Breakout Session 8: Track A

Applying Gerchberg-Saxton Algorithm on Biomedical Data to Mitigate Sampling Bias on Under-Represented Populations

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Developing Unbiased AI/Deep Learning Pipelines to Address Lung Cancer Health Disparities Research

Applying Gerchberg-Saxton Algorithm on Biomedical Data to Mitigate Sampling Bias on Underrepresented Populations

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Agenda

1. Project Motivation
2. Gerchberg-Saxton Algorithm
    - Previous Studies and Results
3. Project Plan
4. Current Phase and Initial Results
5. Future Directions and Expected Outcomes

Project Motivation - Challenges in Medical AI

- **PHI data regulations** poses challenges on data distributions.
- Upholding **data integrity and privacy** is paramount yet challenging.
- There is a noticeable scarcity in the **availability of public medical datasets**.

Project Motivation - Data Quality and Representation

- The imperative to improve **the quality of data generated** by individual institutions is clear.
- The **distribution among population** groups in the US is **uneven**, which is mirrored in medical data, potentially biasing AI model predictions.
- Existing AI-based solutions, such as synthetic data generation, face challenges like **inadequate source data quality or quantity**.

U.S. Population by Race and Hispanic Origin, 2019

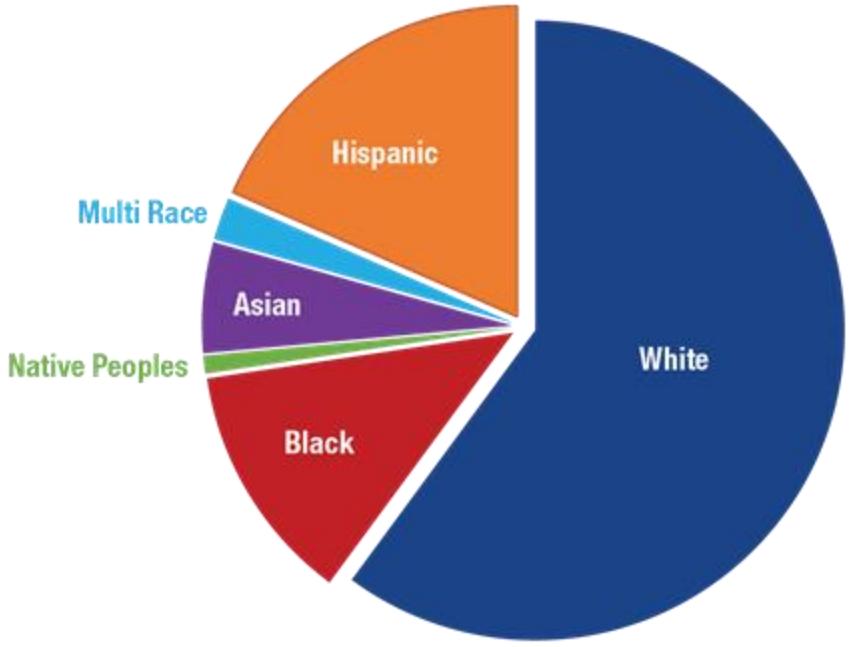


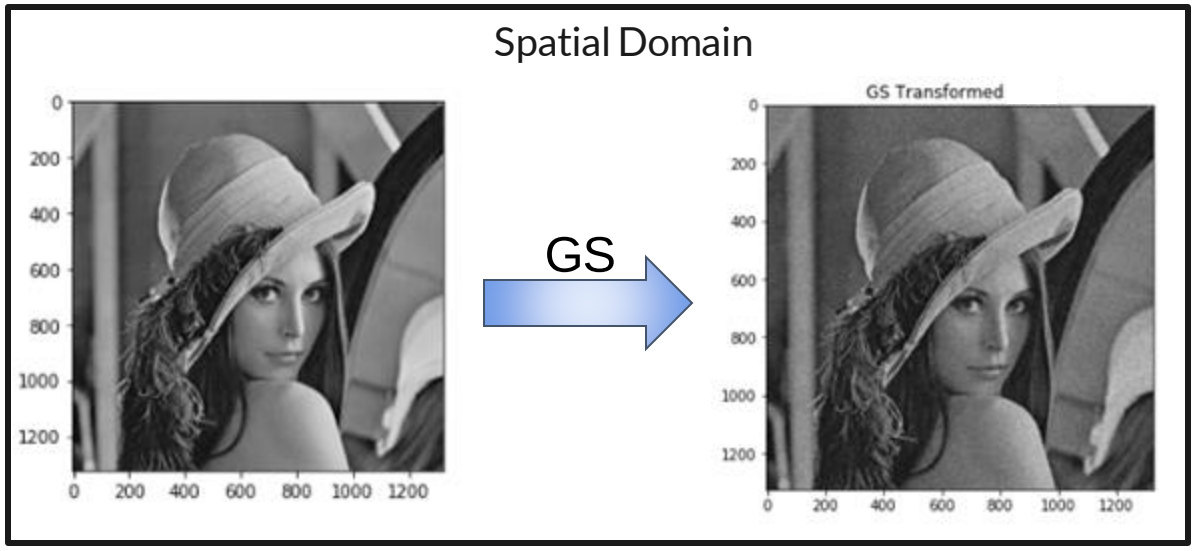
Image Source: U.S Census Bureau, Population Estimates, 2019

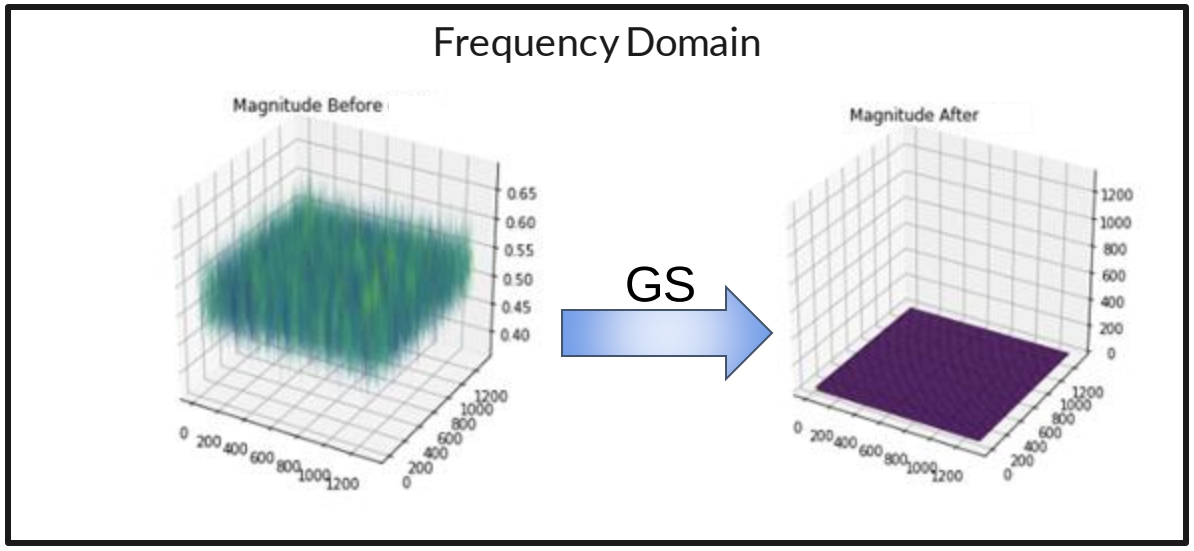
Project Motivation - Innovative Solution

- We propose an innovative data transformation approach utilizing the **Gerchberg-Saxton algorithm** to address data quality and representation issues.
- This algorithm transforms data in the frequency domain, balancing intensity components while preserving phase information, thereby **enhancing data uniformity**.
- The transformed data will more uniformly represent each population group, aiming for **fairer results in machine learning applications**.

Introduction to Gerchberg-Saxton

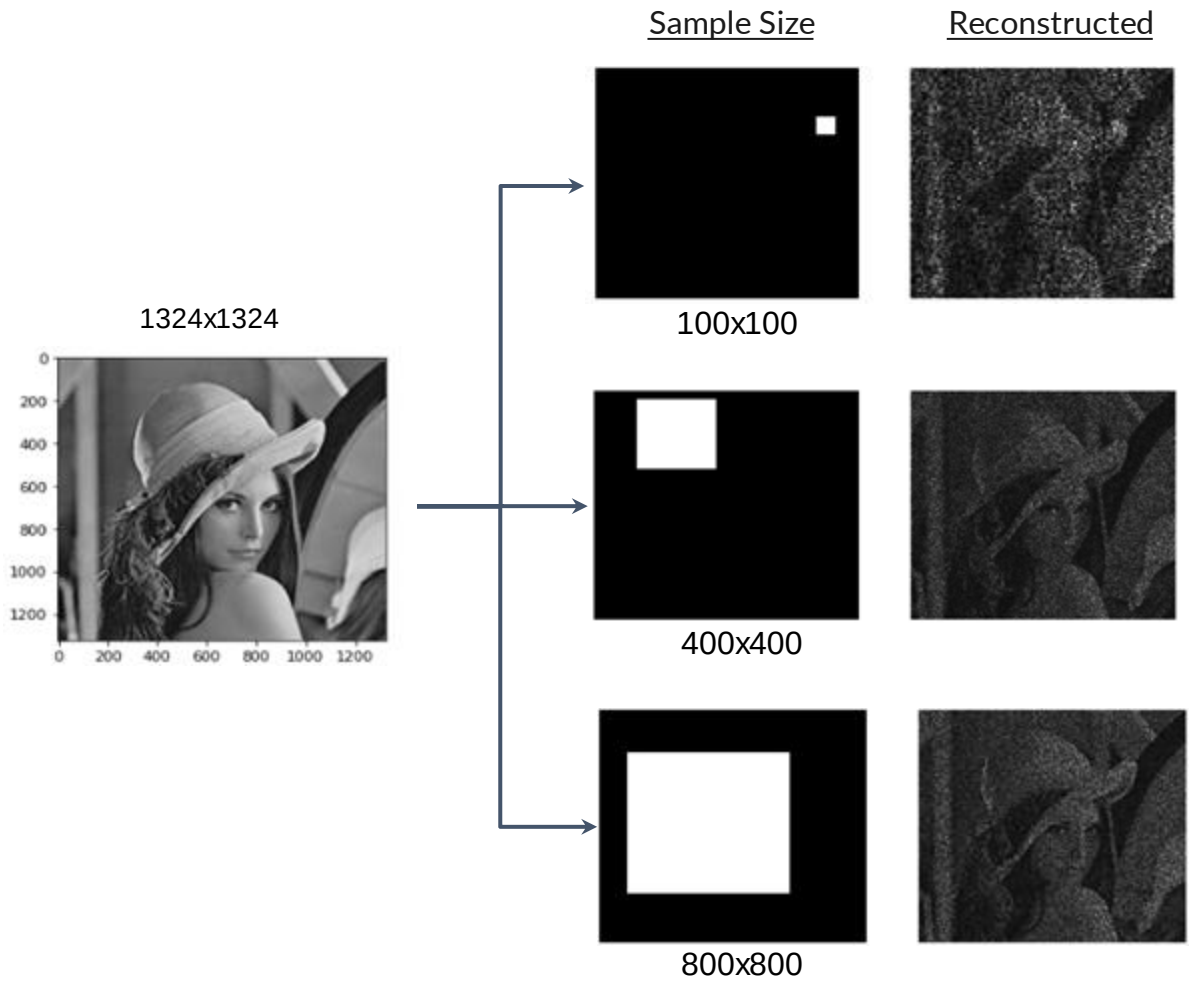
- The Gerchberg-Saxton algorithm is a cornerstone in holographic imaging, enabling the creation of **holographic representations of images in digital environments**.
- We leverage the Gerchberg-Saxton algorithm to utilize two crucial **characteristics of holographic images** to enhance medical data analysis.
  - *Holographic Divisibility*
  - *Information Distribution*





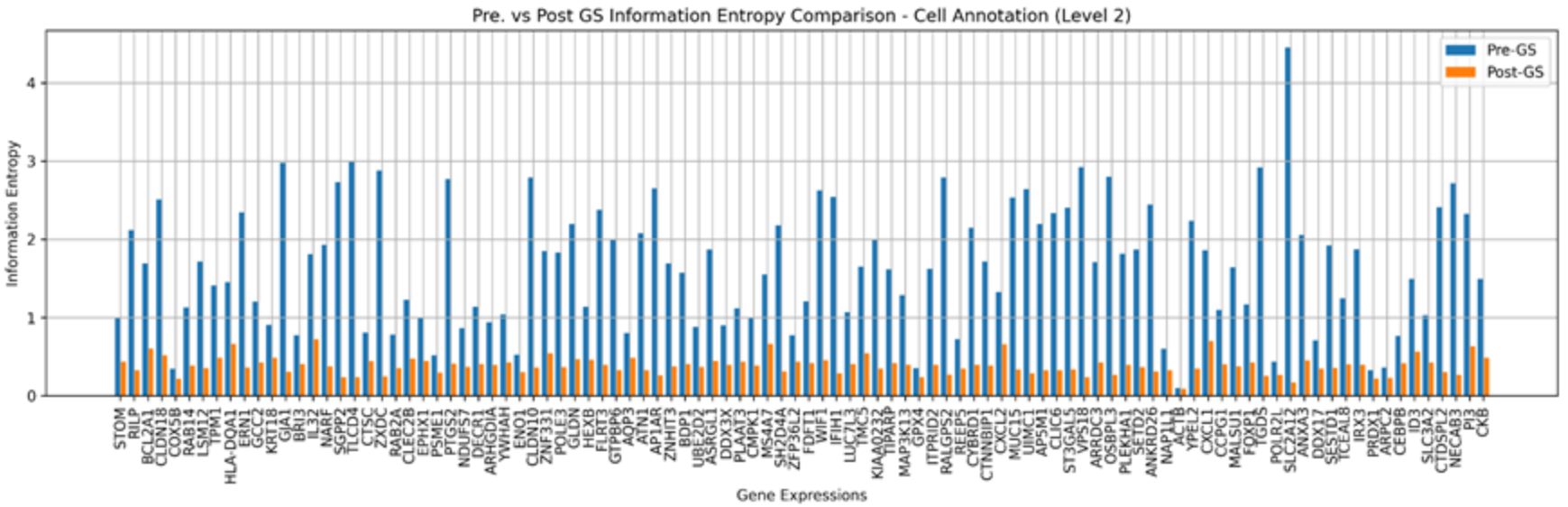
Holographic Divisibility

- Each data sample encapsulates information representative of the entire dataset, echoing the **holistic nature of holograms**.
  - Small Sample, Whole Dataset
- Equitable insights and analysis across diverse patient data.



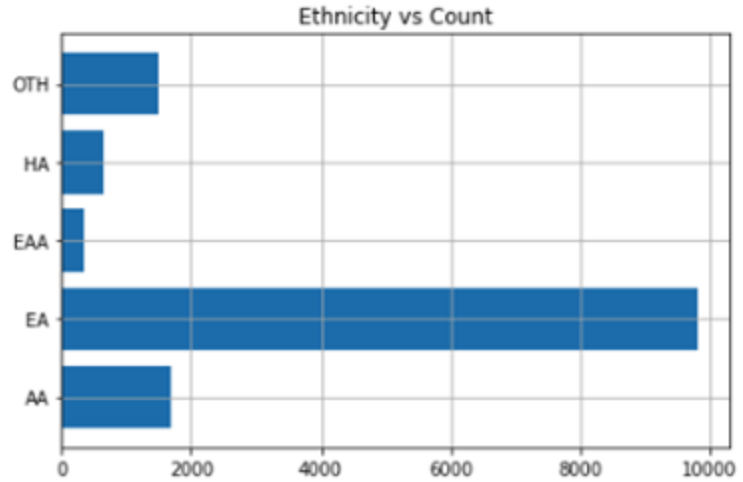
Uniform Information Distribution

- The Gerchberg-Saxton algorithm works in the frequency domain, **balancing intensity components** and preserving phase information during data transformation.
- Such transformation ensures a more **uniform distribution of information across datasets**.
- This uniformity is critical for obtaining **fairer results** from machine learning models and simplifying the **identification of feature model contributions**.



Previous Study - Mortality Prediction

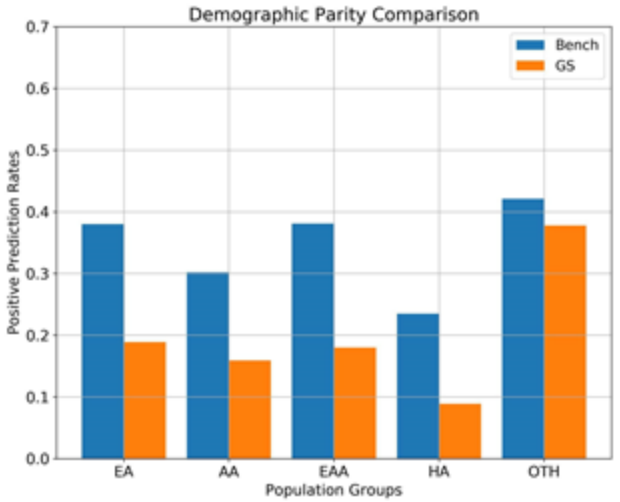
- Study Focus
  - Evaluation of mortality rates among ICU patients, with a particular emphasis on **detecting and correcting bias across diverse population groups**.
- Database Selection
  - The **MIMIC-III database** was chosen for its comprehensive data
  - **Unbalanced population distribution** across different racial groups.

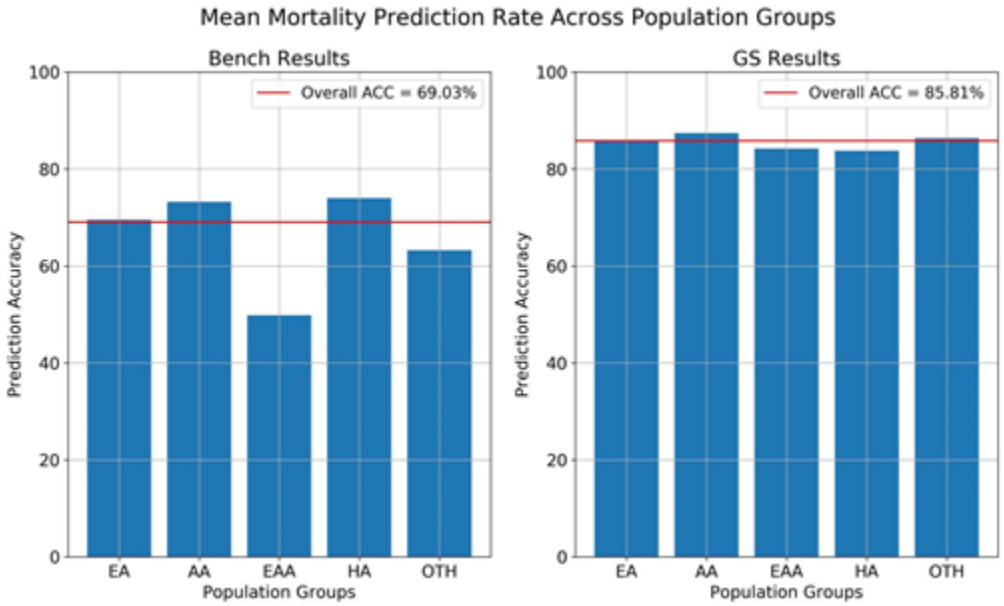


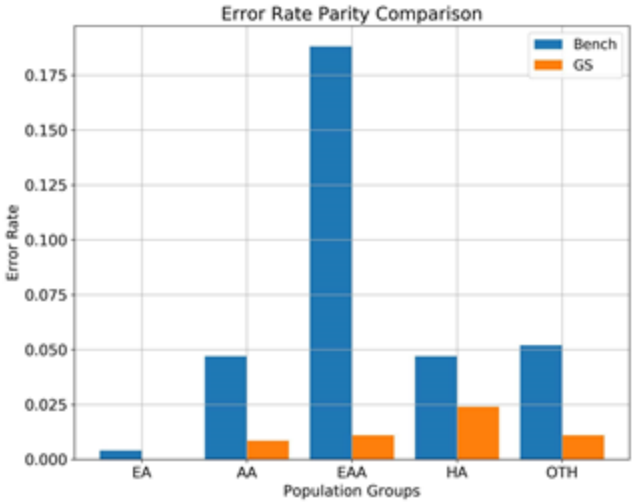
Ay, S., Cardei, M., Meyer, AM., Zhang, W., Topaloglu, U. "*Improving Equity in Deep Learning Medical Applications with the Gerchberg-Saxton Algorithm*". J Healthc Inform Res (2024). https://doi.org/10.1007/s41666-024-00163-8

Previous Study - Results

- Implementation of GS transformations on the dataset **significantly reduced the bias,** enhancing model predictions across different population groups.
- The improvements were quantitatively supported by **demographic parity** and **error rate parity**, demonstrating more uniform model prediction rates across demographics.





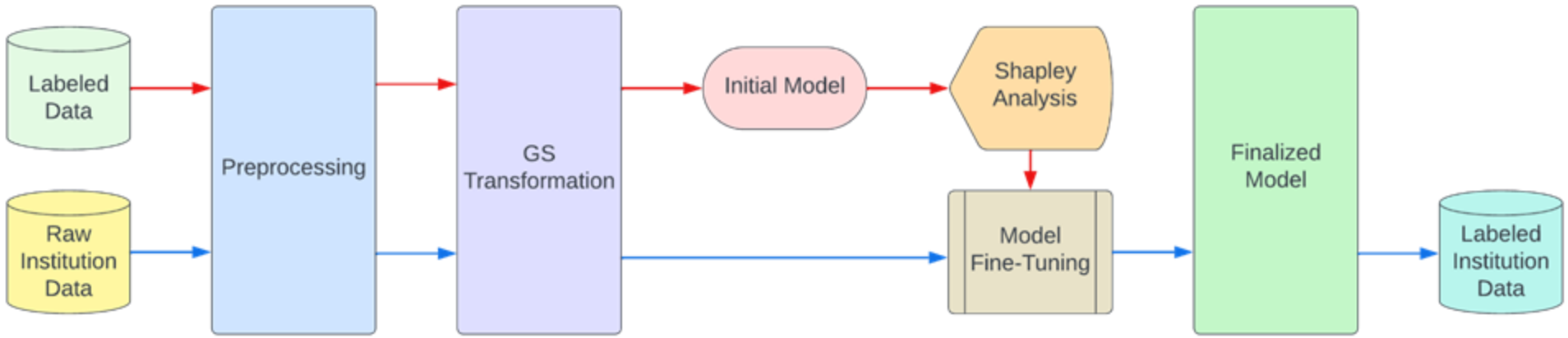


Project Objectives and Approach

- **Goal:** Enable fair data representations for single-cell cancer studies, improving healthcare decision-making.
- **Strategy:** Develop a pipeline to transform sc-RNA sequencing data into an AI-ready format, ensuring fair and uniform data representation through GS transformations.
    - Data Preprocessing and GS transformation
    - Model Development
    - Testing and Implementation

Pipeline

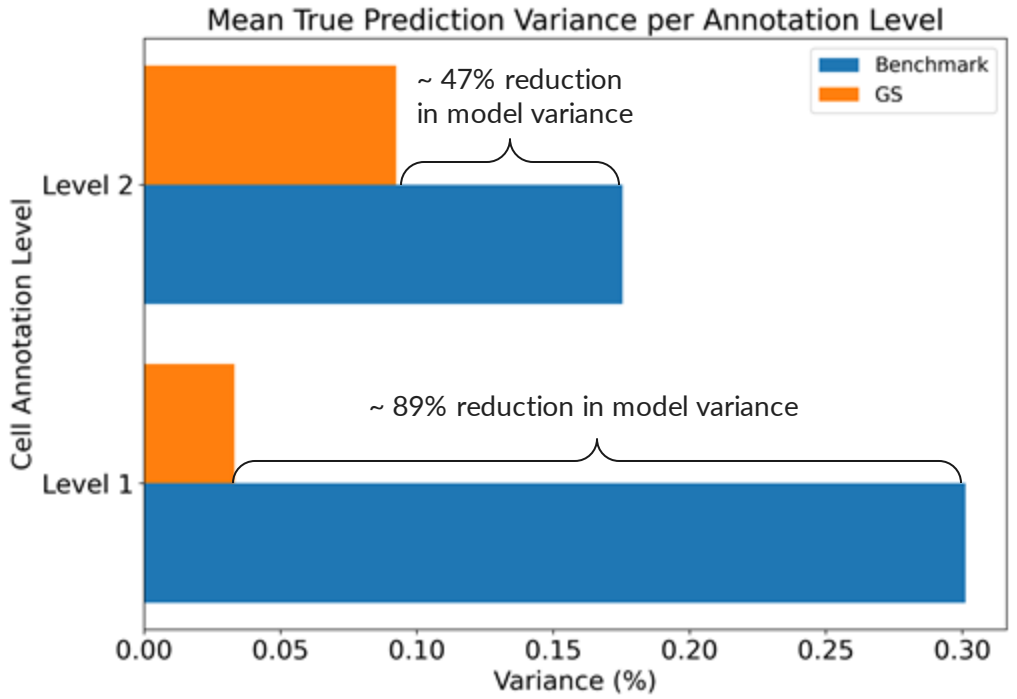
- Raw data **preprocessing** and **GS transformation** for fairness.
- Train models, then refine using **Shapley analysis** to identify and retain only **features that significantly contribute to model performance**.
- Validate model with **labeled public data subsets**.
- Apply to **institutional data** for enhanced decision-making in healthcare.



Initial Results - Model Prediction Uniformity

- Human Lung Cell Atlas, featuring **over 2 million single cell profiles from lung tissue**, with detailed cell annotations.
- Selected 20,000 cells **across diverse populations**, focusing on annotation levels 1 **(39 cell types)** and 2 **(61 cell types)**.

	Pre-GS Accuracy	Post-GS Accuracy
Level 1 (39 cell types)	90.62 %	89.48 %
Level 2 (61 cell types)	89.67 %	88.72 %



Future Directions and Expected Outcomes

- Pipeline Enhancement: Integrating a secondary model for tumor stage prediction to **distinguish between normal and cancer cells**, facilitating tumor microenvironment analysis.
- Comprehensive Analysis: Combination of models will **improve understanding** of *gene regulatory networks*, *cell-to-cell interactions*, and *therapeutic pathways*.
- Impact on Healthcare: Aims for enhanced, **equitable decision-making in healthcare** through better insights into cancer biology and treatment pathways.

Thank you

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