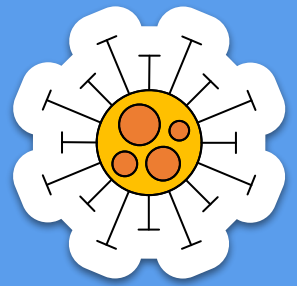
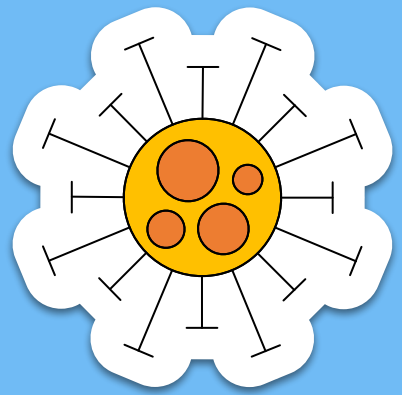
Predictive Modeling of Immune Responses to Pertussis Vaccination





Group 4:

Javier Garcia (Business Manager & Data Engineer)

Weikang Guan (Data Analyst & Visualization Developer)

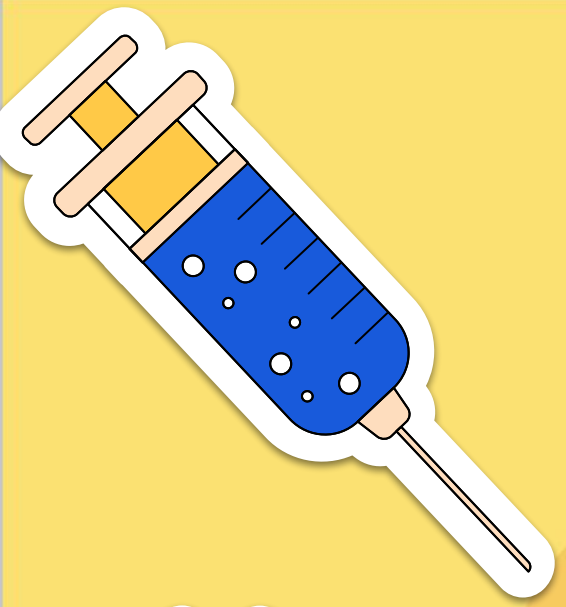
Brian Qian (Data & Dashboard Developer)

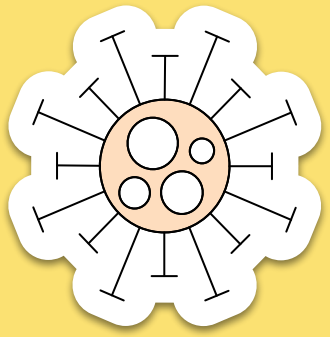
Peng Cheng (Solution Architect & Budget Controller)

Advisors:

Barry Grant (Professor)

Jason Hsiao (Biological Sciences PhD Student)



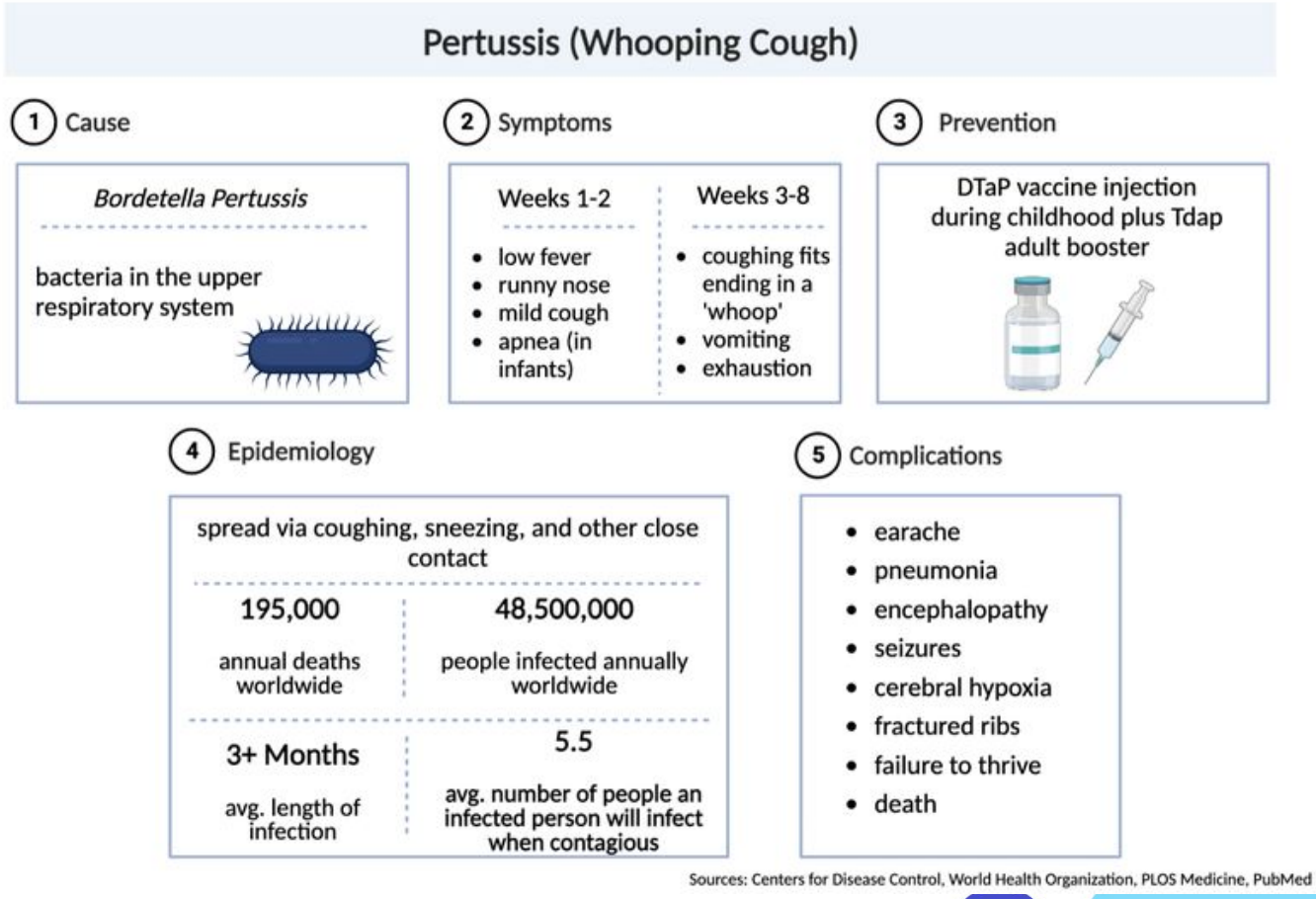


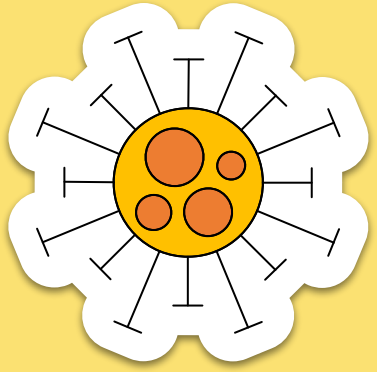
01

Project Background and Definition

1. Background and Definition

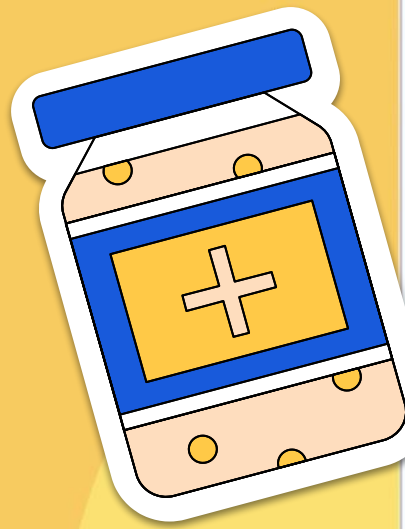
- Pertussis, or Whooping cough, is a highly contagious lung infection
- Two vaccines: whole-cellular (wP) and acellular (aP)
- Challenges of balancing vaccine safety and efficacy
- Importance of ongoing research and monitoring of vaccine effectiveness over time
- How does vaccine induced immunity change over time per person?





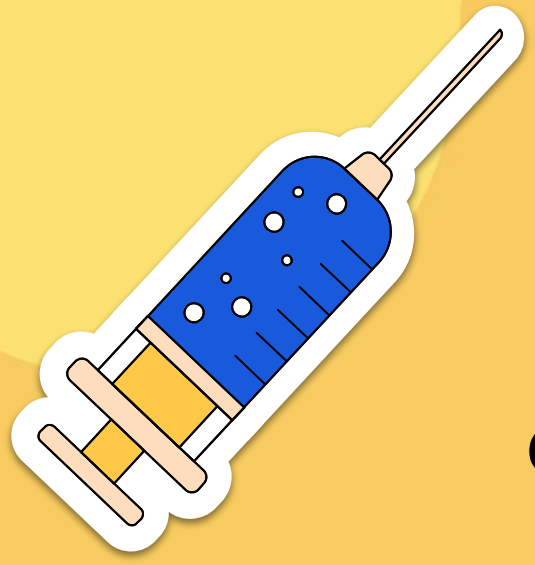
16 Million

Estimated Annual Pertussis Cases Worldwide



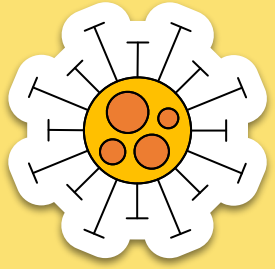
195,000

Annual Deaths Due to Pertussis



85%

Global Vaccination Coverage for DTP3 in 2021



1. Background and Definition

Goals

- Help save lives from preventable pertussis cases
- Share academic research with growing community
- Advance the understanding of immunology and use models in the real world to improve vaccine effectiveness

UC San Diego

JACOBS SCHOOL OF ENGINEERING

MAS Data Science and Engineering

CMI-PB

COMPUTATIONAL MODELS OF IMMUNITY

PERTUSSIS BOOST

02

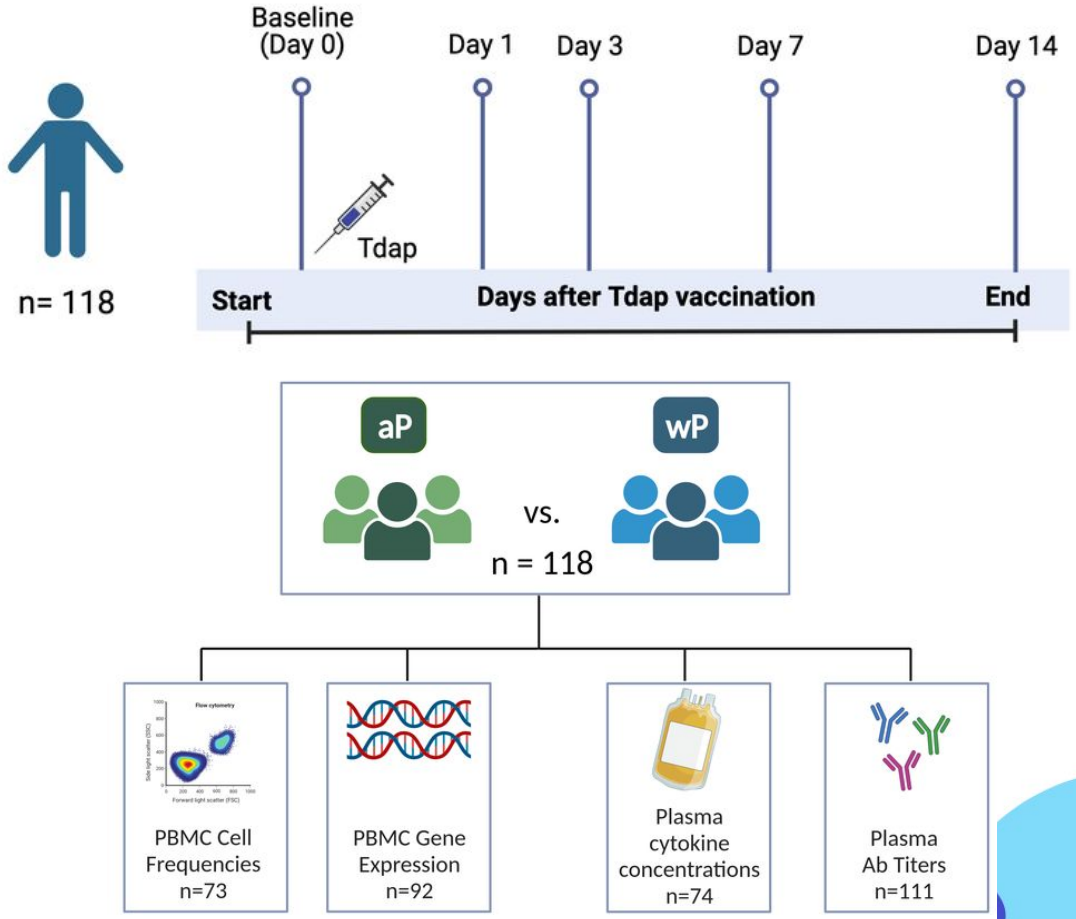
Datasets Overview

2. Overview of Data Sets

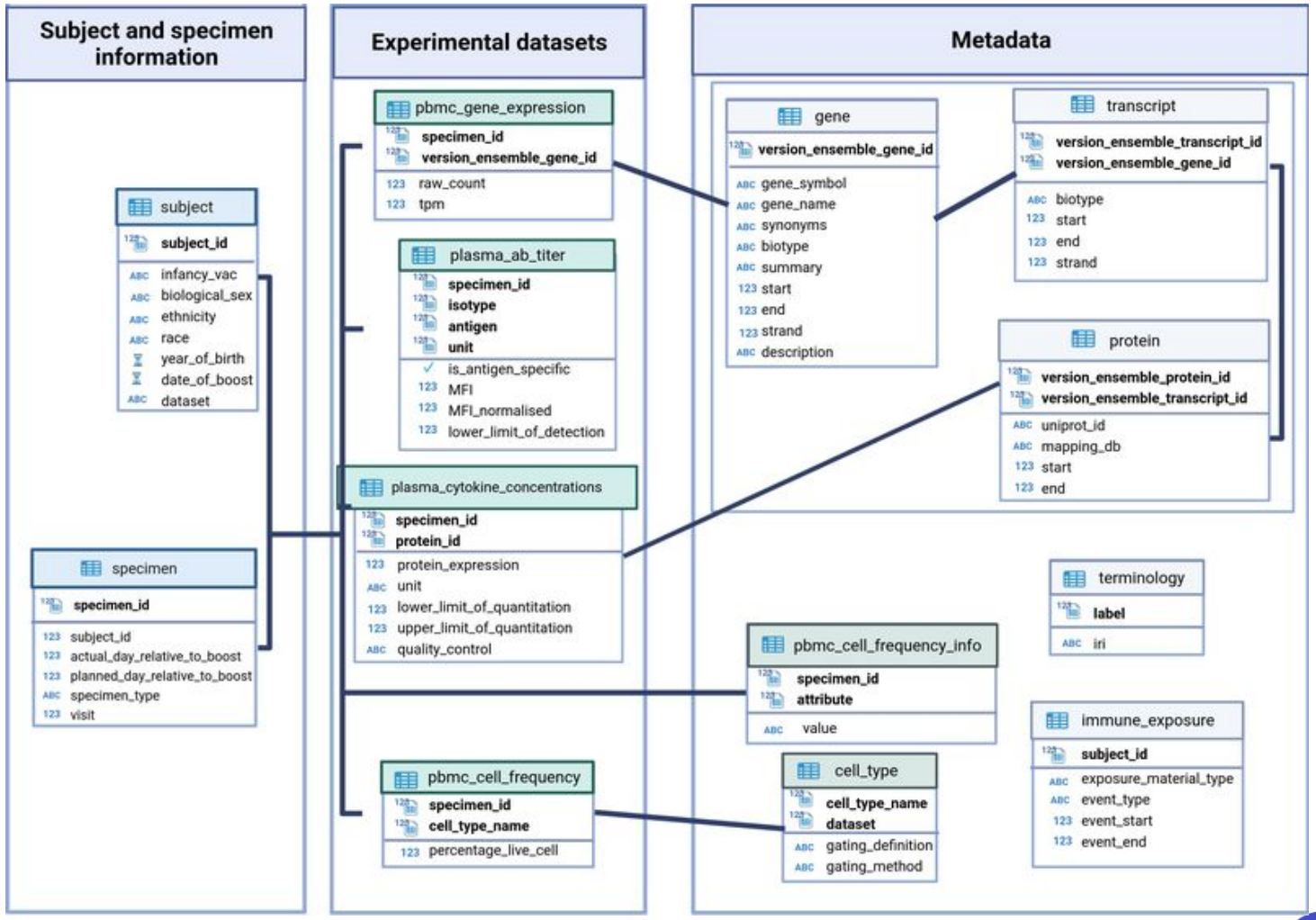
Objective: Analyze immune responses post-Tdap booster vaccination.

Subjects: 118 individuals contributing 500+ blood specimens.

Timeframe: Pre- and post-vaccination (days 1, 3, 7, and 14).

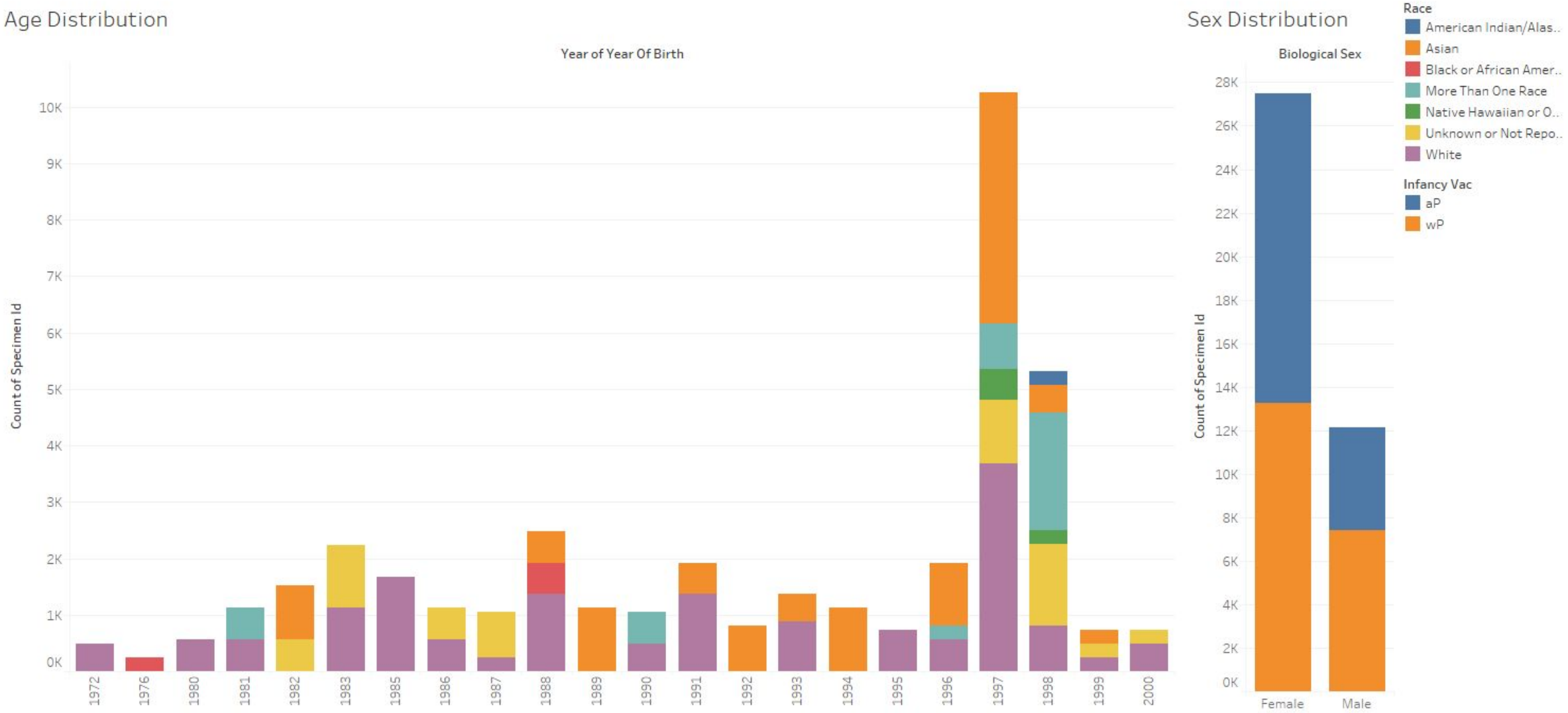


2. Overview of Data Sets



Source: CMI-PB

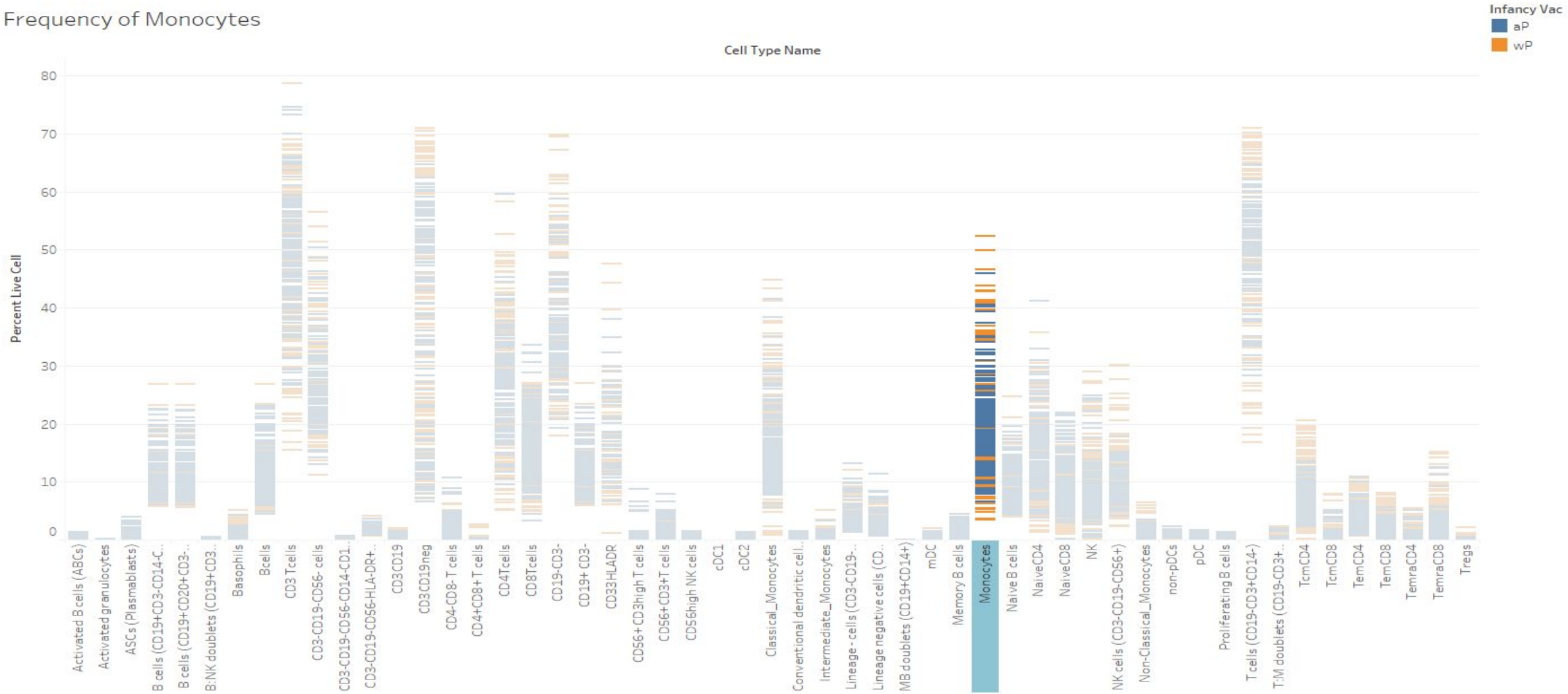
2. Overview of Data Sets



2. Overview of Data Sets

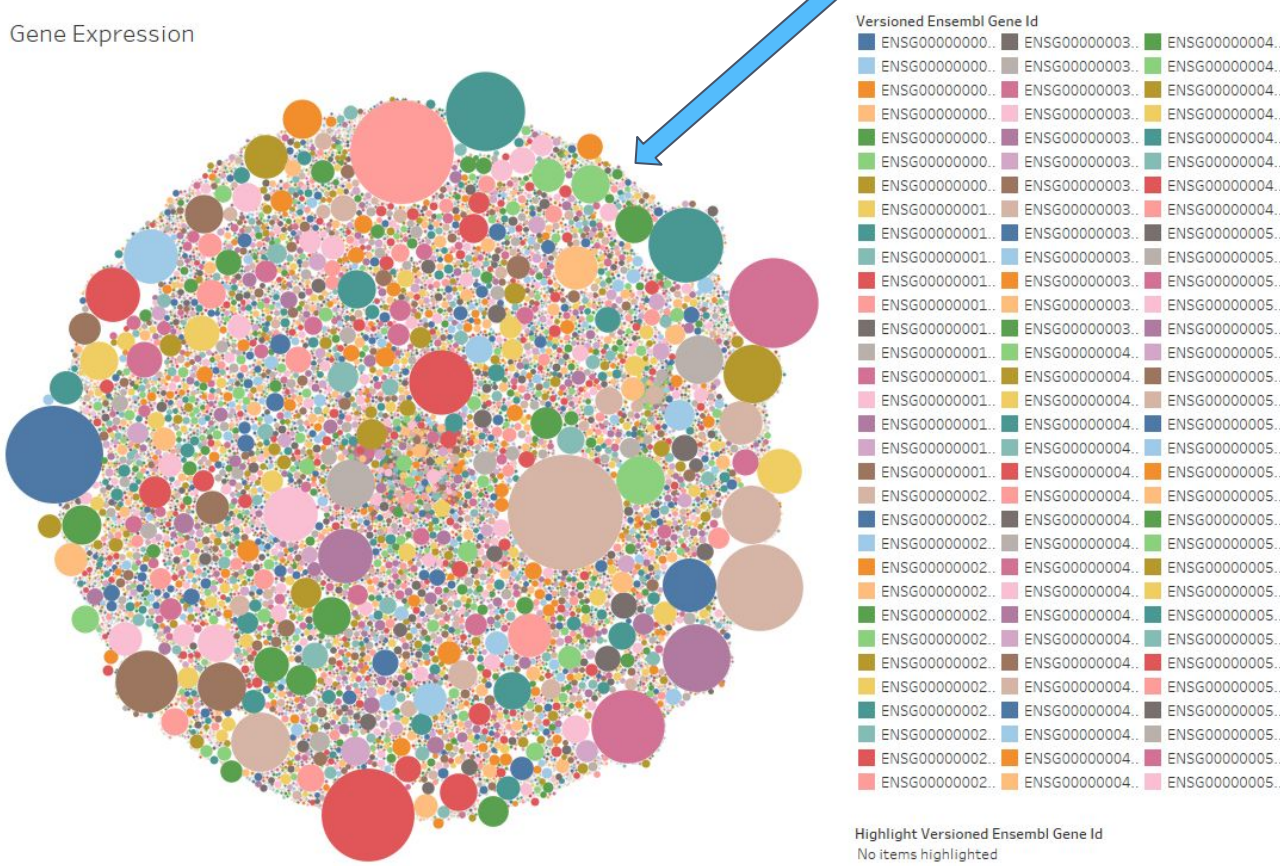
Immunoglobulin

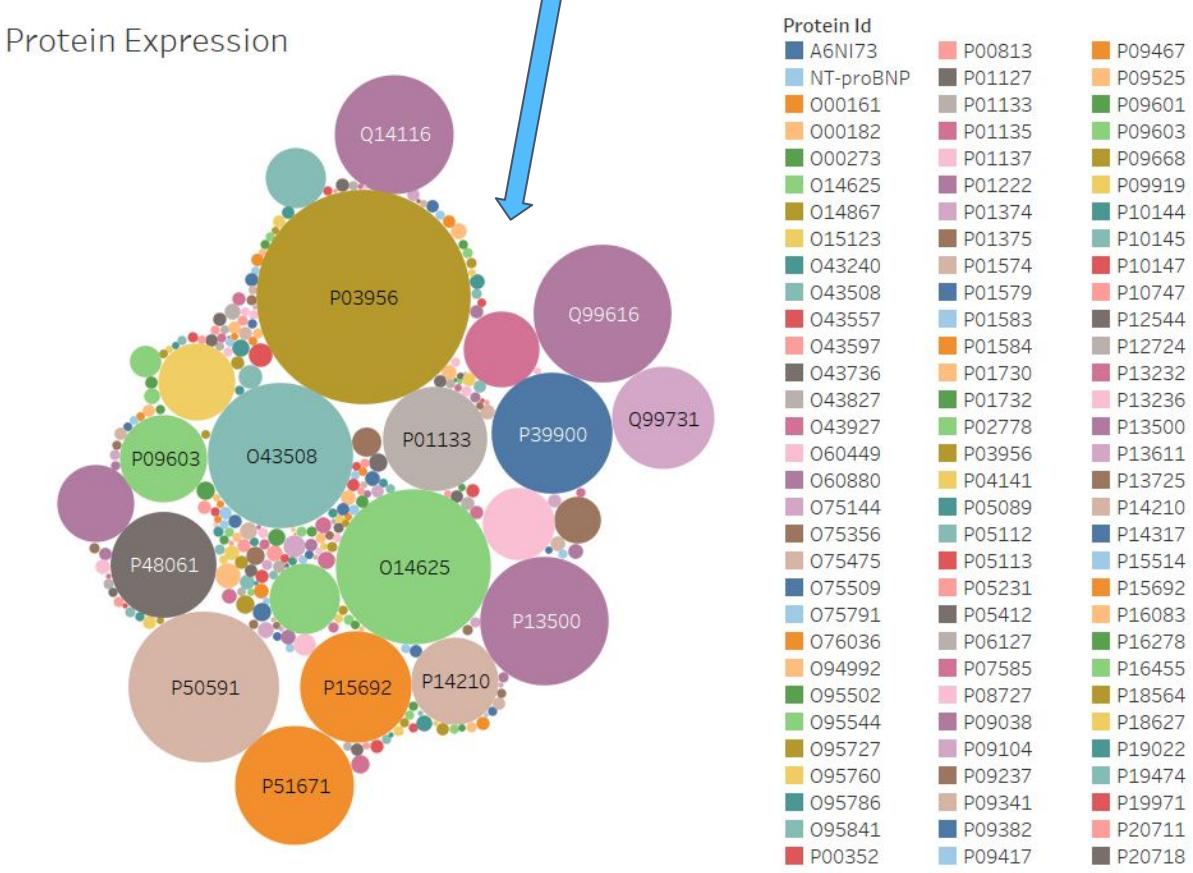
2. Overview of Data Sets

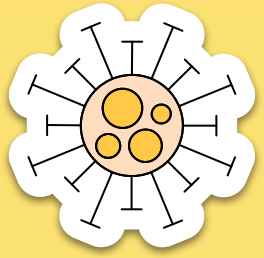
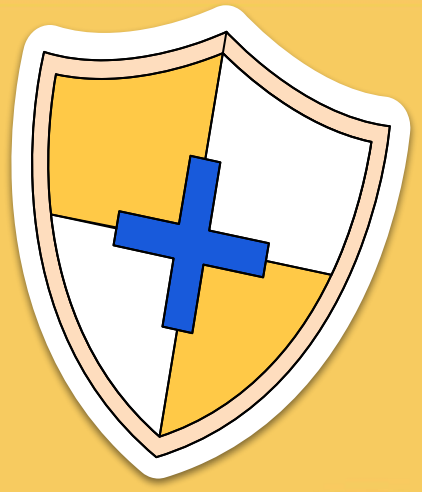


2. Overview of Data Sets

DNA → mRNA(Gene Expression) → Protein Expression → CCL3

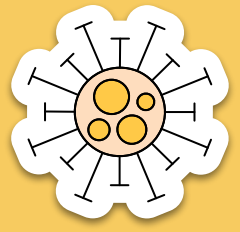
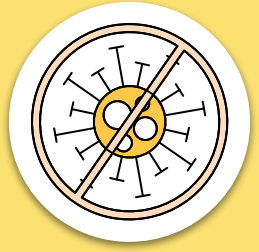




03

Project Objectives

3. Project Objectives

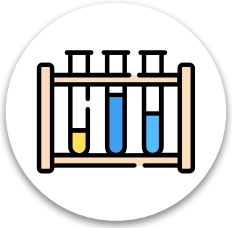
- **Building Computational Models:** To predict vaccination outcomes for newly tested individuals.

- **Participation in the Prediction Challenge:** Showcase intuition and analytical skills by engaging in the community prediction challenge

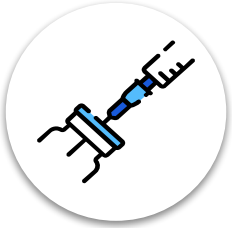
	Annual prediction challenge title	Contestants	Number of subjects		Current status
			Training dataset	Test dataset	
1	**First Challenge:** Internal dry run	CMI-PB consortium	60 (28 aP + 32 wP)	36 (19 aP + 17 wP)	Concluded in May 2022
2	**Second Challenge:** Invited challenge	Invited contestants	96 (47 aP + 49 wP)	22 (13 aP + 9 wP)	Will be announced in September 2023
3	**Third Challenge:** Open Challenge 1	Public	118 (60 aP + 58 wP)	32 (16 aP + 16 wP)	Will be announced in April 2024
4	**Fourth Challenge:** Open Challenge 2	Public	150 (76 aP + 74 wP)	32 (16 aP + 16 wP)*	Will be announced in December 2024

*Goal

3. Project Objectives



- Accurate prediction of immune responses



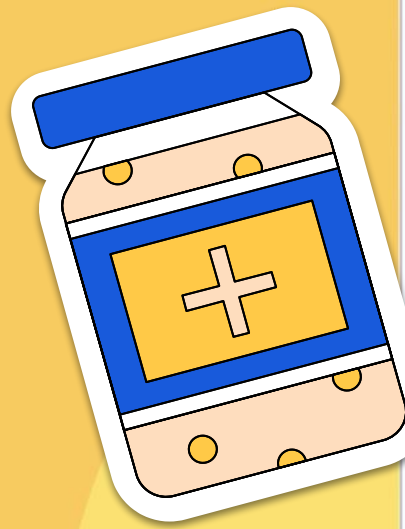
- Identifying what variables induce a strong response

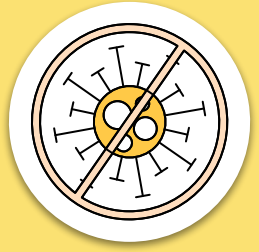
- Real-time access to dynamic immune response data

- Efficient handling of diverse features

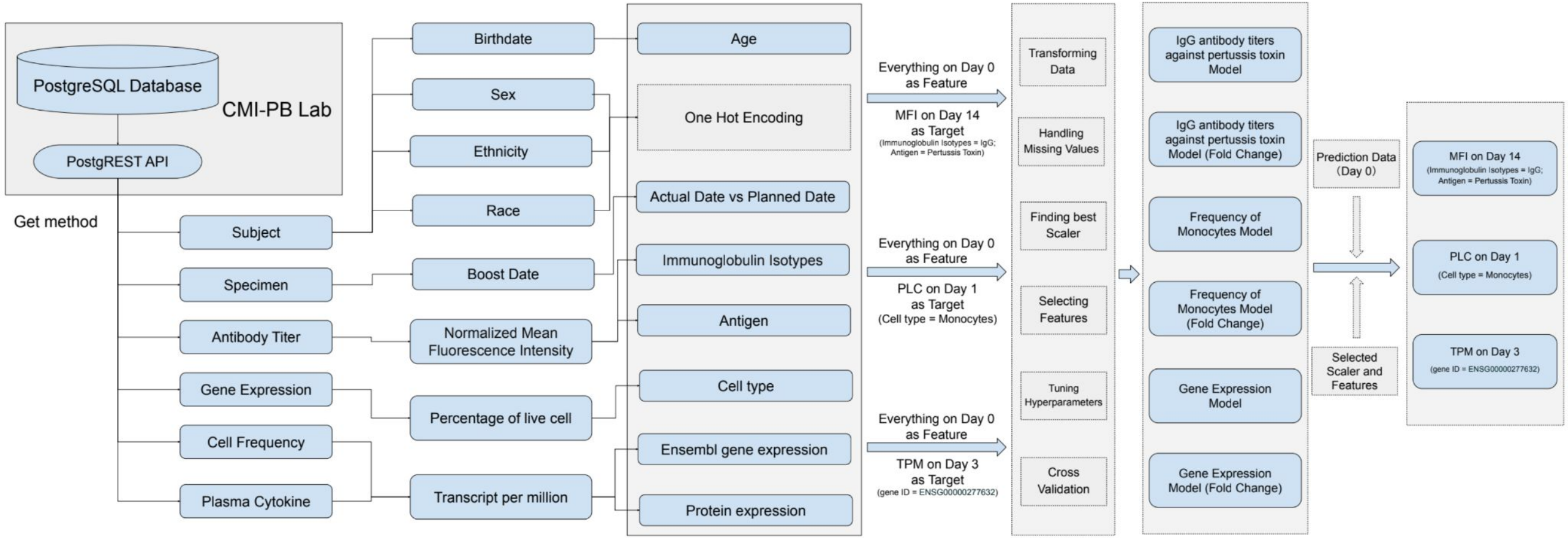
04

Methods and Techniques



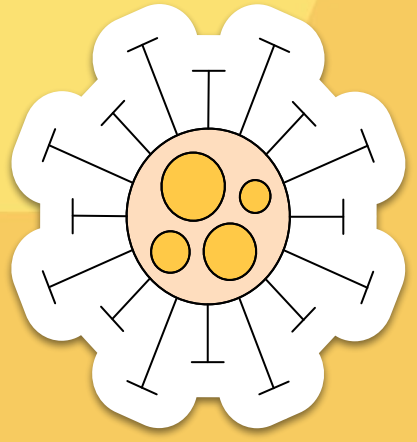


4. Methods and Techniques

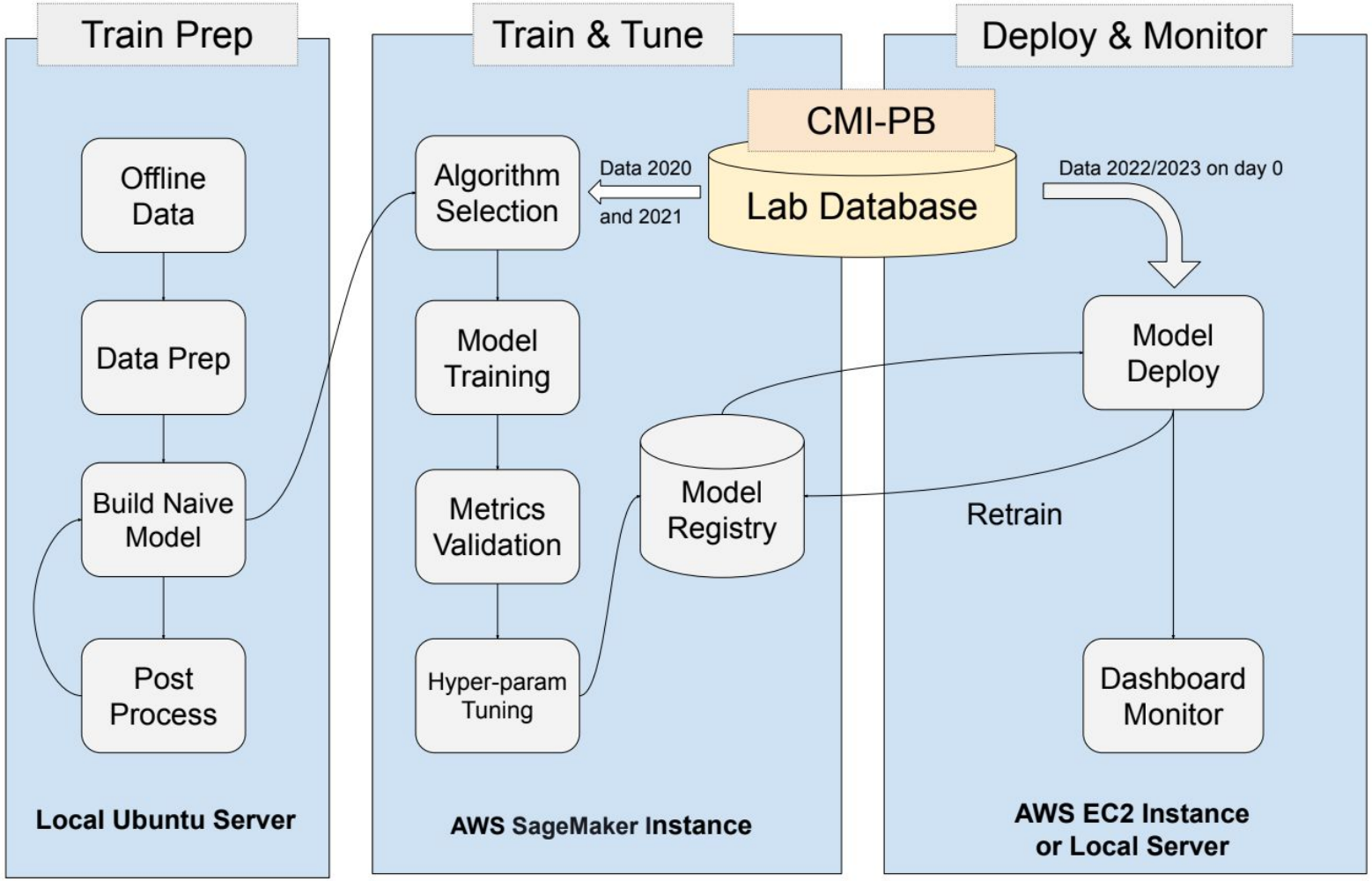


05

Solution Architecture



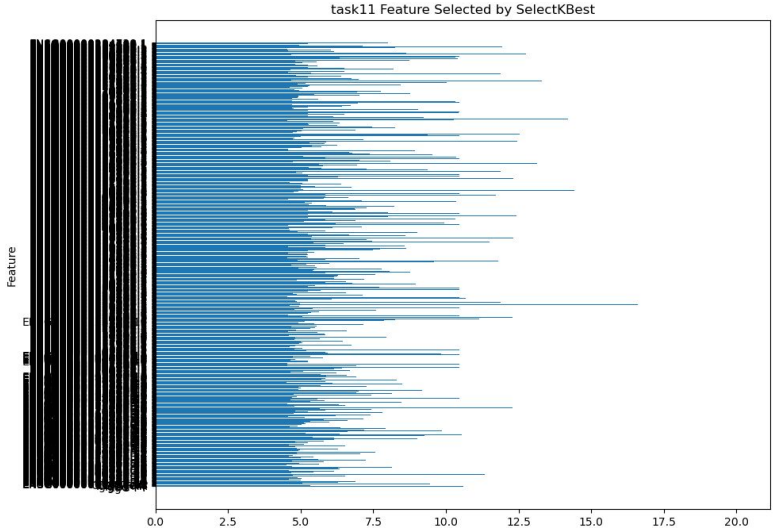
5. Solution Architecture

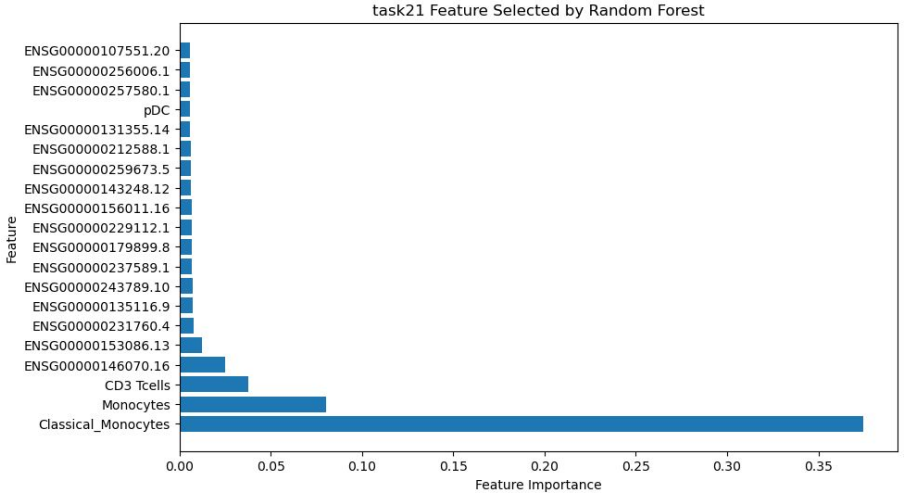


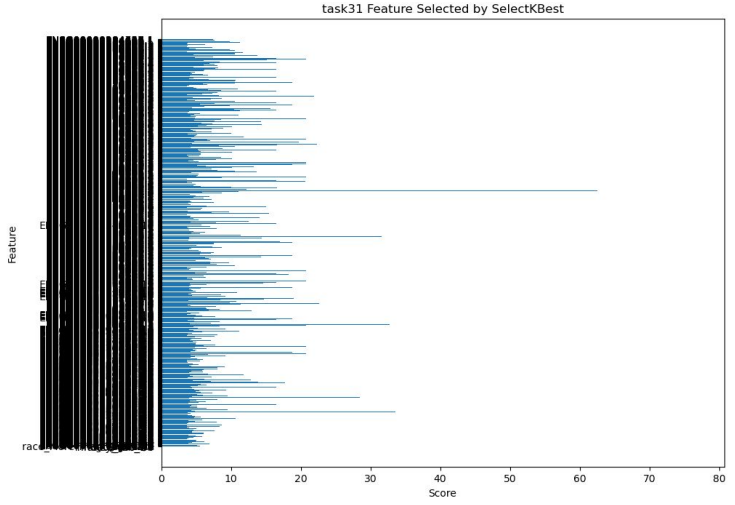
06

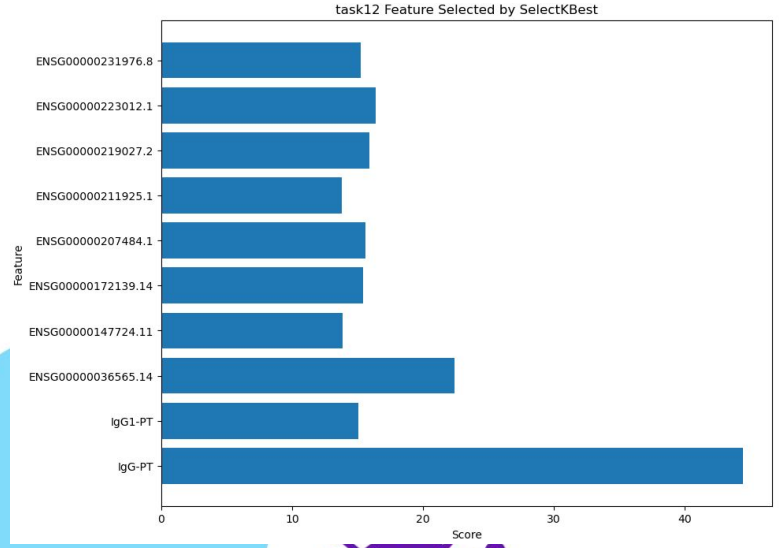
Analysis of Results

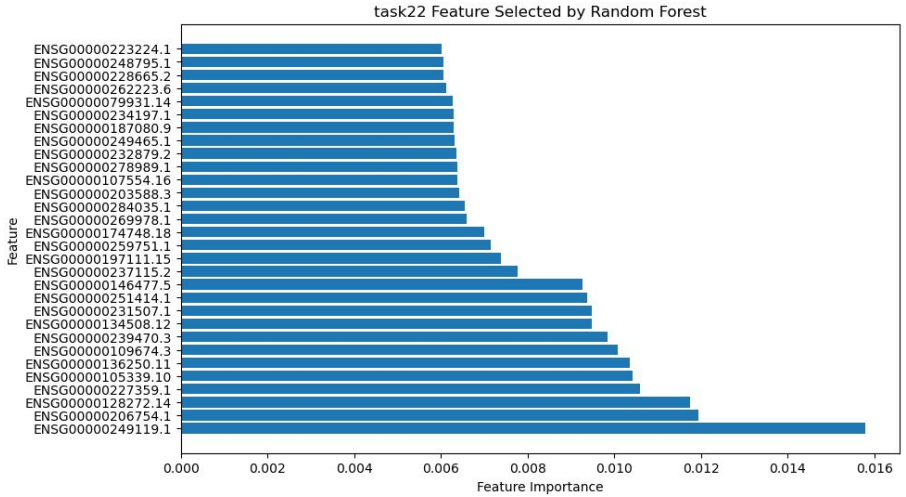
6. Analysis of Results

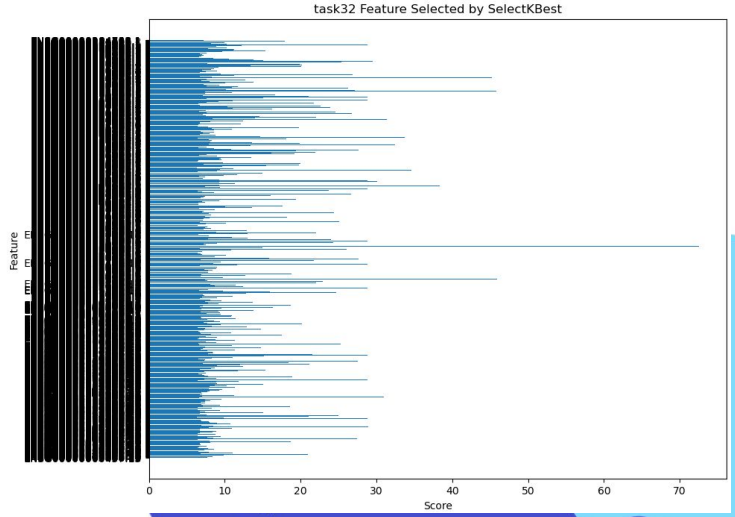




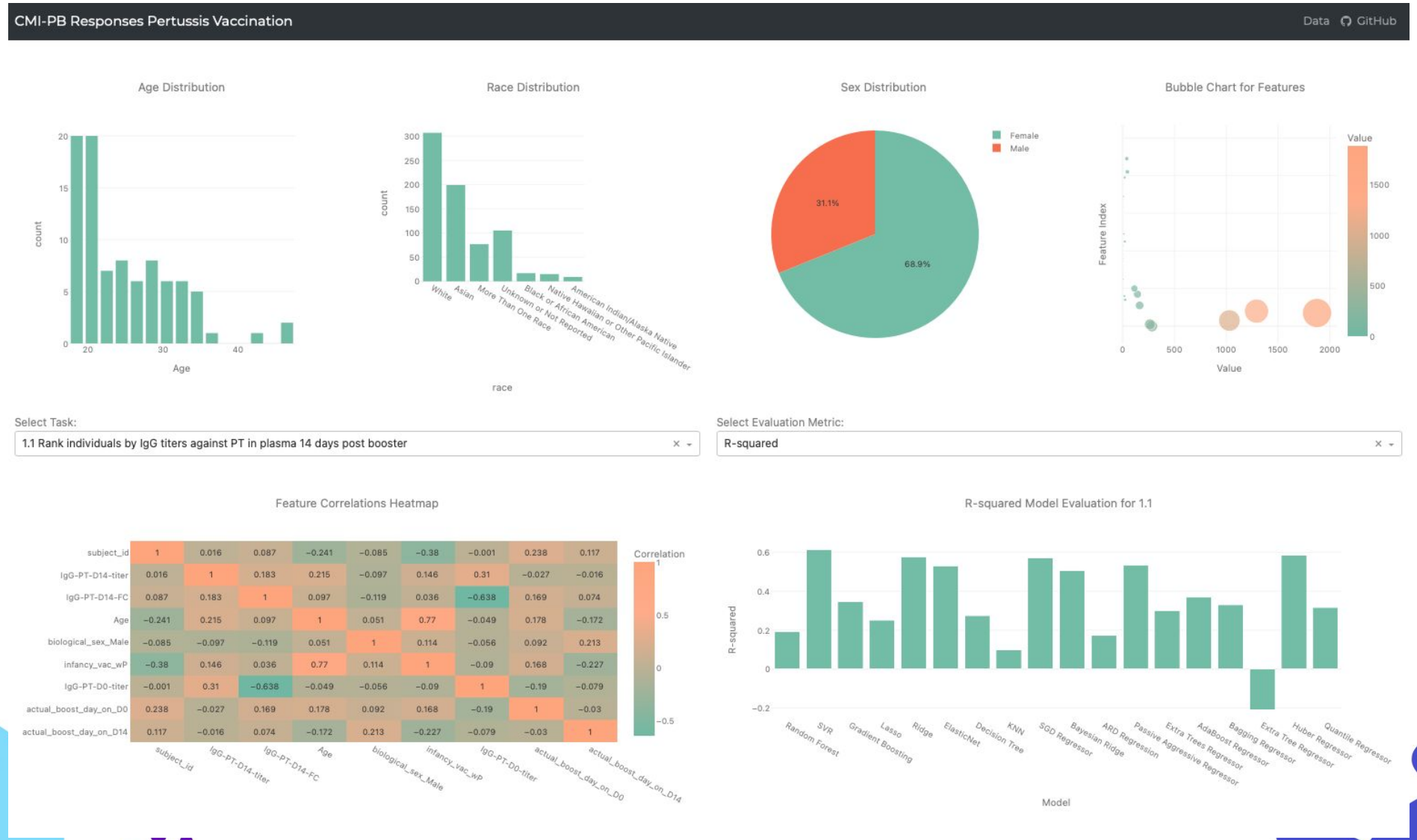




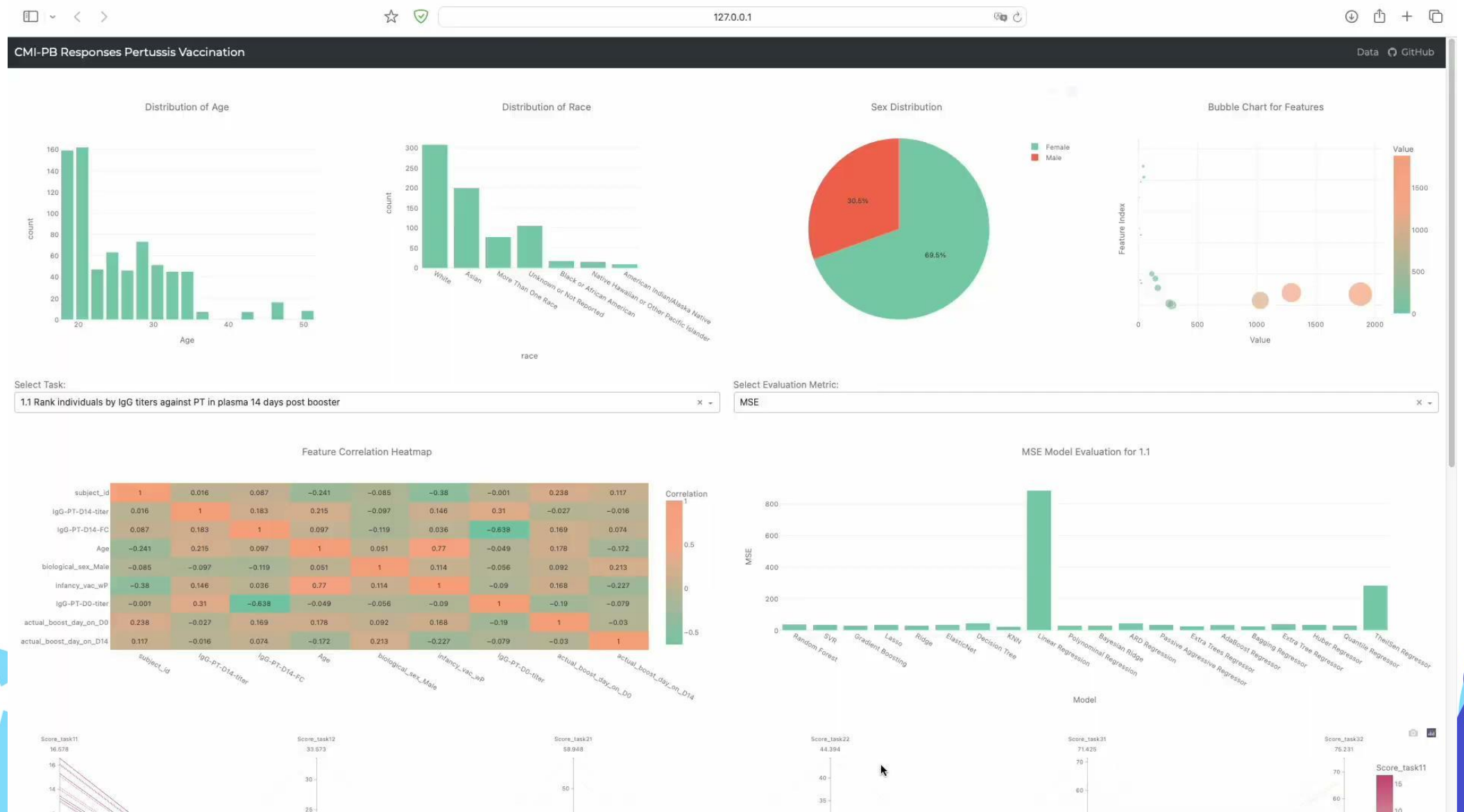




6. Dashboard

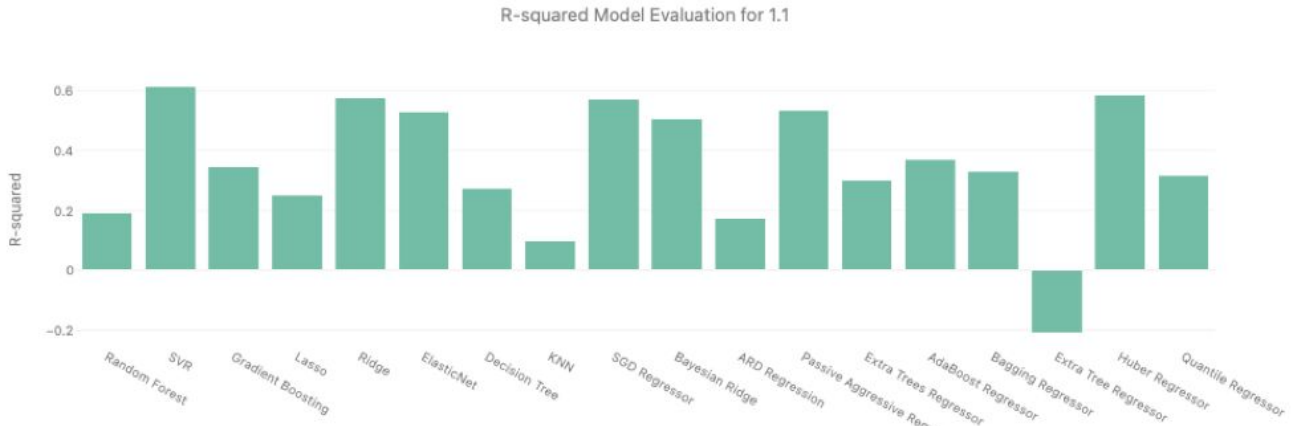

CMI-PB Responses Pertussis Vaccination
Data
GitHub
Age Distribution
count
Age
Race Distribution
count
race
White
Asian
More Than One Race
Unknown or Not Reported
Black or African American
Native Hawaiian or Other Pacific Islander
American Indian/Alaska Native
Sex Distribution
Female
Male
31.1%
68.9%
Bubble Chart for Features
Feature Index
Value
Select Task:
1.1 Rank individuals by IgG titers against PT in plasma 14 days post booster
Select Evaluation Metric:
R-squared
Feature Correlations Heatmap
subject_id
IgG-PT-D14-titer
IgG-PT-D14-FC
Age
biological_sex_Male
infancy_vac_wP
IgG-PT-D0-titer
actual_boost_day_on_D0
actual_boost_day_on_D14
Correlation
R-squared Model Evaluation for 1.1
R-squared
Model
Random Forest
SVR
Gradient Boosting
Lasso
Ridge
ElasticNet
Decision Tree
KNN
SGD Regressor
Bayesian Ridge
ARD Regression
Passive Aggressive Regressor
Extra Trees Regressor
AdaBoost Regressor
Bagging Regressor
Extra Tree Regressor
Huber Regressor
Quantile Regressor

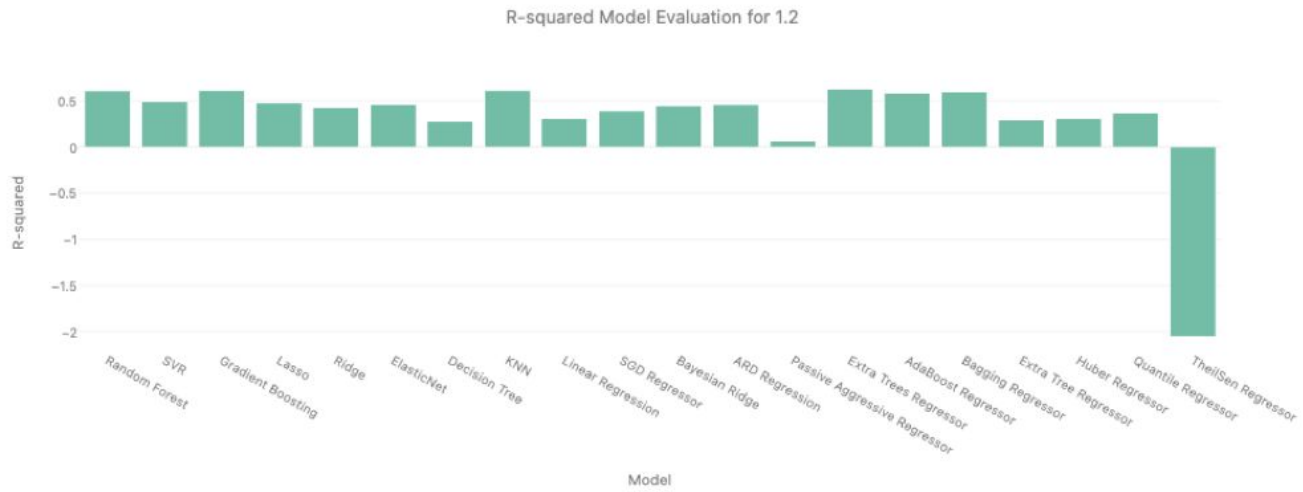
6. Dashboard - Demo



6. Analysis of Results

– Predict IgG antibody titers against pertussis toxin on day 14



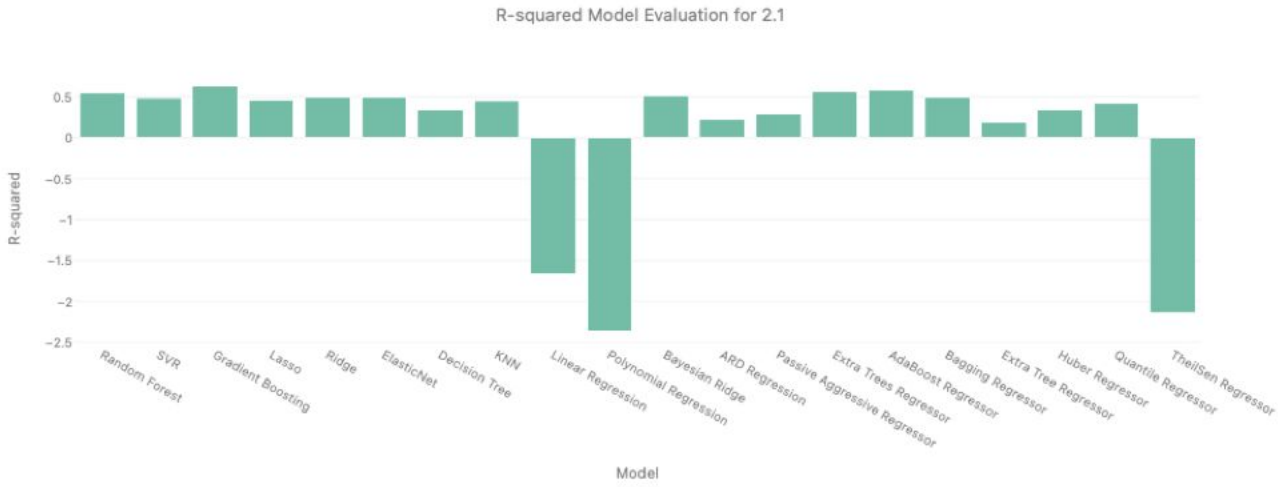


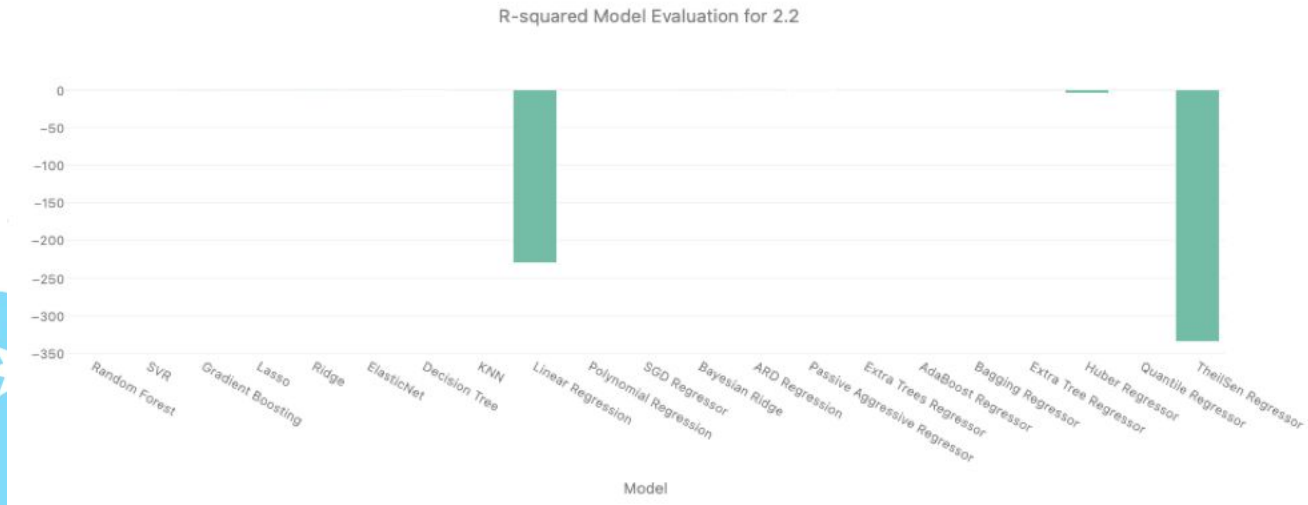
Take Log2 Fold Change
the Target

$$\log_2\left(\frac{MFI\ on\ day\ 14}{MFI\ on\ day\ 0} - 1\right)$$

6. Analysis of Results

– Predict frequency of Monocytes on day 1





Take Log2 Fold Change
the Target

$$\log_2\left(\frac{PLC\ on\ day\ 1}{PLC\ on\ day\ 0} - 1\right)$$

6. Analysis of Results

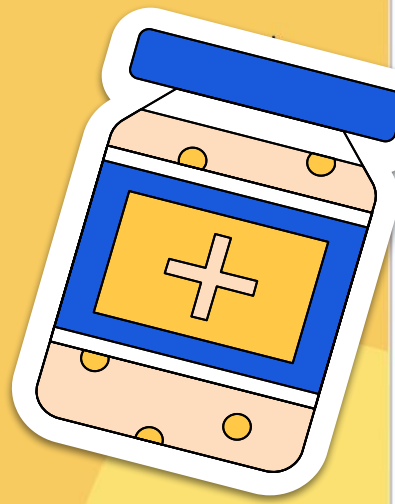
– Predict gene expression of CCL3 on day 3

Take Log2 Fold Change
the Target

$$\log_2\left(\frac{TPM\ on\ day\ 3}{TPM\ on\ day\ 0} - 1\right)$$

07

Insights



7. Insights

- *Support Vector Regression (SVR)*: The model performed well in predicting antibody titer levels. SVR is effective in high-dimensional spaces and can handle nonlinear relationships, making it suitable for handling our complex biological data.
- *Extra Tree Regressor and Gradient Boosting*: These ensemble methods outperformed other methods in predicting the Log2 fold change of antibody levels at day 14 relative to day 0. They were able to reduce overfitting through bagging and boosting techniques, making them a good fit for our dataset.

7. Insights

- *Gradient Boosting for Monocyte Frequency*: Gradient Boosting showed the best performance in predicting monocyte frequency at day 1. The approach of this model helps minimize the prediction error, making it applicable to a variety of tasks.
- *ElasticNet for Gene Expression Levels*: Initially, ElasticNet performed best in predicting CCL3 gene expression levels at day 3. However, simpler models such as Stochastic Gradient Descent(SGD) Regressor and TheilSen Regressor outperformed ElasticNet when predicting the Log2 fold change of the target variable. This shift highlights the importance of model simplicity and regularization in dealing with large amounts of gene expression data.

08

Next Steps Plan

8. Next Steps Plan

Model performance metrics:

- *Regular re-evaluation*: Continuously monitor performance metrics (MSE, MAE, R^2) to ensure the model remains accurate as new data becomes available.
- *Model retraining*: Regularly retrain the model with updated datasets to maintain prediction accuracy and adapt to any changes in data patterns.

Operational metrics:

- *Data quality:* This involves regular data cleansing and validation processes. High-quality data is critical to maintaining the integrity of the model and ensuring reliable predictions.
- *System availability*: Monitor user feedback on dashboard usability for iterative improvements. Usability metrics include user satisfaction scores, system response time, and frequency of use, which can provide insight into the effectiveness of the dashboard and areas for improvement.


Thank you!