcohol, diarrhoea, vomit, weight loss, abdomen, swelling	sweats, lose weight, vomit, weak, hiv, water drips, diarrhoea, hallucinating, swollen stomach
A9: sweating, cough, low breath, urine, weight loss, paralysed, alcohol	cough, heavily, rot, worms, rotting, spread, thigh, buttocks, waist, extent, intestines, visible, abdomen
A10: fever, cough, vomit, weight loss, alcohol	cough, signs, vomits, low, energy, cough critical, tried, natural, fever
A11: hypertension, fever, low breath	fell, forehead, improve, speak, tears, rolled eyes, mixed blood, accident, urinate
A12: fever, cough, low breath, abdomen, swelling, headache, injury	initially, swollen ears, swollen, abdomen, critical, puss, ears, fever, cough
A13: nil	swollen, wounds, top, feet, wounds, burst, puss, swollen, feet, cuts, razor blade, rubbed
A14: fever, low breath, chest pain, diarrhoea, vomit, weight loss, hair, eyes sunken	committing, thinner, diarrhoea, oral, dehydration, solution, vomit
A15: chronic, fever, skin, weight loss, swollen legs, alcohol, smoking	pain, toe, long, kneel, cut, flesh wound, toe, swollen toe, infected
A16: fever, cough, diarrhoea, blood diarrhoea, vomit, weight loss	diarrhoea, vomit, weight loss, oral, dehydration, thrush
A17: hiv, stroke, low breath, weight loss, alcohol, chest pain	fell, weak, touch, hold, feeling, pains, arv, years, clear, pass, stools, giving, arv, sweats, minutes

<https://doi.org/10.1371/journal.pone.0308452.t002>

# We studied how different AI/ML methods classify cause of death

## Comparing KNN, SVM, BERT, and GPT-4

The screenshot shows the OpenReview.net website. At the top, there's a red header bar with the OpenReview.net logo, a search bar, and a login button. Below the header, a grey navigation bar includes a backlink to the COLM 2024 Conference homepage. The main content area displays a research paper titled "From Narratives to Numbers: Valid Inference Using Language Model Predictions from Verbal Autopsies" by Shuxian Fan, Adam Visokay, Kentaro Hoffman, Stephen Salerno, Li Liu, Jeffrey T. Leek, and Tyler McCormick. The paper was published on 10 Jul 2024 and last modified on 25 Aug 2024. It has a CC BY 4.0 license. The abstract discusses the use of verbal autopsies to predict causes of death (COD) using language models like GPT-4.

### From Narratives to Numbers: Valid Inference Using Language Model Predictions from Verbal Autopsies

Shuxian Fan, Adam Visokay, Kentaro Hoffman, Stephen Salerno, Li Liu, Jeffrey T. Leek, Tyler McCormick

Published: 10 Jul 2024, Last Modified: 25 Aug 2024 | COLM | Everyone | Revisions | BibTeX | CC BY 4.0

Research Area: Data, Science of LMs, Inference algorithms for LMs, LMs for everyone

Keywords: multiclass, inference, transportability, public health, verbal autopsy

TL;DR: We show how to perform valid statistical inference when using NLP predictions instead of directly observed data.

#### Abstract:

In settings where most deaths occur outside the healthcare system, verbal autopsies (VAs) are a common tool to monitor trends in causes of death (COD). VAs are interviews with relatives that are used to predict the decedent's COD. Turning VAs into actionable insights for researchers and policymakers requires two steps (i) predicting likely COD using the performing inference with predicted CODs (e.g. modeling the breakdown of causes by demographic factors using a sample of deaths). In this paper, we develop a method for vi outcomes (in our case COD) predicted from free-form text using state-of-the-art NLP techniques. This method, which we call multiPI++, extends recent work in "prediction-power multinomial classification. We leverage a suite of NLP techniques for COD prediction and, through empirical analysis of VA data, we demonstrate the effectiveness of our approach: transportability issues. multiPI++ recovers ground truth estimates, regardless of which NLP model produced predictions and regardless of whether they were produced by a n GPT-4-32k or a less accurate predictor like KNN. Our findings demonstrate the practical importance of inference correction for public health decision-making and suggests that end goal, having a small amount of contextually relevant, high quality labeled data is essential regardless of the NLP algorithm.

Supplementary Material: [zip](#)

Code Of Ethics: I acknowledge that I and all co-authors of this work have read and commit to adhering to the COLM Code of Ethics on <https://colmweb.org/CoE.html>

Author Guide: I certify that this submission complies with the submission instructions as described on <https://colmweb.org/AuthorGuide.html>

Submission Number: 496

<https://openreview.net/forum?id=QbCHIqbDj>

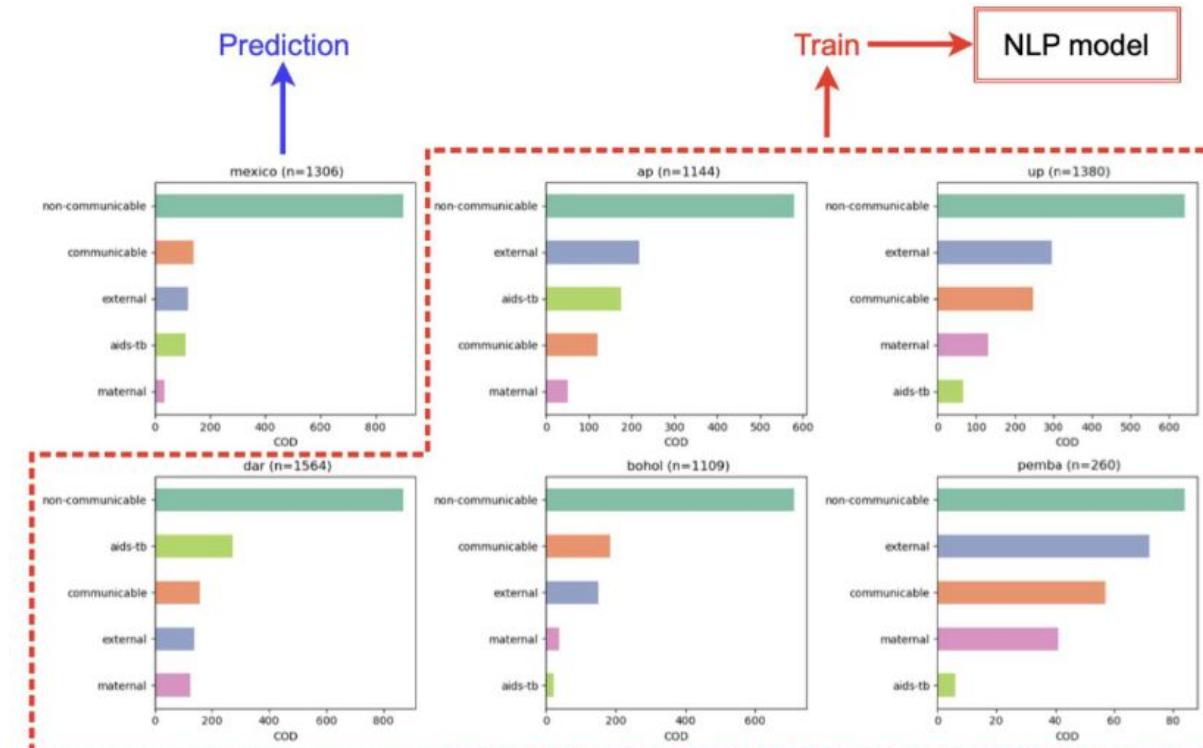
The screenshot shows a GPT-4 zero-shot prompt for cause of death (COD) prediction. The prompt is structured as follows:

- INPUT:** <narrative> [REDACTED] **Each narrative gets plugged in here**
- Labels:**
  - aids-tb: Patient died resulting from HIV-AIDS or Tuberculosis.
  - communicable: Patient died from a communicable disease such as pneumonia, diarrhea or dysentery.
  - external: Patient died from external causes such as fires, drowning, road traffic, falls, poisonous animals, suicide, homicide, or other injuries.
  - maternal: Patient died from pregnancy or childbirth including from severe bleeding, sepsis, pre-eclampsia and eclampsia.
  - non-communicable: Patient died from a non-communicable disease such as cirrhosis, epilepsy, acute myocardial infarction, copd, renal failure, cancer, diabetes, stroke, malaria, asthma.
  - unclassified: narrative does not contain enough information to predict cause of death.
- Options:** aids-tb, communicable, external, maternal, non-communicable, unclassified **Explicitly require output in this format**
- Instructions:** Which label from options best applies to the narrative? If you are not sure, return your best guess. Limit your response to one of the options exactly as it appears in the list. **Instructions**

A large red curly brace on the right side of the labels section is labeled **Context**, indicating that the narrative input is the context for the classification task.

# Population Health Metrics Research Consortium

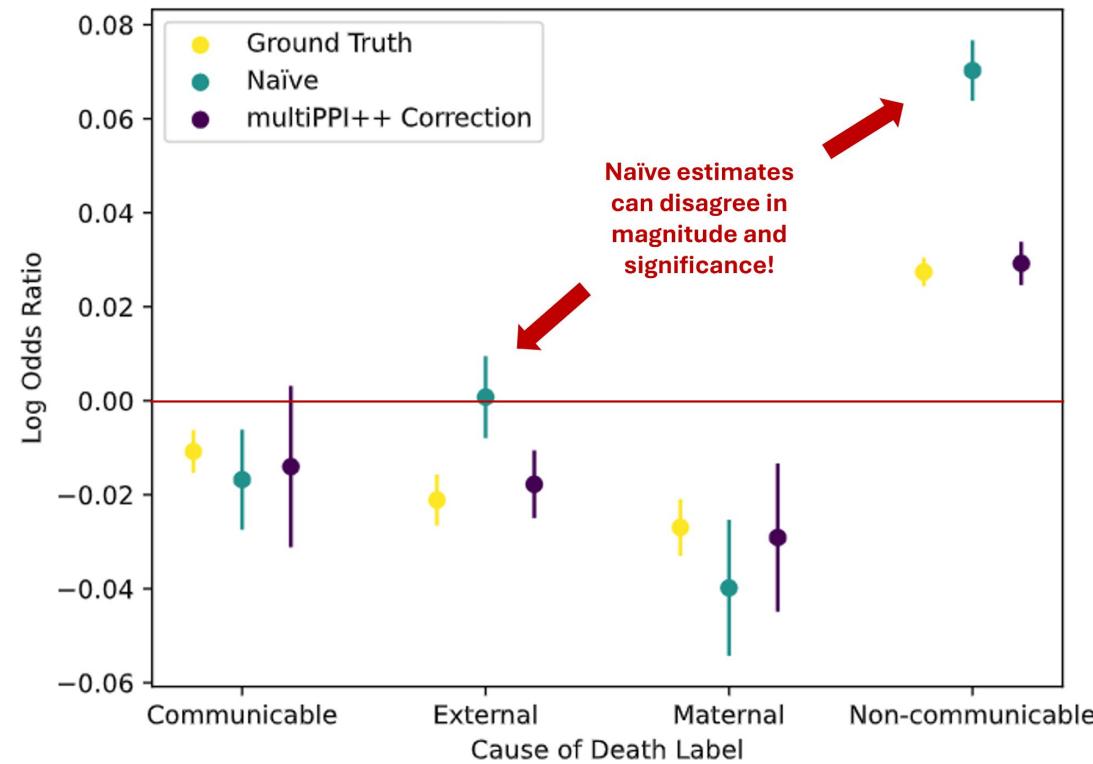
N = 6,763 observations from 6 sites in 4 countries; adults only, 5 cause of death labels



<https://openreview.net/forum?id=QbCHIIqbDJ>

# And how IPD corrects inference on predicted cause of death

By extending an existing method (PPI++) for multiclass prediction



<https://openreview.net/forum?id=QbCHIqlqDJ>

# Case Study: Body Mass Index

# ‘Predictions’ don’t have to be complex to bias inference

The case of body mass index (BMI; kg/m<sup>2</sup>) as an *imperfect* measure of adiposity

**Three-Quarters of U.S. Adults Are Now Overweight or Obese**

A sweeping new paper reveals the dramatic rise of obesity rates nationwide since 1990.

Listen to this article • 7:32 min [Learn more](#) Share full article 2.2K



Getty Images

By Nina Agrawal  
Published Nov. 14, 2024 Updated Nov. 15, 2024, 2:17 a.m. ET

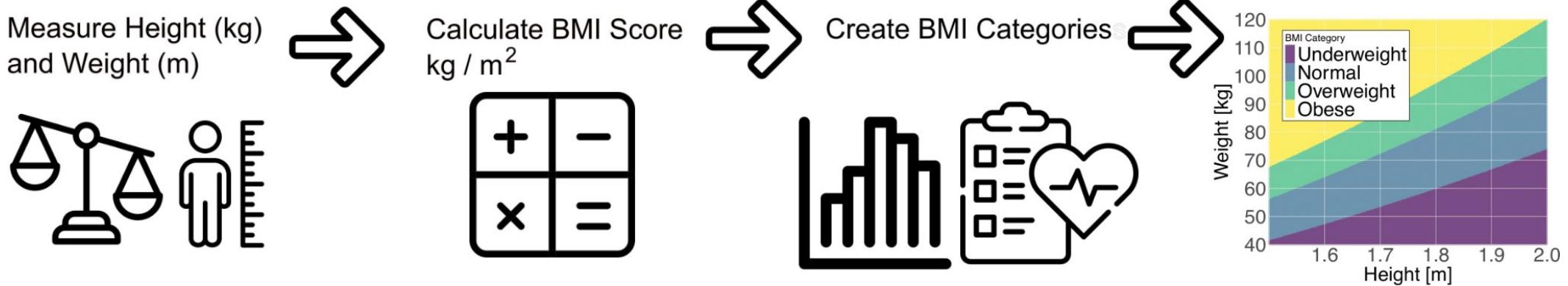
The paper defined “overweight” adults as those who were age 25 and over with a body mass index at or over 25, and “obese” adults as those with a B.M.I. at or over 30. The authors acknowledged that B.M.I. is an imperfect measure that may not capture variations in body structure across the population. But from a scientific perspective, experts said, B.M.I. is correlated with other measures of body fat and is a practical tool for studying it at a population level.

<https://www.nytimes.com/2024/11/14/well/obesity-epidemic-america.html>

# An ‘algorithm’ is just a set of steps that map inputs to outputs

BMI is one of several potential adiposity prediction algorithms

- BMI ( $\geq 30 \text{ kg/m}^2$ )
- Waist circumference (men  $\geq 102 \text{ cm}$ ; women  $\geq 88 \text{ cm}$ )
- DXA % body fat ( $> 30\%$  men;  $> 42\%$  women)



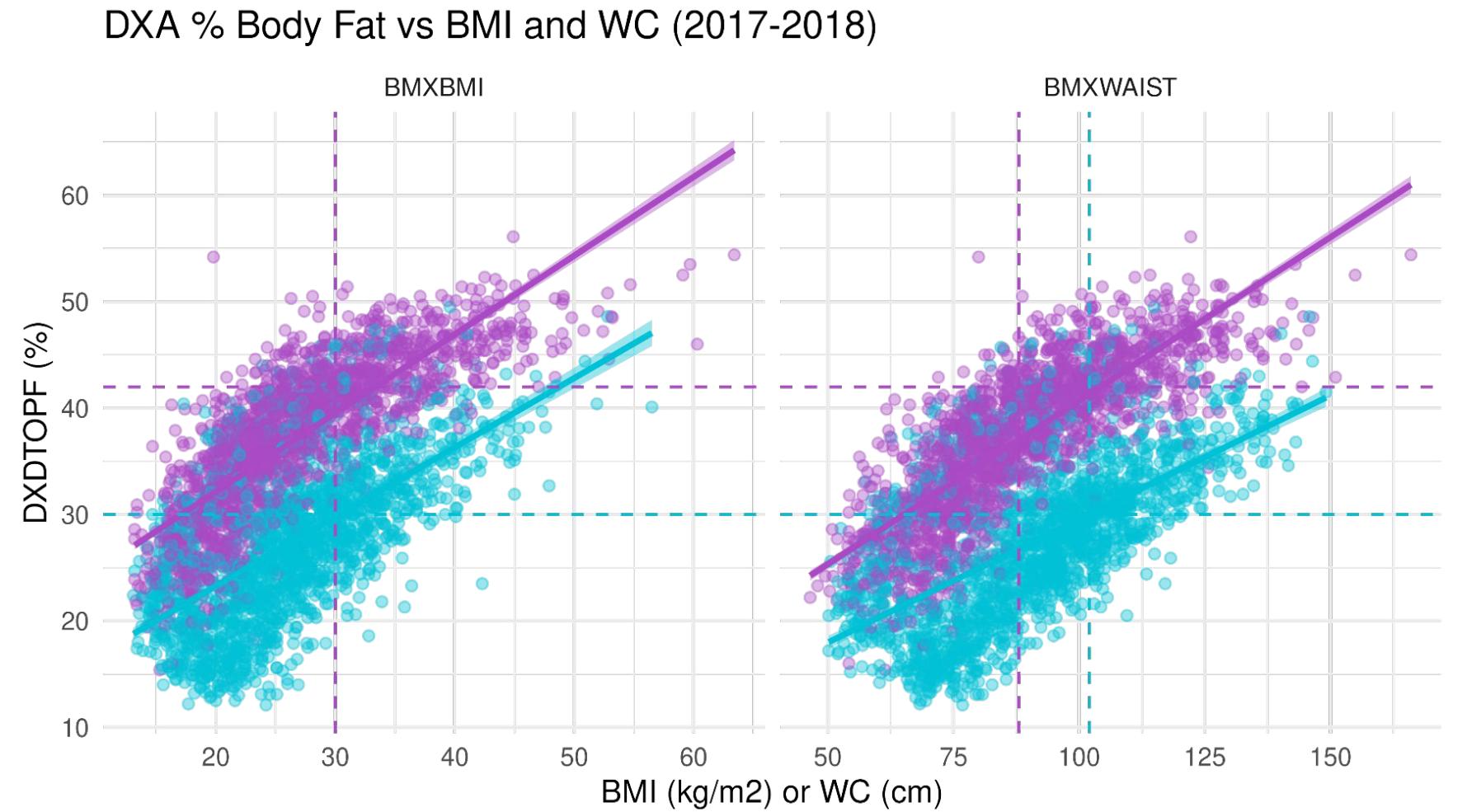
<https://www.medrxiv.org/content/10.1101/2025.04.01.25325037v1.full.pdf>

# Using NHANES to understand population-level inference

BMI/WC/DXA all collected up until COVID-19, when DXA collection was suspended

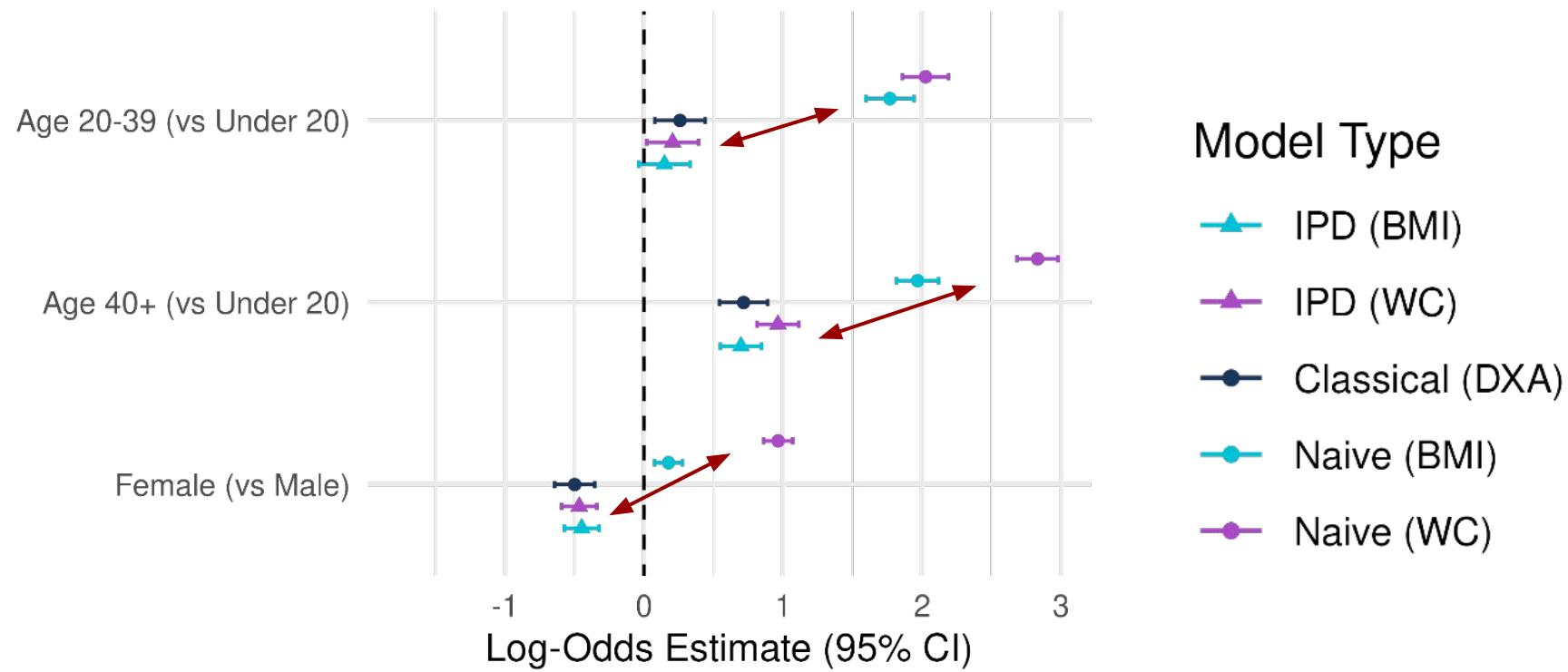


# Mismatched quadrants suggest limitations in BMI/WC



# Differences in sign and magnitude depending on the measure!

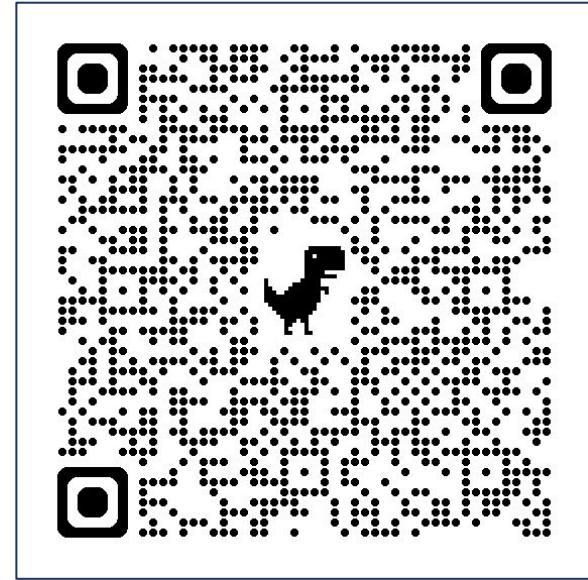
But IPD correction aligns with gold-standard DXA-based measure of obesity



# Some final thoughts

This area is only becoming more relevant in this AI/ML era

- Increasing reliance on AI/ML raises questions about data quality/validity
- IPD is rapidly evolving, driven by need for rigorous methods to domain-specific problems
- We believe that open-source collaboration is the fastest way to success!



These Slides

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<https://github.com/ipd-tools>



# Thank you!

