# Let's Take It Personal: Maximizing patient care in late-stage prostate cancer through Al-based approaches in precision medicine

Ralf P. Dagdag<sup>1,2\*</sup>, James C. Costello<sup>1,2‡</sup>, Christopher R. Gignoux<sup>1,3‡</sup> \*Corresponding Author: ralf.dagdag@cuanschutz.edu

## Study Overview:

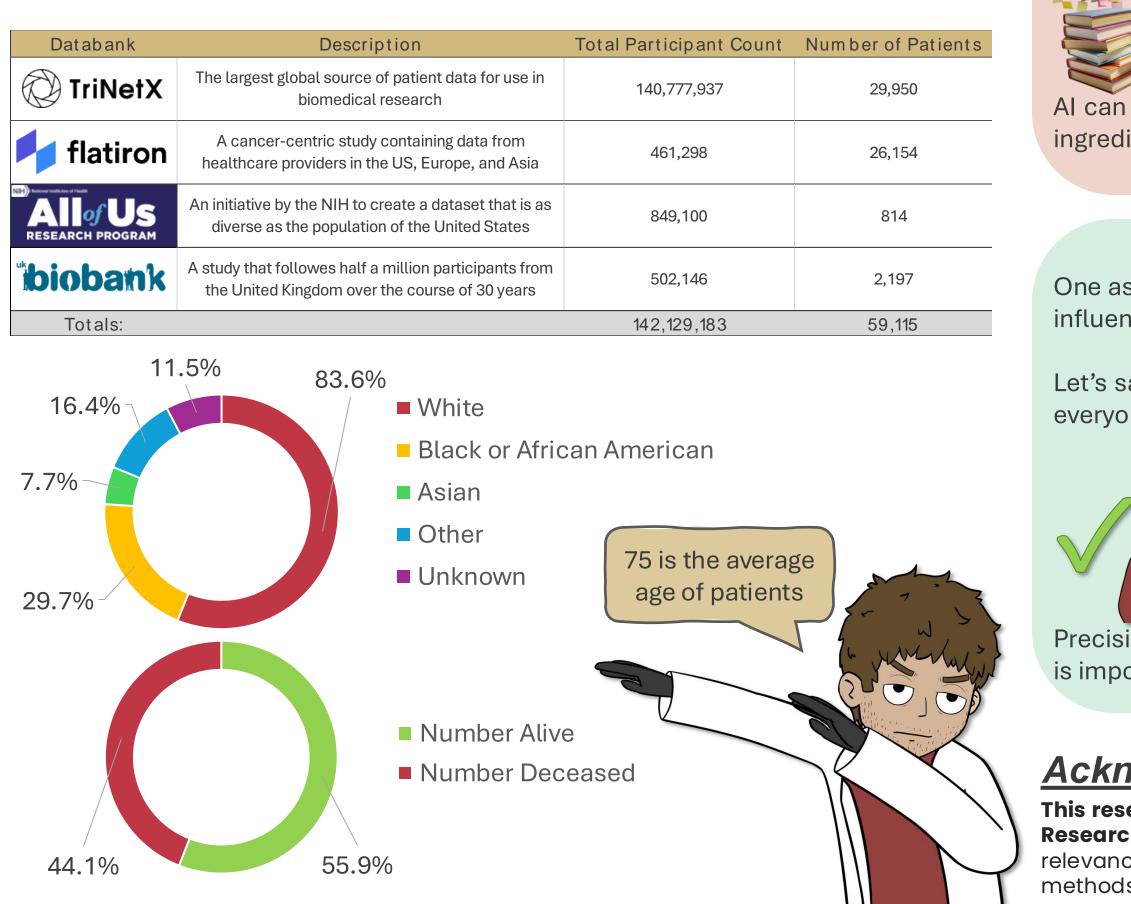
**Prostate cancer** is the most commonly-diagnosed cancer in men and is the second leading cause of cancer-related death. Current research efforts focus on understanding patient's risk of developing prostate cancer, their risk of their cancer spreading in the body, and improving treatments for patients with early-stage prostate cancer.

While this is helpful for patients whose cancer is caught early, information for treating patients with later diagnoses is not nearly as strong. This represents in a **critical need** in the field – a better understanding of late-stage prostate cancer at as it relates to drug response will improve patient outcomes.

To address this need, my project tests the **hypothesis** that a patient's response to drugs used for treating late-stage prostate cancer can be better understood by looking at their health history, as well as their DNA. Understanding this relationship can improve and maximize patient care, providing them better armor during their fight against cancer.

## Who are the participants?

This research project uses patient health records from four different research studies:



The overall <u>approach</u> used in this study consists of the three main objectives:



Patient data can be messy, so it's important to **preprocess** the data to ensure the rest of the process goes smoothly.

Think of this like baking: trying to grab every ingredient as you go can make things hard, especially if your kitchen is disorganized...



Artificial intelligence (AI) uses data from pre-existing information to predict a certain outcome.

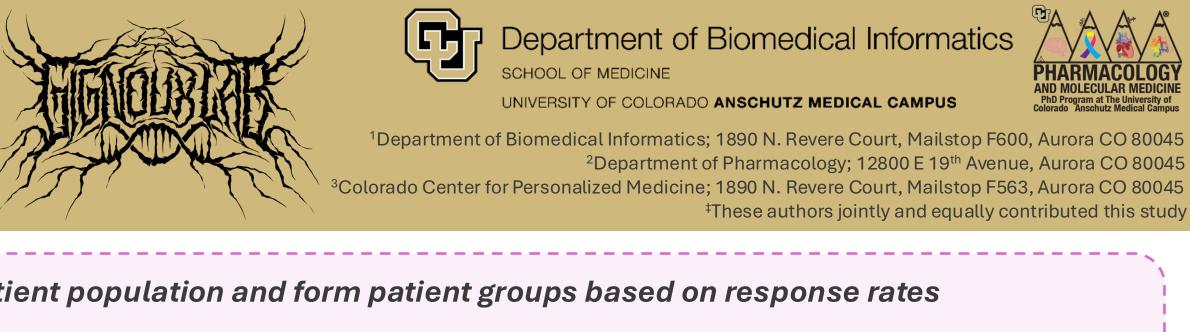
Pretend you just had THE best brownie ever – you have a full pantry to recreate it, but don't know which ingredients are important.



AI can "learn" from every brownie recipe you have to predict which ingredients are important for a "good" vs "bad" brownie.

One aspect of precision medicine studies how a patient's DNA can influence how well a treatment works for them.

Let's say that the best brownie in the world has a secret ingredient – everyone loves them, but some people have an allergic reaction.



**Preprocessing:** Define the patient population and form patient groups based on response rates **Specific Aim 01:** Determine what aspects of healthcare records are most predictive of response to treatment Specific Aim 02: Detect aspects of patient DNA that can be useful for precision medicine

## What is the main concept?



But if you preprocess your ingredients and get them ready to go before you start, the cooking process will be much easier!



Precision medicine can tell us why some people are allergic, which is important in allowing everyone to enjoy the World's Best Brownie<sup>™</sup>

### Goal:

To ensure we have all the "ingredients" needed for our project set in place, we must:

Define the patient population

- Select patients who meet this definition to form cohorts
- Split the cohorts based on how well they respond to therapy

### Goal:

To predict the "recipe" for a good or poor responder and the "ingredients' needed for each, we want to:

- Build AI models to predict whether a patient will have a good or poor response
- Test how well the models perform
- Identify which data are important for deciding response rate

### <u>Goal:</u>

To determine how DNA can explain why some patients respond poorly to a treatment "brownie", we will:

- Analyze the DNA of patients who had a poor response to treatment
- Find differences in patient DNA that are consistent with poor response
- Predict how these differences affect and influence the body

### Acknowledgments:

This research would not be possible without the partnership and contributions of the participants within UC Health and the Colorado Center for Personalized Medicine, the TriNetX Research Network, the NIH All of Us Research Program, UK Biobank, and Flatiron Health. Additionally, I would like to thank the following individuals for their contributions: Laura S. Graham, MD for providing guidance on framing the clinical scope and relevancy of this project; Michael Orman, Lily Elizabeth Feldman, and Cailin Deiter for their guidance and feedback regarding cancer biology; Lucas Gillenwater and Sutanu Nandi, PhD for their guidance on computational methods; Maizy Brasher for her guidance on UK Biobank and HIPAA and GDPR compliance; Sean Davis, MD, PhD for his guidance on Flatiron; Luke M. Evans, PhD and Chris Arehart for their guidance on drug repurposing.

Research reported in this publication was supported by the National Cancer Institute of the National Institutes of Health under award number R01CA276826. The content is solely the responsibility of the authors and does not necessarily reflect the official views of the NIH. Additionally, this research has been conducted using the UK Biobank Resource under Application Number 100578.

## How is the work done?

